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Varietal Evaluation of Promising Spring Rice Genotypes in Bagdula, Pyuthan, Nepal

Evaluación varietal de genotipos prometedores de arroz de primavera en Bagdula, Pyuthan, Nepal

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Abstract

A field experiment was carried out in order to assess the performance (growth, yield, and yield-attributing characteristics) of five different spring rice genotypes. The study was conducted in a farmer's field in Bagdula, Pyuthan, under the supervision of Prime Minister Agriculture Modernization Project (PMAMP), Rice Zone, Pyuthan, from March 2021–July 2021. Five spring rice genotypes, including PR-126, HHZ 25-DT9-Y1-Y1, IR 103575-76-1-1-B, IR 99742:2-11-17-1-9-B, and IR 86515-19-1-2-1-1-1-1, were evaluated in a randomized complete block design (RCBD) with four replications each. Plant growth and yield-attributing parameters were measured, entered into MS-Excel, and analyzed using the R-Studio software. Rice seedlings were raised in a wet nursery bed and transplanted at a spacing of 20 cm x 20 cm (3 seedlings per hill). The highest plant height (82.25 cm) and number of tillers per hill (10.40) were recorded in IR 86515-19-1-2-1-1-1-1, whereas the lowest plant height was observed in genotype IR 99742:2-11-17-1-9-B (64.30 cm). The highest number of effective tillers per square meter (247.125), panicle length (24.43 cm), number of grains per panicle (206.35), thousand grain weight (25.90 g), and grain yield (6.630 $t.ha^{-1}$) were recorded in PR-126, whereas the highest straw yield was recorded in IR 86515-19-1-2-1-1-1-1 (5.78 $t.ha^{-1}$). Similarly, the lowest numbers of effective tillers per square meter (150.73), panicle length (18.51 cm), number of grains per panicle (158.30), and thousand grain weight (22.53 g) were recorded in IR 99742:2-11-17-1-9-B. Thus, based on the yield and other growth parameters, the PR-126 genotype was found to be the most suitable for achieving greater productivity in Bagdula, Pyuthan, Nepal. However, further multilocation yield trials, including assessments of nutrient content, should be conducted for validation.

Key words: *Biological Yield; Effective Tillers; Harvest Index; Panicle length; Straw yield*

Resumen

Se llevó a cabo un experimento de campo para evaluar el comportamiento (crecimiento, rendimiento y características que contribuyen al rendimiento) de cinco genotipos diferentes de arroz de primavera. El estudio se llevó a cabo en el campo de un agricultor en Bagdula, Pyuthan, bajo la supervisión de PMAMP,

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Rice Zone, Pyuthan, desde marzo hasta junio del 2021. Fueron evaluados cinco genotipos de arroz de primavera, incluidos PR-126, HHZ 25-DT9-Y1-Y1, IR 103575-76-1-1-B, IR 99742:2-11-17-1-9-B e IR 86515-19-1-2-1-1-1-1, mediante un diseño de bloques completos al azar (DBCA) con 4 repeticiones cada uno. Se midieron los parámetros que contribuyen al rendimiento y crecimiento de la planta, se ingresaron en MS-Excel y se analizaron usando el software R-Studio. Las plántulas de arroz se sembraron en una cama húmeda en un vivero y se trasplantaron a una distancia de 20 cm x 20 cm (3 plántulas por golpe). La mayor altura de planta (82.25 cm) y número de macollos por golpe (10.40) se registró en IR 86515-19-1-2-1-1-1-1, mientras que la menor altura de planta se registró en el genotipo IR 99742:2 -11-17-1-9-B (64.30 cm). PR- 126, mientras que el mayor rendimiento de paja se registró en IR 86515-19-1-2-1-1-1-1 (5.78 $t.ha^{-1}$). De igual forma, los menores números de macollos efectivos (150.73 por m^2), longitud de panoja (18.51 cm), número de granos por panoja (158.30) y peso de mil granos (22.53 g) se registraron en IR 99742:2-11-17-1- 9-B. Así, con base en el rendimiento y otros parámetros de crecimiento, se encontró que el genotipo PR-126 era el más adecuado para lograr una mayor productividad en Bagdula, Pyuthan, Nepal. Sin embargo, para su validación se deben realizar más ensayos de rendimiento en múltiples ubicaciones, incluidas evaluaciones del contenido de nutrientes.

