Nepal Agriculture Research Journal
Vol. 15, No. 1, pp. 115-124, 2023
DOI: https://doi.org/10.3126/narj.v15i1.51533

Evaluation of panicle architecture traits in rice genotypes using PTRAP

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ARTICLE INFO

Research Paper

Received: July 23, 2022
Revised: November 20, 2022
Accepted: January 17, 2023
Published: February 01, 2023

Contents available at
http://www/sasnepal.org.np

Published by Society of Agricultural Scientists Nepal (SAS-Nepal).

ABSTRACT

An experiment was conducted with the objective of evaluating panicle architecture traits of different genotypes of rice in relation to yield during June to November 2020. The experiment was conducted in randomized complete block design with three replications and forty-two treatments. The graphical user interface used image analysis tool Panicle Trait Phenotyping (PTRAP) was used to record architecture and yield related traits. Among genotypes, the highest yield was found in high yielding late variety Sampurna (6.1t/ha) with highest number of both primary (16.33) and secondary branches (53.33). Four different types of panicle size-irregular, conical, diamond like and pyramid shaped panicle were identified in 42 genotypes. Correlation analysis revealed significant (p=0.05) and positive correlation of grain yield with architecture traits i.e., number of primary branches (r=0.88), length of primary branches (r=0.89), number of secondary branches (r=0.69), number of nodes (r=84). The correlation between spikelet number and other variables related to number of primary branches was higher than correlation with variables related to length of primary branch. The increase in number of panicle rachis length, number of primary and secondary branches and length of primary branches resulted in increased spikelet number per panicle and grain yield. It can be concluded the architectural traits like rachis length, number of primary secondary branches, and secondary branches and length of primary branches were the most important in improving panicle architecture and crop yield.

Keywords: Rachis length, Rice, Panicle architecture, Panicle length, Grain yield

Cited as: Gautam A and A Shrestha. 2023. Evaluation of panicle architecture traits in rice genotypes using PTRAP. Nepal Agriculture Research Journal **15**(1): 115-124.
DOI: https://doi.org/10.3126/narj.v15i1.51533

INTRODUCTION

Rice (*Oryza sativa*) is the major staple food crop for more than half of the world's population. Rice is grown in wide range of agro-climatic conditions. The global rice production accounts 503.901 million metric tons (FAOSTAT 2019). Global rice production is still insufficient to meet the increasing food demand which has to be increased by 1-2.4% by 2050 (Ray et al 2013). Rice occupies about half of total cereal grains production in Nepal. It covers one third of overall country's crop area supplying 40% of calories for the people (Gauchan et al 2008).

The rice yield is the result of the interaction of genetic, abiotic and biotic factors (Newton et al 2011) determined by plant growth especially panicle traits, total number of grains, percent of filled grains per panicle, seed setting rate and grain weight (Yoshida 1981).Rice panicle architecture is spatial arrangement of primary and secondary branches and spikelet distribution in branches (Weberling 1989). In rice, the panicle architecture has nine successive stages starting from transition of vegetative shoot apical meristem to an inflorescence meristem which later forms branch meristem followed by generating spikelet meristem and finally developing grains (Zhang and Yuan 2014). There is a wide range of rice panicle architecture among varieties (Faroq et al 2013). Each spikelet meristem produces one floral meristem. Therefore, the number of grains per panicle depends on number of differentiated spikeletper panicle (Yoshida and Nagato 2011), which is further determined by primary, secondary and tertiary branching (Xing and Zhang, 2010).

Variation in spikelet branching and grain formation results in superior and inferior grains in the panicle affecting grain quality (Mohapatra et al 2011). Rice shows wide range of variation in morphological traits and tolerance to abiotic and biotic stresses. Improvement on plant architecture is considered to be best approach to boost grain yield, because crop plants such as rice with desirable architecture are able to yield higher (Wang and Li 2008). Considering the relationship among plant architecture, grain yield, further molecular mechanism, hormonal and genetic diversity behind panicle architecture was studied (Wu et al 2016). This resulted in identification of specific genes (Wu et al 2016, Li et al 2016). However, systematic study of physiological parameters of panicle architecture and agronomic traits were limited to evaluate panicle architecture. The manual phenotypic procedure and analysis is time consuming, unreliable, ineffective and destructive for screening of panicles. It is almost impossible to quantify and evaluate all traits for obtaining an accurate overview of panicle architecture. The development of an easy high throughput panicle phenotyping tools like PTRAP standardizes the measurement and extraction of panicle traits.

