

## Characterizing Genotypic Diversity: Flowering pattern, Grain Yield and Yield Attributes in Rice for Crop Improvement

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(Received 02 September 2022, Accepted 27 October, 2022)

(Published by Research Trend, Website: [www.researchtrend.net](http://www.researchtrend.net))

**ABSTRACT:** Rice is an important staple food crop in the world. With increase in climate change rice production is getting affected and reduces the yield and production, increasing the yield production is necessary to meet the demand by the population. Understanding the genetic diversity of rice genotypes is crucial for enhancing breeding programs and improving agricultural productivity. The present study was investigated on the genotypic variation in flowering time, total grains, and yield attributes in diverse genotypes of Rice. The objective was to gain insights into the phenotypic traits of these genotypes and provide a traits for future breeding efforts. Flowering time was assessed by recording the number of days to 50% flowering, revealing a wide range of flowering duration between 60 to 80 days after sowing. Total grain production per panicle was examined between 20 and 40 days after flowering, with genotypes displaying significant variation in grain counts. Filling of grains in the panicle increased with maturity, while the number of unfilled grains decreased. The study also analyzed other agronomic traits, including the number of tillers per hill, 100 grains weight, and panicle length. Genotypes exhibited diverse tillering patterns, with 7 to 8 tillers being predominant. The weight of 100 grains ranged from 2.0 to 2.5 grams, while panicle length varied within the 24 to 28 cm range. This investigation provides valuable insights into the genotypic diversity of rice, enabling future breeding strategies focused on improving flowering time, grain production, and other important agronomic traits to enhance crop productivity and sustainability.

**Keywords:** Flowering, grain production, genotypic diversity, Rice, yield attributes.

### INTRODUCTION

Asian cultivated rice (*Oryza sativa* L.), feeding more than 90% of the human population in Asia, is one of the world's most important crops. Wild ancestors and landraces with rich genetic diversity and wide adaptation to various environments provide valuable and useful genetic resources for crop improvement (Dwivedi *et al.*, 2016; Sang and Ge 2013). Genetic diversity within crop species is a critical factor in agricultural research and breeding programs as it provides the foundation for developing improved crop varieties with enhanced productivity and adaptability (Vavilov, 1992). Understanding the range of genotypic variation in key traits such as flowering time, grain production, and agronomic characteristics is crucial for targeted breeding efforts (González *et al.*, 2019).

The flowering time in rice is influenced by a complex interplay of genetic and environmental factors. Flowering time is a key phenological stage that plays a vital role in determining the synchronization of reproductive processes and the overall yield potential of crops (Yan *et al.*, 2014). Genetic variations within rice genotypes contribute to the diversity observed in flowering time, with different varieties exhibiting

variations in the duration from sowing to the onset of flowering. Some genotypes flower early, while others exhibit a delayed flowering response (Cao *et al.*, 2017). Studying the diversity of rice genotypes in flowering time is essential for crop breeding programs aimed at developing varieties with desirable flowering characteristics, such as early or late flowering to suit specific agro-climatic conditions or cropping systems. Additionally, understanding the genetic basis of flowering time variation can help unravel the underlying molecular mechanisms controlling this trait and facilitate targeted genetic manipulation for crop improvement Shrestha *et al.* (2014).

The diversity of rice genotypes in terms of grain number per panicle is immense, with different varieties exhibiting significant variations in their grain-filling capacity. Some genotypes have high grain numbers, resulting in dense and heavily filled panicles, while others have relatively lower grain numbers. This diversity offers valuable opportunities for crop improvement programs aimed at enhancing grain yield potential (Swamy *et al.*, 2016). Studying the diversity of rice genotypes in grain number per panicle is essential for understanding the genetic basis of this trait and

identifying superior genotypes with desirable grain-filling characteristics. Furthermore, it enables breeders to develop varieties that maximize grain production by optimizing the number of grains per panicle, while maintaining other important agronomic traits. Grain production, including the total number of grains per panicle and the proportion of filled and unfilled grains, directly impacts crop yield and quality (Dingkuhn *et al.*, 2015). These traits are influenced by genetic factors and environmental interactions.