Palabras llave: *Rendimiento Biológico; Macollos efectivos; índice de cosecha; Longitud de la panícula; Rendimiento de paja*

Introduction

Oryza sativa has been domesticated for millennia, evolving from a wild Asian grass to a cultivated crop that is a staple food for half the world's population (Callaway, 2014). About two-thirds of the global population relies on rice as a staple food. Among them, 90 % live in Asia, while the remaining 10 % are distributed across America, Africa, Australia, and Europe (Chauhan & Johnson, 2011; Dahipahle & Singh, 2018). According to the statistical database of the (Food and Agriculture Organisation of the United Nations [FAOSTAT, 2020]), rice ranks third in the world in terms of cultivated area and second in terms of productivity among the main cereal crops, with 164 192 164 ha, 756 743 722 t, and 4.60 $t.ha^{-1}$, respectively. In Nepal, rice contributes approximately one-fourth of the Gross Domestic Product (GDP), with more than 75 % of the working population engaged in rice farming for at least six months of the year (Tripathi et al., 2019). Rice alone contributes 20.8 % to the agriculture GDP (AGDP) among major crops in Nepal (Development Vision Nepal [DVN], 2018). The total area under cultivation, total production, and productivity of rice in Nepal are 1 458 915 ha, 5 550 878 t, and 3.804 $t.ha^{-1}$, respectively (Ministry of Agriculture and Livestock Development [MoALD, 2020]). There is a diverse habitat for rice cultivation in Nepal, with the Terai region alone covering about 73 % of the total rice-cultivating area (Begho, 2021).

Food insecurity has become a major concern in the current scenario in Nepal, exacerbated by rapid population growth that has increased daily food demand. Despite efforts, Nepal's rice self-sufficiency ratio remains below 100, indicating insufficient domestic production to meet consumption needs (Tripathi et al., 2019). Nepalese farmers, overseeing complex and geographically diverse farming systems, require a diverse portfolio of crop genotypes with agro-morphological and agronomical traits (Joshi et al., 2017). Given the increasing demand for rice due to population growth and the decreasing availability of land and water resources for cultivation, the development and adoption of rice technologies leading to higher yields are critical (Virmani & Kumar, 2004).

Spring rice, characterized by its short duration, resistance to diseases and pests, photoperiod insensitivity, and high yield potential, presents a promising solution. Spring rice constitutes only 8 % of all rice varieties, with main-season rice accounting for the remaining 92 % (Ministry of Agricultural Development [MoAD, 2015]). Spring rice is typically sown in the last week of February to the first week of March and follows the transplanting of 30 to 40-day-old seedlings. Beyond grain yield, farmers also consider maturity days, plant performance, and other yield components (Subedi, 2018). The shorter duration of spring rice allows it to escape abiotic stresses, insects, and diseases, resulting in lower cultivation costs. Additionally, the straw load is lower, offering benefits in terms of efficient straw management. Therefore, cultivating spring rice not only strengthens food security but also provides opportunities for the adoption of multiple cropping systems.

Farmers prefer novel rice varieties with attributes such as high yield, good cooking quality, early maturity, and good drying ability, driven by increased demand and resource constraints (Joshi et al., 1995). Moreover, as most farmers in Nepal rely on rain-fed farming systems, the development of better rice genotypes for rain-fed environments is crucial, despite being often overlooked or rarely successful (Adhikari et al., 2018). Varietal evaluation and participatory selection are crucial steps to improve food security and address malnutrition in Nepal (Subedi, 2018). Conducting varietal trials in specific locations is essential to recommend suitable genotypes with desired agro-morphological and agronomical traits (Tiwari et al., 2019). Farmers, facing challenges in meeting customer demands for rice due to a lack of knowledge about variety suitability, benefit from experimental studies evaluating the appropriateness of promising locally available rice genotypes. Given the varying adaptability of different locations, it is essential to conduct multi-location trials to identify the best genotype for each specific area. Consequently, this experiment was undertaken to determine suitable genotypes for Pyuthan during the spring season, aiming to enhance production and meet the food requirements of the region.