PTRAP measures the panicle structure parameter and grain traits which automatically detects structure of panicle from a spread panicle image consisting of different morphological traits (Faroq et al 2013). The present study was conducted with objective of evaluating the panicle architecture traits of different rice genotypes using PTRAP.

MATERIALS AND METHODS

Study area and planting materials

The field experiment was conducted in agronomy farm of Regional Agriculture Research Station (RARS), Parwanipur, Bara, Nepal. It is located at 27°.07’°N latitude and 84°.91’ °E longitude with an elevation of 115 meter above mean sea level. The soil was silty loam in texture and olive gray with common fine to medium distinct dark yellowish-brown mottles. The experimental site experienced the average minimum and maximum temperature of 10.25 °C and 43.6 °C, respectively. A total of 1215 mm of rainfall recorded from June 2020 and October 2020, of which 1045 mm was recorded during the rice-growing season (June to October), as shown in Figure 1.

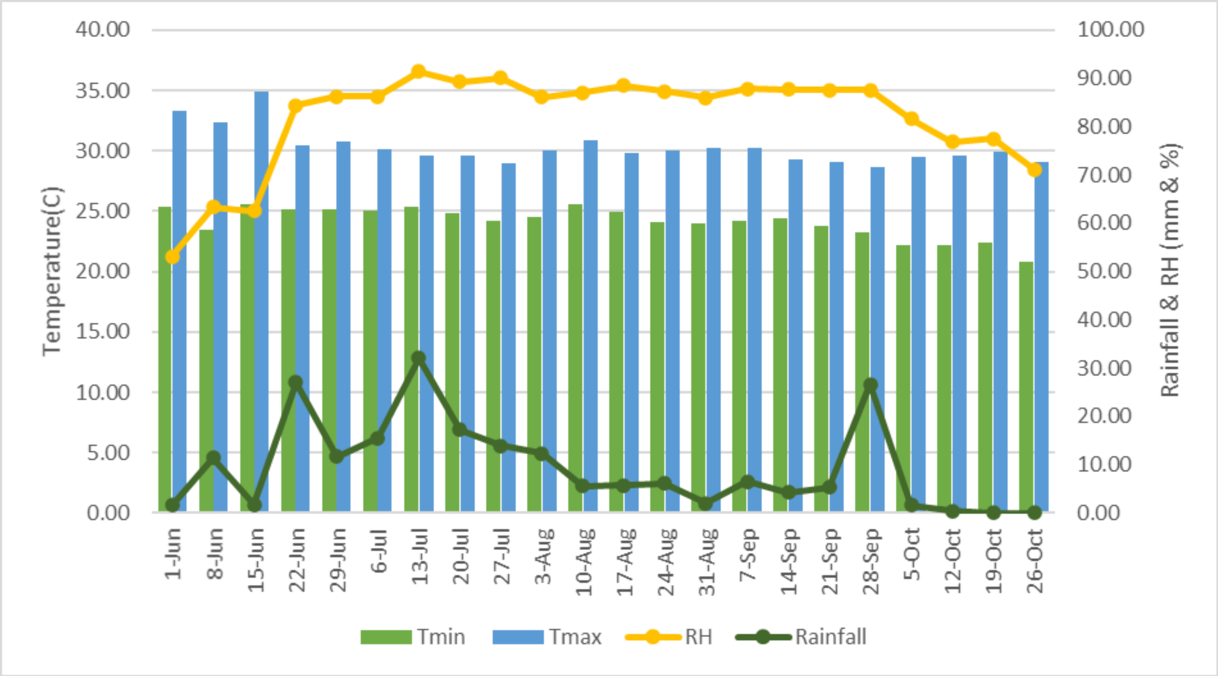

Figure 1: Weather data of research station Parwanipur, Bara from June to October 2020 (Source:https://power.larc.nasa.gov)

The experimentalmaterials comprised of 42 genotypes of rice available at Regional Agriculture Research Council, Parwanipur Bara.

