

Evaluating Panicle Architecture and Yield Characteristics in Medium Duration Rice Genotypes Through Correlation and Principal Component Analysis

Abstract

Panicle architecture is a crucial factor that significantly improves economic grain yield. The panicle exhibits considerable variation in its structure, including the number of branches, the length and weight of the panicle, and arrangement of the grains. These traits are not only vital for the plant reproductive efficiency but also for optimizing yield potential. This study focuses on assessing variation in panicle architecture among 31 different medium duration rice genotypes by employing principal component analysis and correlation analysis. This study aimed to dissect the complex relationship between different panicle characteristics. The findings revealed that the first three principal components together explained 60.3% of the total variability. In the first principal component (PC1), the traits SF, PBL, YPH, and HI had the highest positive eigenvalues, indicating their significant impact on overall genotype variations. The second principal component (PC2) was mainly influenced by TSP and SBN, while the third principal component (PC3) was driven by PW and SBL. These results suggest that grain yield is significantly affected by the traits SF, PBL, YPH, HI, TSP, SBN, PW, and SBL. The correlation analysis revealed that, the number of secondary branches showed a positive association with unfilled spikelet. Spikelet fertility exhibited a strong positive correlation with yield hectare⁻¹ and harvest index, highlighting its significance in overall yield improvement. Therefore, these components are crucial for differentiating rice genotypes with higher grain yield potential. By evaluating correlation and principal component analysis, we aimed to identify traits that can be targeted for crop improvement initiatives. The findings will contribute to the development of rice varieties that are better suited to specific growing conditions and have enhanced yield potential. This approach will enable the identification of key panicle architecture and yield and yield traits that optimize resource allocation and improve grain filling efficiency, ultimately leading to rice varieties with higher productivity and adaptability.

Keywords: Rice, medium-duration genotype, panicle architecture, spikelet fertility, grain filling, grain yield

Introduction

Rice (*Oryza sativa* L.) is a crucial cereal crop globally, providing sustenance to more than half of the world's population. The genus *Oryza*, comprising about 25 species, experienced two distinct domestication events in Asia and Africa, with *Oryza rufipogon* cultivated in Asia around 9000 years ago and *Oryza glaberrima* in Africa about 3000 years ago (Spengler *et al.*, 2021). Rice cultivation has risen in global rice production is predicted to increase by 58 to 567 million tonnes by 2030 (Mohidem *et al.*, 2022). The changing climate poses a threat to rice production due to the sensitivity of modern cultivars to external fluctuations beyond their physiological range (Rezvi *et al.*, 2022), while production has only improved by 0.5% in recent times, rice consumption has increased by 1% annually. Further growth of rice lands is unlikely if prices are set at levels that billions of customers may afford. The rate of yield increase must be greater than it has been recently. In the short to medium term, demand is expected to exceed the supply of rice unless existing trends of slow

productivity development and unsustainable resource management are reversed. Increasing rice yields requires improving the crop (Rashmi *et al.*, 2017).

Medium duration rice genotypes play a crucial role in rice cultivation, offering a balance between growth period and yield potential. Studies have shown that selecting for specific traits like plant height, 1000 seed weight, and panicle length can significantly improve grain yield per hectare in medium duration rice varieties (Gayathri *et al.*, 2023). Additionally, stability analysis of elite medium duration rice genotypes has highlighted the importance of genetic variability, heritability, and genetic advance for traits like plant height, total number of grains panicle⁻¹, and grain yield plant⁻¹, indicating the potential for further improvement through selection and breeding (Shiva kumar, 2014).

The cultivars have different physiological and morphological characteristics, and proper crop management depends on the growth characteristics of various cultivars to achieve maximum benefit (Hussain *et al.*, 2014). High-yielding rice varieties with extra-large sink capacity often have unstable grain filling. Therefore, understanding the factors that limit grain filling is essential for further improvement of rice grain yield (Okamura *et al.*, 2018)

Due to the continuous cultivation of a single variety, it has become generally susceptible to pests and diseases, resulting in low yields and low net returns for farmers (Kumar *et al.*, 2020). In rice, grain size and the number of grains are the major determinants of yield potential. Since grain size is genetically constant, in terms of yield improvement, increasing the number of grains has received more attention (Makino *et al.*, 2020).