Materials and methodology

Experimental site

The research was conducted at a farmer's field in Bagdula, situated in the warm temperate zone of Nepal, during the months of early March to late June 2021. The study site was located within the command area of Rice Zone under the Prime Minister Agriculture Modernization Project (PMAMP). This zone, located in Pyuthan Khalanga Municipality, is approximately 500 meters above the Jhimrukh Khola floodplain and about 15 kilometers north of the Mahabharat range in the middle hills. The geographical coordinates of the site are 28°06'N latitude and 82°52'E longitude, covering a total area of 128.96 km^2. The site is characterized by a low-land area dominated by alluvial clay soil at an elevation of about 1038 m above sea level.

Treatment details and cultural activities in the experimental field

The major experimental materials used in the research were five varieties of rice: PR 126, HHZ 25-DT9-Y1-Y1, IR 103575-76-1-1-B, IR 86515-19-1-2-1-1-1-1, and IR 99742:2-11-17-1-9-B. Urea (1.5 kg), di-ammonium phosphate (DAP) (0.72 kg), and muriate of potash (MOP) (0.48 kg) were used as per the recommended dose suggested by Agriculture Information and Training Center (AITC, 2019) in 120 m^2. All relevant aspects were meticulously recorded, including germination duration, transplantation days, number of tillers per hill, maturity duration, disease and insect pest infection, and yield.

The nursery bed was prepared with a rotavator and leveled. MOP and DAP, along with farmyard manure (FYM), were applied at the rates of 0.5 kg, 0.7 kg, and 3 kg, respectively, in the nursery bed (6 m^2). Seeds were sown after lightly watering the nursery bed in the evening, with urea applied 14 days after sowing (DAS) to promote seedling growth. The seedlings were ready within 30 days.

For the main field, measuring 14.5 m by 13 m and divided into 20 plots of 2 m x 3 m each, extensive plowing and tilling were conducted three times, followed by puddling. Nearby river water served as the main source of irrigation. NPK was applied at a rate of 0.072 kg, 0.024 kg, and 0.024 kg, respectively, in each plot. Seedlings were manually transplanted in lines 20 cm x 20 cm apart. Moreover, due to increased weed infestation in the spring rice, pre-emergence weedicides were applied, and manual weeding was performed 25 days after transplanting (DAT) and 45 DAT.

Design of the experiment

The experiment was conducted in a one-factor randomized complete block design (RCBD) with five treatments representing different varieties, and each treatment was replicated four times. The total area allocated for the experimental field was 188.5 m^2, arranged in a rectangular layout measuring 14.5 m^2 x 13 m^2. A 50 cm margin was maintained between replications and along the outer borders of the field. The space between individual plots was set at 0.5 m, both between rows and within rows. In total, there were 20 plots in the experimental field, each separated by a distance of 0.5 m. The net production area, excluding margins and the border, was 120 m^2. The layout further included a 0.5 m space between different replication blocks. Each individual plot measured 2 m × 3 m, resulting in a total plot area of 6 m^2. Within each plot, there were 10 rows and 15 columns (Figure 1).

Parameters observed

Morphological observations

Plant height (cm)

Within each plot, a systematic sampling approach was employed, selecting five random hills. The measurement of plant height commenced 30 days after transplanting (DAT) and continued at 15-day intervals until 90 DAT. Plant height was measured as the length from the base of the plant to the tip of the longest leaf, or panicle.