The diversity of rice genotypes in terms of total filled and unfilled grains per panicle is vast, with different varieties exhibiting significant variations in their grain-filling capacity and efficiency. Some genotypes have higher percentages of filled grains, resulting in dense and well-filled panicles, while others may have a higher proportion of unfilled grains (Liu *et al.*, 2019). This diversity offers valuable opportunities for crop improvement programs aimed at enhancing grain yield and quality. Studying the diversity of rice genotypes in terms of total filled and unfilled grains per panicle is essential for understanding the genetic and physiological factors that influence grain development and determining the underlying mechanisms that contribute to variations in grain-filling efficiency. This knowledge can help breeders identify and select superior genotypes with desirable grain-filling characteristics and develop varieties that optimize the balance between filled and unfilled grains for maximum grain yield (Chen *et al.*, 2021).

Agronomic traits, such as the number of tillers per hill, 100 grains weight, and panicle length, serve as important indicators of crop performance and can contribute to breeding efforts aimed at improving yield potential and stress tolerance (Khush, 2005). By conducting a comprehensive analysis of diverse genotypes, we can gain valuable insights into the genetic variation present within rice and identify potential targets for breeding programs (Varshney *et al.*, 2018). This knowledge will inform future breeding strategies, allowing for the development of improved crop varieties with desirable traits and increased resilience to environmental challenges.

The diversity of rice genotypes in terms of test weight and panicle length is extensive, with different varieties exhibiting significant variations in these traits. Test weight reflects the density and quality of rice grains, with higher test weights indicating denser and more desirable grains. Panicle length, on the other hand, influences the number of grains per panicle and overall yield potential (Zhong *et al.*, 2021). Studying the diversity of rice genotypes in terms of test weight and panicle length is essential for understanding the genetic and physiological factors that contribute to variations in these traits. It helps breeders identify and select superior genotypes with desirable grain characteristics and agronomic performance. By harnessing this diversity, breeders can develop rice varieties with higher test weights, longer panicles, and increased grain yield, thus meeting the demands for quality rice in both domestic and international markets (Zhu *et al.*, 2018). In this study, we aimed to explore the genotypic diversity of rice and

investigate the relationships between flowering time, grain production, and agronomic traits across a diverse panel of genotypes. These findings will provide a solid foundation for targeted breeding efforts and contribute to sustainable agriculture and global food security.

## MATERIALS AND METHODS

**Plant materials and growth conditions.** A diversified set of 96 rice accessions from the Short Term Gene Bank of ICAR-National Rice Research Institute, Cuttack, representing PB (Western Odisha Collections), HT (Assam Rice Collections) and NHN (popular varieties) were used in the present study. Thirty-day-old seedlings were transplanted with 20×10 cm spacing between rows and plants. NPK (40:20:20) kg ha<sup>-1</sup> as baseline dosage and supplemental nitrogen (40:20:20 kg ha<sup>-1</sup>) at 30 and 50 days after transplanting were applied. NRRRI used conventional measures for insect, disease, and weed management. The experiment was laid out in Alpha lattice design with three replications.

**Days to flowering and 50% flowering** were recorded as numbers of days from the date of transplanting to the date of appearance of flower and flowers in 50 per cent plants in each genotype of the three replication and separately.

**Number of tillers hill<sup>-1</sup>.** The number of effective tillers in the five randomly selected plants was counted and the mean number of effective tillers per plant was calculated.

**Panicle length (cm).** The length of the panicle was measured from five uniformly sized panicles, and the average panicle length was calculated and expressed in centimeters.

**Filled grains panicle<sup>-1</sup> from 20 to 40 DAF.** The total number of filled grains from each panicle of the ten selected plants were separated and counted at 20 to 40 DAF. The mean number of filled grains per panicle was calculated.

**Unfilled grains panicle<sup>-1</sup> from 20 to 40 DAF.** The total number of unfilled grains from each panicle of the ten selected plants were separated and counted at 20 to 40 DAF. The mean number of unfilled grains per panicle was calculated.