Grain number plays a crucial role in determining crop yield and food security by directly impacting the overall productivity of staple crops like wheat and rice. Studies have shown that grain number is a major determinant of yield. New rice (*Oryza sativa* L.) genotypes characterized by a high number of spikelets occasionally do not achieve their full yield potential due to a lower grain-filling rate. (Kobata *et al.*, 2013) A complex genetic control involving various quantitative trait loci (QTLs) and causal genes (Mizuno *et al.*, 2021). While there is often a trade-off between grain size and number, targeted genetic modifications, such as overexpressing specific proteins like expansins, can lead to an increase in grain size without compromising grain number boosting yield potential (Daniel *et al.*, 2021). The association between panicle architecture and yield attributes in medium-duration rice genotypes is crucial for enhancing crop productivity. The branch number, branch length, and grain arrangement of rice panicles exhibit remarkable variability; however, not much is known about the process that produces this diversity in patterns (Agata *et al.*, 2023). The present study was conducted to identify the correlation and multivariate analysis, principal component analysis between panicle architecture and yield attributes which will improve the efficiency of genetic selection in plant breeding programs. Understanding and manipulating these factors are essential for achieving higher yields and ensuring food security for a growing global population.

2. Material and method

2.1 Experimental location and design

The trial was conducted during two consecutive *Kharif* season 2021 and 2022 at Indira Gandhi Krishi Vishwavidyalaya, Raipur. The farm is situated between 22°33'N to 21°14'N Latitude and 82° 6' to 81° 38'E Longitude with an altitude of 289.60 m above mean

sea level. The study material comprised 31 medium-duration genotypes with a growth duration between 125 and 140 days. The genotypes were grown in an alpha lattice design with two replications.

2.2 Data collection

The data collected panicle length (PL), panicle weight (PW), primary branch length per panicle (PBL), primary branch number per panicle (PBN), primary branch grain number per panicle (PBGn), secondary branch number per panicle (SBL), secondary branch number per panicle (SBN), secondary branch grain number per panicle (SBGn), number of unfilled spikelet/panicle (NUFS), spikelet fertility (SF), harvest index (HI) and yield per hectare (YPH). The panicle from the harvested plant was selected. The length of each panicle was measured from the base to the tip using a ruler. Each panicle was weighed using a precision balance. The panicle weight was recorded to assess its contribution to overall yield. The number and length of primary branches and secondary branches were measured. The length was measured from where the branch joins the main panicle axis to its tip. Spikelet fertility was calculated by the percentage of spikelets that are filled (*i.e.*, successfully developed into grains) out of the total number of spikelets present on a panicle. This is an important measure for assessing the reproductive success and potential yield of the rice panicle.

2.3 Statistical analysis

The data on panicle architecture and yield components were analysed using Excel 2016. Pearson's correlation coefficient was employed to assess the direction of the relationship between panicle architectural traits and yield attributes in medium-duration genotypes. Principal component analysis (PCA) was then performed and identify the key variables contributing to the variation in panicle architecture and yield characteristics among the medium-duration rice genotypes. Both PCA and correlation analyses were conducted using GRAPES (General R-based Analysis Platform Empowered by Statistics) Version 1.1.0 to further elucidate the relationships and patterns within the dataset.