Number of tillers per hill

Tillers per plant were recorded by randomly selecting five hills per plot, excluding those along

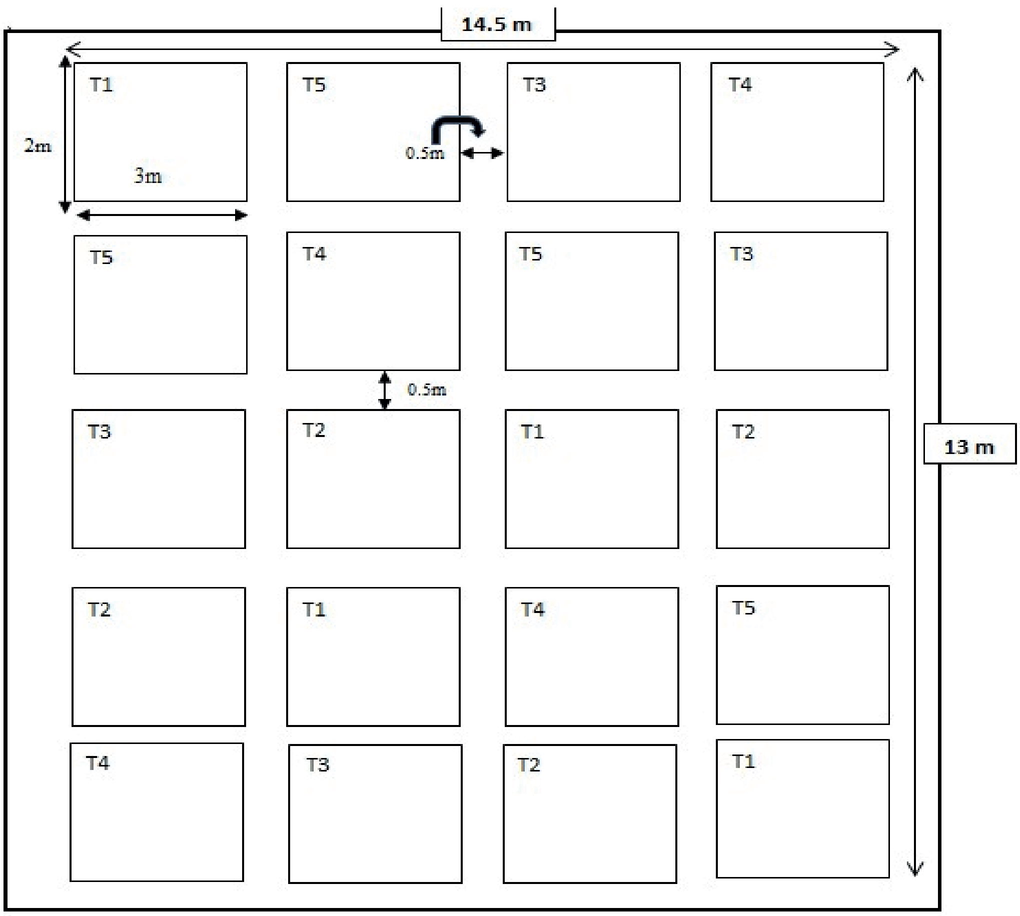

Figure 1. Layout of the experimental field.

the border, and counting the number of tillers per hill. The average values were then calculated to obtain the tillers per hill. The data were collected at 30, 45, 60, 75, and 90 days after transplanting (DAT).

Yield-attributing characters

Number of effective tillers per square meter

The number of effective tillers per square meter was determined by assessing the tagged plants just before harvesting the crop. Effective tillers were identified as those with filled grains, and their count was recorded.

Panicle Length (cm)

Panicle length was measured by randomly selecting five panicles from each hill, and the average value was recorded. The measurement, taken in centimeters, extended from the base of the rachis to the tip of the panicle.

Number of grains per panicle

The total number of grains per panicle was manually counted from panicles chosen at random from five hills in each plot. The mean of the counts from five randomly selected panicles within each plot was then calculated to determine the average number of grains per panicle.

Thousand grain weight (g)

A thousand grains were randomly selected from the yield of each plot and weighed using a portable automatic electronic balance. The weights were then adjusted to 14 % moisture using a specific formula. The thousand-grain weight was expressed in grams (g).

Number of days until maturity

The duration from seed sowing to complete maturity was recorded to determine the number of days required for maturity.

Yield

After winnowing and cleaning, the grain yields from each plot were measured using a double-pan balance. These weights were then converted to grain yield in quintals per hectare (which is equivalent to 100 kg/ha) by applying the necessary multiplication factors.