**Total grains panicle<sup>-1</sup> from 20 to 40 DAF.** The pre-harvest sprouting variation was assessed by counting the number of filled grains (both filled and unfilled) per panicle. Three panicles were randomly selected, and the counting was performed at five different flowering stages: 20, 25, 30, 35, and 40 days after flowering (DAF).

**100 grains weight (gm).** The weights of one hundred randomly selected seeds from each genotype were counted and expressed in grams.

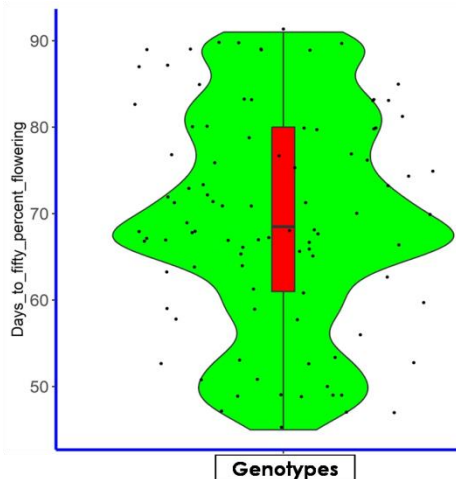
**Statistical analysis.** The yield and yield attribute data were analyzed using Excel (MS Office, 2021) and graphs were generated using R Studio (version 4.2.2) and the Past 4.0 project for visualization.

## RESULTS

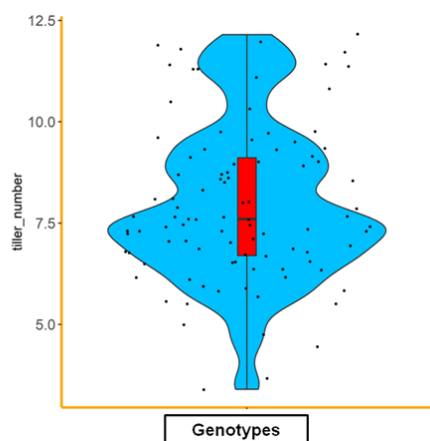
**Days to 50 % flowering.** To assess the variation in 50% flowering among diverse rice genotypes, the timing of flowering was recorded and depicted in Fig. 1. The findings revealed that a significant number of genotypes

exhibited flowering between 60 and 80 days after sowing, indicating a consistent pattern across both seasons. The range of 50% flowering across all genotypes duration from 43 to 86 days after sowing, highlighting the diverse flowering times observed within the population.

**Number of tillers hill<sup>-1</sup>.** The diversity of genotypes in terms of the number of productive tillers was examined at the harvesting stage (Fig. 2). The findings revealed a predominant range of 7 to 8 tillers among many genotypes, while a few genotypes exhibited exceptionally high tiller numbers (11 to 12). Conversely, only a small number of genotypes produced lower tiller counts ( $\pm 5$ ).

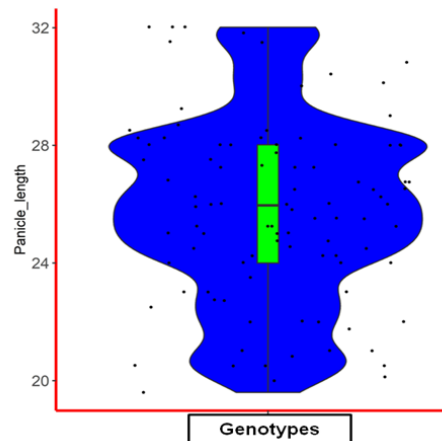


**Fig. 1.** Diversity of the genotypes for days to 50 % flowering (Distribution of jitters indicates the distribution of genotypes).