Table 1: List of early, medium and late genotypes used in the experiment

Genotypes		**Background**	**Source**	**Remarks**
1. HHZ25-DT9-Y1-Y1 2. IR 15 L1717 3. IR16L 1637 4. IR 16L 1831 5. NR 2169-10-4-1-1-1-1-1 6. PR12 7. IR 17 L 1415	8. SVIN 188 9. IR 103587-22-2-3-B 10. TP 30529 11. IR 16L 1678 12. SVIN 189 13. SVIN 224 14. IR 16 L 1704	Breeding line	National Rice Research Program (NRRP)	Early
15. HHZ26-DT1-L11-L11 16. SVIN 207 17. NR2157-122-1-21-1-1-1 18. IR14L 363 19. IR98853-6-1-3-2	20. GSR 310 21. SVIN 141 22. IR 16 L 1844 23. IR 16L 1753	Breeding line	National Rice Research Program (NRRP)	Medium
24. Hardinath-3 25. Radha-4 26. HardinathBoro	27. Hardinath-2 28. Ram dhan	Improved variety	Farmer's field	Medium
29. Sampurna		Improved variety	Farmer's field	Late
30. TP 30535 31. IR 101465-5-25 32. TP 30539 33. IR 17 L 1341	34. IR 99993-B-B-RGA-1RGA-2RGA 35. IR41008	Breeding line	National Rice Research Program (NRRP)	Late
36. Sabitri37. Khumal 4 38. Makwanpur-1	39. Samba Mansuli 40. Hardinath Saba	Improved variety	Farmer's Field	Late
41. JethoBudo	42. Gurchi	Landraces	Farmer's Field	Late

Experimental design, data collection and analysis

The experiment was laid out in randomized complete block design with 42 treatments with three replications of each. Each plot size was 3 m× 2 m with 20 × 20 spacing of plants. The space between treatments and replication was 0.5m and 1m, respectively. The total number of plots was 126 withnet plot area of 483.84 m^2. The 21-day-old seedlings were transplanted with twoseedlings per hill at 20 cm × 20 cm spacing. Ten plants were selected randomly for recording observations for different biometrical, phenological and yield attributing characters and inter-relationships for the following traits. Panicle architecture and grain related traits were measured by using a free open-source software, Panicle traits phenotyping tool (Faroq et al 2013).

PTRAP captured images of spread panicles taken using a camera at a fixed distance, lighting, shutter speed, ISO and minimum camera resolution of 1024 × 768 pixels, where images were loaded into the software as a "project". From then on, pre-processing of the images within PTRAPis done by cropping out non-panicle areas without altering the resolution of the images. PTRAP was calibrated to the precise cm/pixel ratio to accurately measure the panicle and grain parameters. The data collected from the processed images were exported in two different formats i.e. XML and CSV. A CSV file generated allowed direct visualization of the results and easy transfer to spreadsheet software like Microsoft Excel. PTRAP generated two different files for the panicle analysis results i.e. MainTraits.csv and GrainsTraits.csv, respectively. Each image had a result file that describes each grain trait individually in the particular folder. PTRAP measures nine architecture traits and spikelet traits of rice panicle. The panicle architecture traits includedrachis length, rachis diameter, length of primary and secondary branches, number of nodes, number of primary and secondary branches, interval length between both primary and secondary branches measured from panicle skeleton and are presented in Figure 2.

For panicle shape categories, the total rachis length was partitioned into top, middle, bottom gradients and mean profile for each gradient was determined. Then, the mean of primary branches was compared with mean of each gradient. For instance, if primary rachis branches at the lower gradient had a mean length longer than the middle gradient, and the mean length at the middlelonger than that at the top, then the panicle shape was categorized as pyramidal. The inverse of this mean length comparisons was categorizedas a conical shaped panicle. If the mean length of primary rachis branches was longer at the middle gradient, the panicle can be described as diamond-like. Otherwise, panicle shape was categorized as irregular.