3. Result

The descriptive statistics including mean, minimum, maximum, standard error of difference and coefficient of variation were calculated and are summarized in (Table 3.1). All panicle architecture and yield trait showed significantly different among 31 medium duration genotype. The panicle length ranges from 23.88 to 31.58 cm with mean of 27.68. The panicle weight exhibited range from 3.2 to 6.9 g with the mean of 3.7. The mean for number of primary branches panicle⁻¹ was 11.65 and it range from 9.5 to 7.5. The length of primary branches panicle⁻¹ ranges from 6.56 to 14.58 cm with the mean of 9.85. While, the mean for number of secondary branches panicle⁻¹ 39.55, ranges from 20.33 to 57.33. The length of secondary branches panicle⁻¹ ranges from 1.9 to 3.7 cm with the mean of 9.8. The grain number on primary branches panicle⁻¹ exhibited a range from 4.5 to 11.5 and the mean was 7.35. Additionally, the mean grain number on secondary branches panicle⁻¹ was 3.6, with a range of 3 to 5. The number of unfilled spikelet panicle⁻¹ exhibited mean 45.6 and it range from 17 to 130.83. While, the total spikelet panicle⁻¹ range from 130.25 to 310.83 with the mean of 224.96. Similarly, spikelet fertility ranges from 40.53 to 86.82 with the mean of 68.42. Also the yield and harvest index were also significantly differed among 31 genotype. The yield hectare⁻¹ ranges from 1934.38 to 4658.91 kg h⁻¹ with the mean of 3382.3 kg h⁻¹ while the harvest index ranges from 25.87 to 45.08 with the mean value of 35.72. Among the

genotypes, the coefficient of variation (CV) ranged from 0.07 to 0.46. Remarkably, the highest CV obtained by number of unfilled spikelet panicle⁻¹ (0.46) followed by; yield hectare⁻¹ (0.26), the number of unfilled spikelet panicle⁻¹ (0.26) and total spikelet panicle⁻¹ (0.24). Conversely, the lowest CV obtained by panicle length (0.07) and grain number on primary branches panicle⁻¹ (0.3).

Table 3.1 Descriptive statistics of panicle architecture and yield characters of 31 medium duration rice genotypes

	PL	PW	PBN	PBL	SBN	SBL	PBGn	SBGn	NUFS	TSP	SF	HI	YPH
min	23.88	3.2	9.5	6.56	20.33	1.9	4.5	3	17	130.25	40.53	25.87	1934.38
max	31.58	6.9	17.5	14.58	57.33	3.76	15.33	5	130.83	310.83	86.82	45.08	4658.91
range	7.7	3.7	8	8.02	37	1.86	10.83	2	113.83	180.58	46.29	19.21	2724.53
sum	858.13	147.7	361.26	305.3	1226.19	85.4	227.73	112.5	1413.55	6973.76	2121.13	1107.19	104851.4
median	27.43	4.7	11	9.51	40	2.71	6.66	3.5	40.33	220.5	72.14	35.58	3465.22
mean	27.68	4.76	11.65	9.85	39.55	2.75	7.35	3.63	45.6	224.96	68.42	35.72	3382.3
SE.mean	0.33	0.16	0.35	0.33	1.86	0.08	0.4	0.09	3.79	9.84	2.58	1.09	156.26
var	3.42	0.81	3.71	3.42	107.34	0.19	4.88	0.26	444.21	2999.91	206.98	36.63	756902.1
std.dev	1.85	0.9	1.93	1.85	10.36	0.44	2.21	0.51	21.08	54.77	14.39	6.05	870
coef.var	0.07	0.19	0.17	0.19	0.26	0.16	0.3	0.14	0.46	0.24	0.21	0.17	0.26

PL-Panicle length, PW- Panicle weight, PBN-Primary branch number/panicle, PBL-Primary branch length/panicle, PBGn- Primary branch grain number/panicle, SBN-Secondary branch number/panicle, SBL-Secondary branch length/panicle, SBGn- Secondary branch grain number/panicle, NUFS- Number of unfilled spikelet/panicle, TSP- Total spikelet/panicle, SF- Spikelet fertility, HI-Harvest index, YPH-Yield per hectare

3.1 Principal component analysis (PCA)

The study examined the differences in panicle architectural and yield-related traits that provide overall variance for each component using principal component analysis. The findings showed that three principal component(PCs) had an Eigenvalue of more than one (Table 3.2). The variation was shown in scree plot (Figure i). The highest percentage contribution on PC1 were 28.44% to total variation and it was attributed by traits spikelet fertility, length of primary branch panicle⁻¹, yield hectare⁻¹, harvest index with Eigen value 3.69. PC2 attributes 19.24% and variable were total spikelet panicle⁻¹, number of secondary branches panicle⁻¹, number of primary branch panicle⁻¹ with Eigen value 2.50. Similarly, PC3 contributing percentage was 12.68% and traits that associated were panicle weight and length of secondary branches panicle⁻¹ with Eigen value 1.64 (Table 3). Principal component analysis (PCA) of the studied rice genotypes illustrates the genotypic relationships using a biplot, based on various panicle characteristics. The points in the biplot represent rice genotypes, and the vectors (arrows) represent the traits or variables being studied. The direction and length of the vectors indicate the contribution of each trait to the principal components and the correlation between traits. (Figure ii).