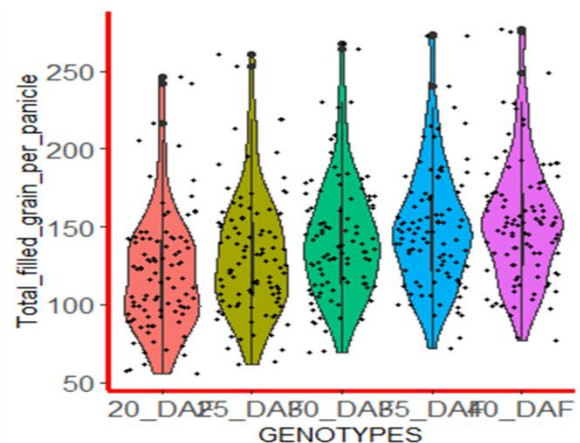
**Fig. 2.** Diversity of rice genotypes for tiller number hill<sup>-1</sup> (Distribution of jitters indicates the distribution of genotypes).

**Panicle length (cm).** Panicle length was measured in 96 diverse genotypes (Fig. 3) and the results revealed that many genotypes had panicle length between 24 to 28 cm long. Whereas few genotypes showed extreme length (>32) while few genotypes showed panicle length between 20 to 23 cm.



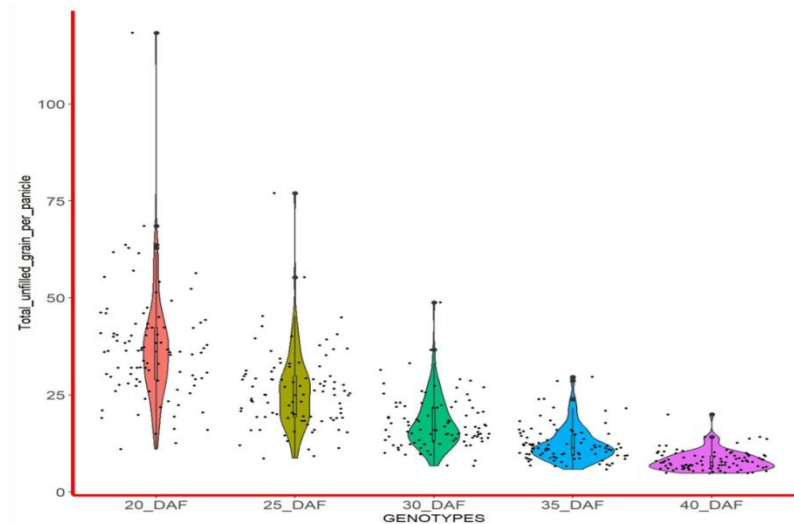
**Fig. 3.** Diversity of rice genotypes for panicle length (Distribution of jitters indicates the distribution of genotypes).

**Number of filled grains per panicle at 20 to 40 DAF.** Total number of filled grains per panicle were recorded at 20 to 40 DAF. Results observed that filling of the grains in the panicle increased towards the maturity. Most of the genotypes had maximum number of filled grains from 30 to 40 DAF compared to 20 and 25 DAF (Fig. 4). At 40 DAF higher number of filled grains was observed in all the genotypes whereas at 20 DAF lower number of filled grains observed in most of the genotypes.



**Fig. 4.** Diversity of the genotypes for total filled grains per panicle at 20 to 40 DAF (Distribution of jitters indicates the distribution of genotypes).

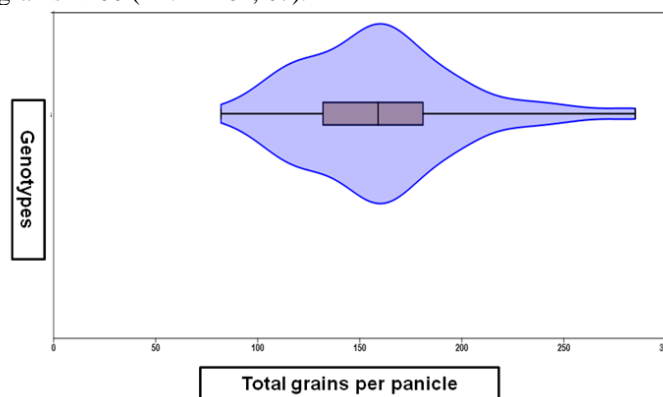
**Number of unfilled grains per panicle at 20 to 40 DAF.** Total number of unfilled grains per panicle at 20 to 40 DAF was recorded. Results observed that with increased maturity the decreased unfilled grains were observed in all the genotypes (Fig. 5). At 20 and 25 DAF unfilled grains number was higher whereas unfilled grains at 30 to 40 shown to be lower than earlier stages. Most of the genotypes had unfilled grains between 25 to 50 at 20 to 25 DAF while <15 unfilled grains was observed at 30 to 40 DAF in all the genotypes.