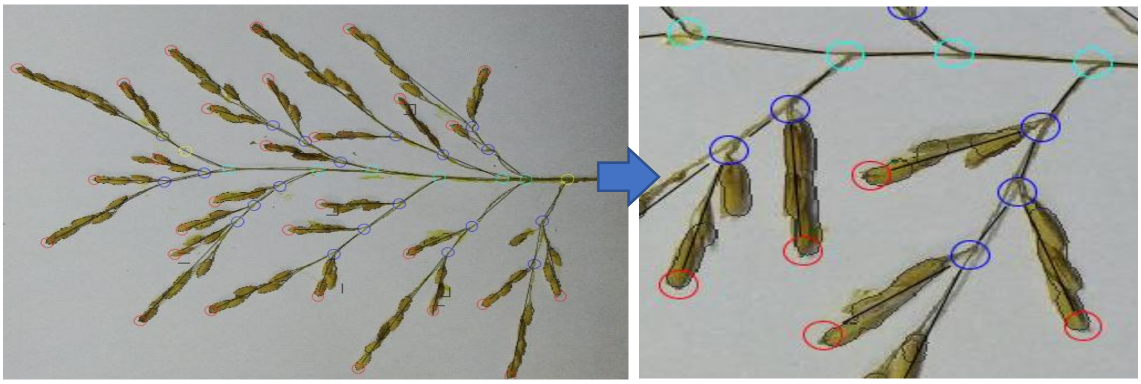

Figure 2: Skeletonized panicle image based on the exact morphology of the panicles. The yellow, sky blue, blue and red circle represented the starting of length of rachis, internodes, nodes and end, respectively.

RESULTS

Panicle architecture traits

The new open access image analysis tool Panicle traits phenotyping (Faroq et al 2013) allowed us to evaluate the phenotypic contribution of panicle architecture to spikelet number per panicle and grain yield. The length of rachis, number of primary branches and secondary branches are the most important panicle architecture traits of rice.

The mean rachis length was between 17.9 cm to 11.37 cm, with a mean of 14.26 cm (Table 1). The highest mean performance of length of rachis was found in genotype PR 126 (17.9 cm). The diameter of rachis varied from 0.39cm to 0.12cm with highest mean performance of GSR 310. Genotype Sampurna had the maximumnumber of primarybranches (16.33), secondary branches (53.33) and number of nodes (15.33). The number of secondary branches ranged from 53.33 to 12.33 and primary branches from 16.33 to 7.67. The maximum length of primary branches (9.72cm) and secondary branches (2.727cm) was noted by the genotype IR 17 L 1341 and IR98853-6-1-3-2, respectively. The analysis of variance showed highly significant difference for of the traits studiedin different rice genotypes whichis presented in Table 1.

Table 1: Mean performance of panicle architecture traits of rice

Values	**Length of rachis (cm)**	**Diameter of Rachis (cm)**	**No. of primary branches**	**Length of primary branches(cm)**	**No. of secondary branches**	**Length of Secondary branch(cm)**	**No. of nodes**
SEM (±)	0.91	0.02	0.71	0.43	2.914	0.11	0.83
LSD 0.05	2.552	0.07	1.99	1.22	8.197	0.30	2.321
CV%	11	17.2	10.70	8.7	17.4	8.5	13.5
Mean	14.26	0.25	11.4	8.59	29	2.1	10.29
F test	***	***	***	***	***	***	***

*** Significant at $p<0.001$, LSD: Least Significant Difference, CV: Coefficient of variation, SEM (±): Standard error of mean

Yield attributing characters

The number of filled grains per panicle being a yield-related trait, determines the grain number per panicle, hence, yield increases in rice. Genotype Sampurna (6.1 t ha^{-1}) and PR126 (5.2 t ha^{-1}) had the highest mean grain yields (Table 2).Plant tillering ability, as well as topological position of tillers affected plant yield potential and tiller contribution to plant yield. The maximum numbers of tillers per m^2 was found in the genotype PR 126(406) followed by genotype Sampurna (402.3) and lowest number of tillers per m^2 was found among genotypes from local landraces Gurdi (209) followed by JethoBudo (224). The grand mean performance of genotypes for 1000-gram weight of rice grains was 24.1 within range of from 37.8 to 14.2. The mean performance of genotypes for total number of grains per panicle is 145.2 with range from 246.7 to 90. The highest mean performance of total number of grains per panicle was found in Sampurna (293.1) followed by Hardinath Saba (241.8) (Table 2). The analysis of variance showed highly significant difference for number of tillers per m^2, total number of grains per panicle, thousand grain weight and grain yield in different rice genotypes which is presented in Table 2.