Table 3.2 Principle component analysis showing the Eigen values and proportion of variance

Prin_comp	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	3.698	28.443	28.443
PC2	2.502	19.243	47.686
PC3	1.649	12.685	60.371

Table 3.3 Percentage contributions of different variables (traits) to each principal component (PC)

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PL	3.869	1.387	0.474	5.956	42.169	17.95	1.131	25.444
PW	0.351	0.274	32.384	0.023	28.246	0.238	1.427	24.036
PBN	0.11	18.747	4.135	7.984	2.813	10.739	16.153	3.176
PBL	18.173	0.901	4.025	5.942	1.114	3.368	10.385	0.504
SBN	2.345	24.699	5.438	0	4.95	1.249	8.406	3.205
SBL	6.66	0.095	25.486	4.247	7.042	4.379	2.686	4.64
PBGn	0.008	6.651	5.245	35.63	0.008	18.473	7.775	0.649
SBGn	4.087	5.383	6.774	12.803	2.625	25.589	4.384	29.653
NUFS	10.711	2.159	2.341	10.372	3.501	11.606	22.286	1.079
TSP	1.243	27.843	2.587	0.002	0.671	4.641	16.54	5.162
SF	22.024	1.065	2.519	0.94	2.214	0.003	3.79	0.238
HI	13.073	4.448	4.123	13.248	3.644	0.415	3.495	2.174
YPH	17.345	6.349	4.469	2.854	1.005	1.35	1.541	0.04

PL-Panicle length, PW- Panicle weight, PBL-Primary branch length/panicle, PBN-Primary branch number/panicle, PBGn- Primary branch grain number/panicle, SBL- Secondary branch length/panicle, SBN- Secondary branch number/panicle, SBGn- Secondary branch grain number/panicle, NUFs- Number of unfilled spikelet/panicle, TSP- Total spikelet/panicle, SF- Spikelet fertility, HI-Harvest index, YPH-Yield per hectare

3.2 Correlation association analysis

The correlation analysis is presented in (Table 4). The length of primary branches panicle⁻¹ had significant negative association with spikelet fertility (-0.724***). The number of secondary branches grain number panicle⁻¹ and the number of secondary branches panicle⁻¹ had a positive association with unfilled spikelet panicle⁻¹ (0.546**) and (0.37*) respectively. Spikelet fertility in the medium-duration genotype had a positive association with yield hectare⁻¹ (0.841***) and harvest index (0.678***).

Discussion

The present study comprehensively evaluated the panicle architecture and yield traits of 31 medium-duration rice genotypes, revealing significant variability among the genotypes. The descriptive statistics highlighted substantial differences in traits such as panicle length, panicle weight, primary and secondary branches, grain number, and total spikelets panicle⁻¹.

The principal component analysis (PCA) revealed three principal components with Eigenvalues greater than one, cumulatively accounting for a significant portion of the total variance. The first principal component (PC1) explained 28.44% of the variation and was primarily associated with spikelet fertility, primary branch length, yield hectare⁻¹, and harvest index. This component's high contribution emphasizes the importance of these traits in defining the yield potential of rice genotypes. Notably, genotypes with better spikelet fertility and optimal primary branch length tended to exhibit higher yields, indicating a strong correlation between these traits and overall productivity. (Shiobara *et al.* 2011). PC2, accounting for 19.24% of the variation, was characterized by the total number of spikelets, secondary branches, and primary branches per panicle. Genotypes contributing significantly to this component displayed a higher number of both primary and secondary branches, suggesting a structural advantage in terms of spikelet accommodation and potential grain number. The third component (PC3) contributed 12.68% of the variance, mainly driven by panicle weight and the length of secondary branches. This indicates that genotypes with heavier panicles and longer secondary branches may not necessarily possess structural features that favours higher grain weight or better yield outcomes. Despite having more substantial panicles, these genotypes might experience challenges in grain filling, potentially due to the increased competition for assimilates among a larger number of grains. Similar finding was reported by (Saito *et al.* 2023).