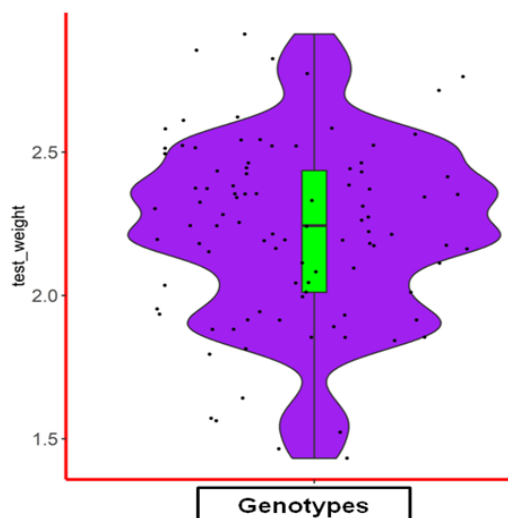
**Fig. 5.** Diversity of the genotypes for total unfilled grains per panicle at 20 to 40 DAF.

**Total number of grains per panicle.** The total number of grains per panicle was recorded (Fig. 6). Results shown that the higher variation was observed in the total grains of diverse genotypes. Total grains per panicle was observed that many genotypes had grains between 140 to 200 and few extreme genotypes had <250 grains per panicle (Ex: HT-87, PB-63) and very few genotypes shown to be very low total grains <100 (Ex: PB-64, 67).

**100 grains weight (gm).** 100 grains weight was weighed in 96 diverse genotypes; results revealed that a majority of the genotypes exhibited 100 grains weight ranging from 2.0 to 2.5 gm. However, few genotypes showed exceptionally high 100 grains weights of around 3 gm, while a small subset exhibited lower 100 grains weights below 1.5 gm. (Fig. 7)



**Fig. 6.** Diversity of the genotypes for total grains per panicle (Width of the violin indicates distribution of genotypes).



**Fig. 7.** Diversity of rice genotypes for 100 grains weight (gm) (Distribution of jitters indicates the distribution of genotypes).



## DISCUSSION

Rice (*Oryza sativa* L.) is a vital cereal crop with diverse genetic variations that influence its yield and yield attributes. Understanding the genetic diversity and its impact on yield-related traits is essential for crop improvement and ensuring global food security (González *et al.*, 2019). The present experiment was conducted to understand the diversity of genotypes for flowering and yield attributes. The present findings revealed that the assessment of variation in 50% flowering among diverse rice genotypes revealed a consistent pattern of flowering between 60 and 80 days after sowing across both seasons. These findings are consistent with previous studies that have reported significant genetic variation in flowering time in rice (Dwivedi *et al.* 2016; Yan *et al.*, 2014). Understanding the genetic basis of flowering time is crucial for crop improvement programs, as it allows for the selection of genotypes better suited to specific environmental conditions (Cao *et al.*, 2017; Awaji *et al.*, 2022). Further research focusing on identifying the specific genes or genetic factors responsible for this variation will contribute to a better understanding of flowering time regulation and facilitate targeted breeding efforts (Sang and Ge 2013). Exploiting the genetic variability in flowering time can lead to the development of rice varieties with improved adaptation and productivity (Shrestha *et al.*, 2014).