Table 2. Mean performance of different yield attributing characters

Values	**Number of tillers per m^2**	**Spikelet's number**	**Thousand grain weight**	**Grain yield**
SEM(+)	20.89	14.69	0.5	0.22
LSD 0.05	58.75	41.32	1.4	0.62
CV%	11.4	18.00	3.6	11
Mean	314.8	141.5	24.1	3.5
F-value	***	***	***	***

*** Significant at p<0.001, LSD: Least Significant Difference, CV: Coefficient of variation, SEM (±): Standard error of mean

Correlation among panicle architecture and yield traits

The grain yield was highly significantly (p=0.01) and positively correlated with all the measured architecture traits i.e., number of primary branches (r=0.88), length of primary branches(r=0.89), number of secondary branches (r=0.69), Number of nodes (r=84).The positive correlation of grain yield with panicle architecture traits indicated positive effect of the number of primary and secondary brancheson determining grain yield.

The number of primary branches was significant (p=0.01) and positively correlated with number of secondary branches(r=0.81), whereas length of primary branches was also highly significant and positively correlated with length of primary branches (r=0.50). The primary branch length was significantly (p=0.05) and positively correlated with number of secondary branches (r=51). The correlation among panicle architecture traits and yield traits is present in Table 3.

Table 3. Correlation among panicle architecture traits and yield traits

	LR	**DR**	**NPB**	**LPB**	**NSB**	**LSB**	**NN**	**SN**	**TW**	**GY**
LR	1									
DR	-0.06	1								
NPB	0.881^{**}	0.022	1							
LPB	0.890^{**}	0.064	0.736^{**}	1						
NSB	0.689^{**}	-0.12	0.812^{**}	0.510^{**}	1					
LSB	0.337^{*}	0.879^{**}	0.359^{*}	0.506^{**}	0.101	1				
NN	0.842^{**}	0.2	0.971^{**}	0.713^{**}	0.773^{**}	0.498^{**}	1			
SN	0.800^{**}	-0.35^{*}	0.840^{**}	0.627^{**}	0.889^{**}	-0.04	0.758^{**}	1		
TW	0.726^{**}	-0.33^{*}	0.528^{**}	0.750^{**}	0.373^{**}	0.069	0.411^{**}	0.548^{**}	1	
GY	0.422^{**}	0.664^{**}	0.504^{**}	0.447^{**}	0.393^{**}	0.776^{**}	0.612^{**}	0.216	-0.03	1

(LR= Length of Rachis, DR= Diameter of rachis, NPB=Number of primary branches, LPB= Length of primary branches, NSB= Number of Secondary branches LSB= Length of Secondary branches, NN= Number of Nodes, SN= Spikelet's number, TW= Thousand grain weight, GY=grain yield

** Correlation is significant at the 0.01 level (2-tailed).

* Correlation is significant at the 0.05 level (2-tailed).

Panicle shape categories

On categorizing panicle shape, four different types panicle shapes were recorded from different all 42 genotypes. The panicle shape included irregular, conical, diamond like and pyramid shaped panicle (Figure 3). Out of 42 genotypes, Diamond like shape was found in 16 genotypes followed by irregular shaped panicle in 15 genotypes. The pyramid shaped panicle was found in 10 genotypes and conical shaped panicle was found in 3 genotypes.