The correlation analysis further elucidated the relationships between various panicle traits. Interestingly, a significant positive correlation between the number of secondary branches and unfilled spikelets per panicle was noted, suggesting a trade-off between spikelet number and grain filling efficiency. This aligns with previous findings by Panda *et al.* (2015) and Sekhar *et al.* (2021), who reported that densely packed panicles often lead to increased unfilled grains, particularly in the basal spikelets. The study by Sahu *et al.* (2021) further supports this observation, indicating that inadequate space between spikelets can impede grain filling, thus affecting both yield and grain quality. Similar findings were reported by (Panda *et al.* 2009; Das *et al.* 2018)

In summary, the results of this study underscore the complex interplay between panicle architecture and yield-related traits in rice genotypes. The significant variation among genotypes provides valuable insights for breeding programs aiming to enhance yield potential through targeted selection of favourable traits. Future research should focus on understanding the genetic basis of these traits and exploring the potential for their improvement through advanced breeding techniques. Additionally, investigating the physiological mechanisms underlying the observed trade-offs between spikelet number and grain filling could provide further insights into optimizing rice yield and quality.

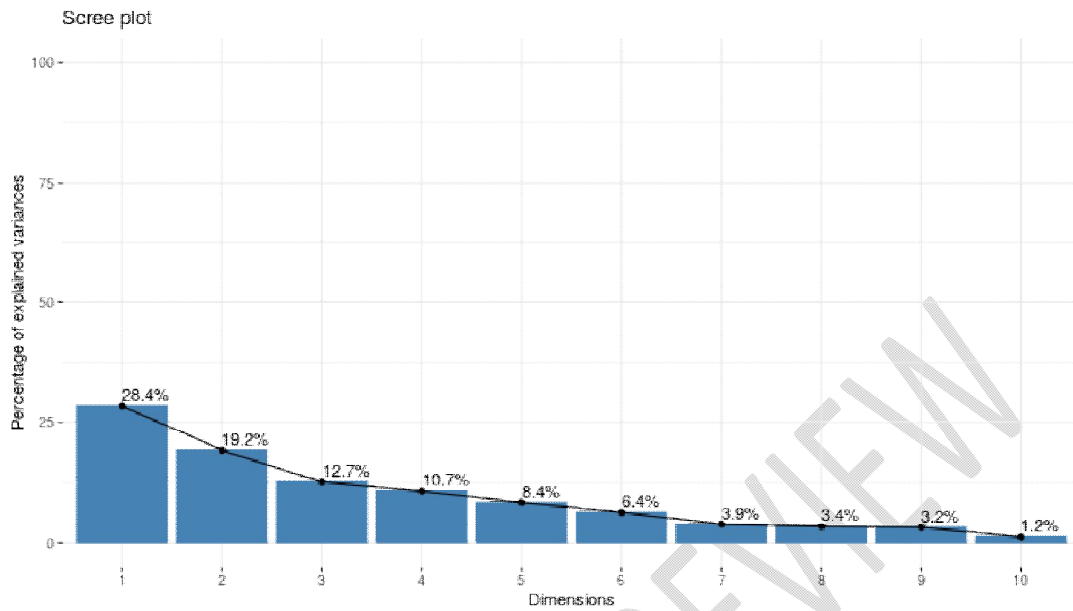


Figure i. Scree plot of percentage variance after PCA

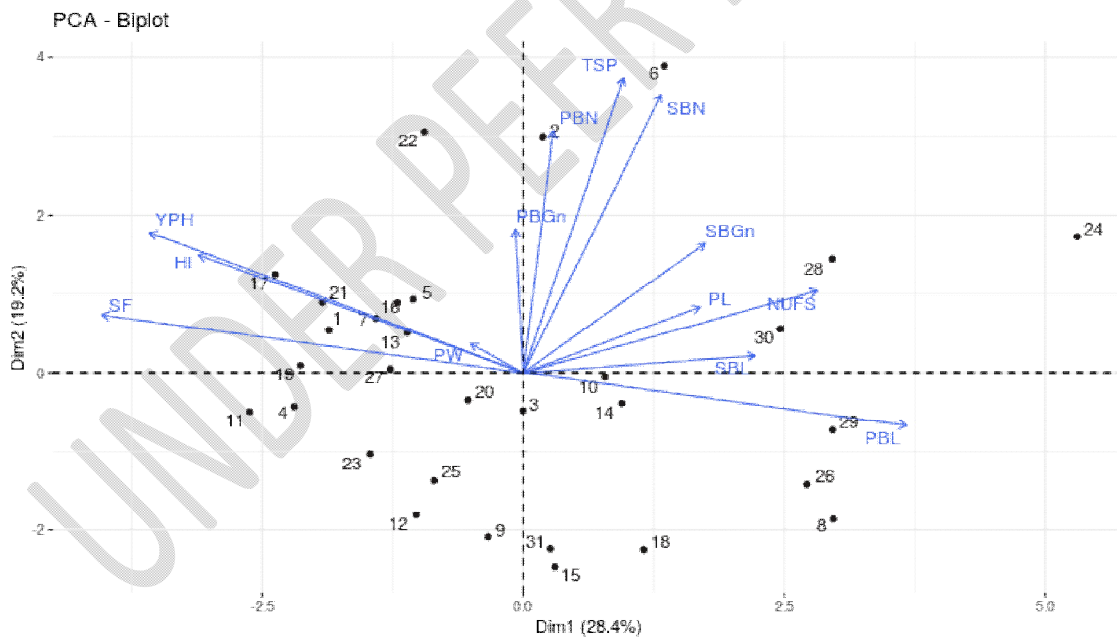


Figure ii. Principal component analysis (PCA) of the studied rice genotypes illustrates the genotypic relationships using a biplot, based on various panicle traits

5. Conclusion