The examination of genotypic diversity in terms of productive tiller numbers at the harvesting stage showed a predominant range of 7 to 8 tillers among many genotypes. These findings highlight significant genetic variability in tillering capacity within the rice population (Swamy *et al.*, 2016). Previous studies have also reported substantial genotypic variation in tiller production in rice, indicating the importance of this trait in determining crop productivity. Understanding the genetic factors underlying tillering can contribute to the development of rice varieties with increased tiller numbers and ultimately improved yield potential. Future research efforts should focus on identifying the genes and molecular mechanisms involved in regulating tillering in rice to facilitate targeted breeding strategies for enhancing tiller production (Chen *et al.*, 2021). Exploiting the genetic diversity in tillering can lead to the development of high-yielding rice cultivars (Dingkuhn *et al.*, 2015).

The measurement of panicle length in 96 diverse genotypes demonstrated a predominant range of 24 to 28 cm, indicating a consistent pattern across the population. These findings reflect significant genetic variation in panicle length among the tested rice genotypes. Further exploration of the genetic factors controlling panicle length can aid in the development of rice varieties with desirable panicle characteristics and improved productivity. The manipulation of panicle length through breeding strategies holds great potential for enhancing rice yield (Sang and Ge 2013).

The assessment of total number of filled and unfilled grains per panicle at different developmental stages (20 to 40 DAF) revealed an increase in grain filling and decreasing unfilled grains towards maturity. These

findings highlight the dynamic nature of grain filling and its impact on overall grain yield (Liu *et al.*, 2019). Previous studies have also emphasized the importance of proper grain filling for achieving optimal yield in rice. Understanding the genetic and physiological mechanisms underlying grain filling can contribute to the development of high-yielding rice varieties (Chen *et al.*, 2021).

The analysis of total grains per panicle in diverse genotypes revealed a wide variation, indicating the genetic diversity in grain production. This variation in total grains per panicle highlights the importance of genetic factors in determining grain yield potential (Khush, 2005). Previous studies have also reported significant genetic variability in grain number per panicle in rice, emphasizing the role of genetic diversity in crop improvement (Chen *et al.*, 2021). Understanding the genetic basis of grain number variation can aid in breeding programs aimed at increasing grain yield in rice (Varshney *et al.*, 2018).

The evaluation of 100 grains weight in diverse rice genotypes demonstrated a significant variation in grain weight. These findings emphasize the genetic diversity in grain weight and highlight the potential for improving grain size in rice through breeding programs. Previous studies have also reported significant variation in grain weight among rice genotypes, underscoring the importance of understanding the genetic basis of grain size for crop improvement (Zhong *et al.*, 2021).

## CONCLUSIONS

In conclusion, the assessment of diverse rice genotypes for various agronomic traits revealed significant variation within the population. The genotypes exhibited diverse flowering times, productive tiller numbers, panicle lengths, and grain characteristics such as filled and unfilled grains, total grains per panicle, and 100 grains weight. These findings indicated the presence of genetic diversity in the studied traits, highlighting the potential for selecting genotypes with desirable agronomic traits. The results revealed valuable insights for rice breeding programs aimed at improving yield potential and grain quality. Further research and selection of genotypes with favorable traits can contribute to the development of high-yielding and superior rice varieties.

## FUTURE SCOPE

The future scope of this article includes utilizing the identified diverse genotypes with desirable agronomic traits for breeding programs to develop improved rice varieties with higher yield potential, stress tolerance, and quality traits. Additionally, further research can focus on understanding the underlying genetic mechanisms and exploring genomic resources to accelerate rice improvement efforts.

**Acknowledgement.** I extend my sincere thanks to ICAR-NRRI for providing fund for research work, facilities and supported by supporting staff.

**Conflict of Interest.** None.

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**How to cite this article:** Repudi Shalem Raju, Prashantkumar S. Hanjagi, Chittaranjan Sahoo, Sushma M. Awaji<sup>2</sup>, K.C. Samal, B.N. Devanna and Manasi Dash (2022). Characterizing Genotypic Diversity: Flowering pattern, Grain Yield and Yield Attributes in Rice for Crop Improvement. *Biological Forum – An International Journal*, 14(4a): 733-738.