(a) (b) (c) (d)

Figure 3. Different panicle shape categories i.e. Irregular (a), upright cone like (b), diamond like(c) and pyramid like (d) obtained from rice genotypes

DISCUSSION

Panicle architecture traits

The number and dimensions of branches among different genotypes (Ikeda et al 2004) and define final panicle architecture. Crowell et al (2016) found the advantage of using different image analysis tool to dissect panicle architecture over manual panicle measurement. Chauhan et al (1989) reported that length of rachis differed significantly among cultivars. In present study, the maximum number of primary branches and secondary branches was found in late rice genotype Sampurna followed by early rice genotype PR 126. Sarwar and Ali (1998) concluded that length of primary branches differed significantly among cultivars. Shafiul et al. (1981) reported variation in number of primary branches in panicle. Greater variation in number of primary and secondary branches (Shafiul et al 1981, Wenging 1981, Wang et al 2009, Sarwar and Ali, 1998) and length of primary branches (Sarwar and Ali 1998) was reported earlier in rice panicle.

Yield attributing traits

Panicle architecture traits such as panicle length, number of primary branches and secondary branches affects yield of rice (Crowell et al 2016). Tillering in rice is an important agronomic trait for panicle number per unit land area as well as grain production. Plant tillering ability as well as topological position of tillers affect plant yield potential and tiller contribution to plant yield (Jaffuel et al 2005). In rice, there was maximum variation in the number of grains per panicle (Chauhan et al 1989, Xu et al 2004, Mei et al 2006). Grain yield is dependent on many yield contributing traits as well as on the environmental influence. The number of filled grains per panicle as being a yield-related trait, determines the grain number per panicle, hence, and yield increases in rice (Mei et al 2006). Chauhan et al (1989) showed that there was maximum difference in the number of grains per panicle in rice.

Correlation among panicle architecture and yield traits

We found in the present study that the grain yield was positively correlated with number of primary and secondary branches and length of primary branches but no significant correlation occurred between spikelet number and length of secondary branches (Table 3). Previously, many studies (Sarwar and Ali 1998, Li et al 2003, Mei et al 2016 and Wang et al 2009) showed correlation between grain yield and others variables related to number of primary branches, the length of primary branches and number of secondary branches.

Interestingly, PTRAP introduces new variables such as number of secondary branches and length of secondary branches. Previous studies (Li et al 2003, Wang et al 2009) showed positive correlation between number of secondary branches and grain yield. In our study, the number of secondary branches wasn't significantly correlated with length of secondary branches (Table 3) Considering the same rank of branching, greater branch number wasn't associated with greater branch length (Rebolledo et al 2016) suggesting two independent ways to increase spikelet's number, either with high number of branches or with long branches and ultimately grain yield. Furthermore, several authors (Xu et al 2004, Mei et al 2006) mentioned the importance of number of secondary branches over primary branches as contributor to grain yield in rice. The grain yield was positively correlated with number of nodes (Table 3). The grain yield can be increased by increasing number of branches (Xu et al 2004, Wang et al 2009) and by increasing the length of branches (Li et al 2003).

Hiroj et al (1990) showed the length of rachis was highly correlated with number of primary and secondary branches, and the length of primary and secondary branches and grain yield were also correlated. Our findings also showed similar trends as Sarwar and Ali (1998) has found in their studies. Yamagishi et al (1992) also reported positive correlation between rachis length and grain yield. This suggested that panicle length isn't a simple trait and it can be affected by several component traits that may have physiologically interacting or may have environmental interaction.

CONCLUSION

The structure or complexity of the panicle in rice varies widely between genotypes. The length and number of primary branches and secondary branches plays a highly important role in determining the architecture of the rice inflorescence. The correlation between grain yield and architecture traits suggested that as panicle length, the number of primary and secondary branches; and the length of the primary branches increased, so did the number of spikelets per panicle and the grain yield. The mosteffective strategy for increasing grain yield is to improve panicle architectural traits.

Acknowledgements

We would like to express our sincere gratitude to the National Rice Research Program and Nepali Army Institute of Agriculture Sciences, Lamjung for valuable support and technical assistance.

Authors' Contributions

All authors listed have made a substantial, direct and intellectual contribution to the experimentation, data recording, and analysis and manuscript preparation.

Conflicts of Interest

The authors have no relevant financial or non-financial interests to disclose.

Publisher's Note

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