The study results emphasize the need to focus on specific panicle architecture traits to enhance rice yield potential. Understanding the relationships between these traits allows for more efficient genetic selection in breeding programs, aiming to develop rice varieties that are better suited to specific growing conditions and have improved yield potential. This research provides valuable insights for future crop improvement initiatives, contributing to the development of rice varieties with higher productivity and adaptability, ultimately aiding in global food security efforts.

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Table 3.4 Correlation analysis between panicle architecture and yield parameters in medium-duration genotype

	PL	PW	PBGn	PBL	PBN	SBGn	SBL	SBN	UFSP	SF	YPH	HI
PL	1											
PW	0.359*	1										
PBGn	0.148	0.114	1									
PBL	0.208	0.057	-0.276	1								
PBN	0.028	0.356*	-0.031	-0.004	1							
SBGn	0.313	0.214	0.318	0.294	0.161	1						
SBL	0.243	0.345	0.114	0.588***	-0.073	0.178	1					
SBN	0.093	0.466**	0.208	0.079	0.546**	0.256	-0.054	1				
UFSP	0.402	0.208	0.626	0.275	0.036	0.546**	0.305	0.37*	1			
SF	-0.161	-0.208	0.181	-0.724***	-0.104	-0.205	-0.279	-0.207	-0.126	1		
YPH	-0.154	0.171	0.065	0.546	0.204	-0.139	-0.139	-0.02	-0.095	0.841***	1	
HI	0.183	0.134	0.072	0.472	0.219	-0.196	-0.061	-0.083	-0.226	0.678***	0.83***	1

PL-Panicle length, PW- Panicle weight, PBGN- Primary branch grain number/panicle, PBL-Primary branch length/panicle, PBN-Primary branch number/panicle, SBGn- Secondary branch grain number/panicle, SBL- Secondary branch length/panicle, SBN-Secondary branch number/panicle, UFSP-unfilled spikelet/panicle,SF- Spikelet fertility, HI-Harvest index, YPH-Yield per hectare

Disclaimer (Artificial intelligence)

The Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

Competing Interests

Authors have declared that no competing interests exist.

Reference

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