Statistical data analysis

All the recorded data were systematically organized treatment-wise across four replications, considering various observed parameters. The experimental data was analyzed using R Studio with R-Stat Software of 3.6.1th edition, and treatment means were separated using Duncan’s Multiple Range Test (DMRT) at a 5 % level of significance. An analysis of variance (ANOVA) was used to test differences among the factors (Gomez & Gomez, 1984).

Result and discussions

Significant variations were observed among the assessed rice genotypes for all yields and their related traits (Tables 1, 2, 3, 4, and 5). Tahir et al. (2002) reported similar results, emphasizing substantial variation among different traits and suggesting that these attributes were under the control of genotypic differences among the evaluated genotypes.

Growth Parameters

Plant height

The observation of plant height at various dates is presented in Table 1. At 30 days after transplanting (DAT), the highest plant height was recorded in IR 86515-19-1-2-1-1-1-1 (45.15 cm), followed by PR-126 (36.26 cm), HHZ 25-DT9-Y1-Y1 (27.9cm), IR 99742:2-11-17-1-9-B (27.25cm), and IR 103575-76-1-1-B (26.875 cm), respectively. Throughout all growth stages, IR 86515-19-1-2-1-1-1-1 consistently achieved the highest plant height, followed by PR-126. No statistical differences were observed among HHZ 25-DT9-Y1-Y1, IR 103575-76-1-1-B, and IR 99742:2-11-17-1-9-B at all the growth stages considered. This variation in plant height among rice varieties is likely attributable to the varietal characteristics, as plant height is primarily influenced by varietal traits rather than other factors (Adhikari et al., 2018; Rahman et al., 2018). The observed differences in plant

Table 1. Plant height of different rice genotypes at various days after transplantation, evaluated at Bagdula, Pyuthan, 2021

Genotypes	Plant Height (cm)				
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
PR-126	36.26[b]	41.10[b]	52.25[b]	63.45[b]	76.20[b]
HHZ 25-DT9-Y1-Y1	27.9[c]	32.80[c]	43.35[c]	55.05[c]	65.20[c]
IR 103575-76-1-1-B	26.875[c]	32.10[c]	42.75[c]	53.05[c]	64.30[c]
IR 86515-19-1-2-1-1-1-1	45.15[a]	49.80[a]	60.4[a]	71.40[a]	82.25[a]
IR 99742:2-11-17-1-9-B	27.25[c]	33.05[c]	43.925[c]	55.05[c]	67.10[c]
SEM (±)	1.70	1.63	1.64	1.66	1.71
$LSD_{0.05}$	3.44	3.45	3.454	4.04	4.46
CV %	6.829	5.93	4.62	4.400	4.083
F Value	***	***	***	***	***
Grand Mean	**32.68**	**37.77**	**48.53**	**59.6**	**71.01**

DAT: Days after transplantation, CV: Coefficient of Variation, LSD: Least Significant Difference, SEM (±): Standard Error of Mean. Letters a, b, c, d represent the ranking of treatment according to Duncan Multiple Range Test (DMRT) at 0.05 level of significance, *represents significance at 5 % level, ** represents significance at 1 % level, *** represents significance at 0.1 % level.

height could also be attributed to the varietal characteristics and were found to vary due to differences in the climatic requirements of each variety (Pervaiz et al., 2010).

Number of tillers per hill

The number of tillers was found to be non-significant at every growth stage as shown in Figure 2.

The highest number of tillers per hill at 30, 45, 75, and 90 DAT was observed in IR 86515-19-1-2-1-1-1-1, followed by IR 103575-76-1-1-B, IR 99742:2-11-17-1-9-B, HHZ 25-DT9-Y1-Y1, and PR-126, respectively. However, at 60 DAT, variety IR 103575-76-1-1-B exhibited a higher number of tillers. At harvest, IR 86515-19-1-2-1-1-1 had the most tillers, while PR-126 had the fewest. Except for the number of tillers, Poudel et al. (2014) also discovered significant

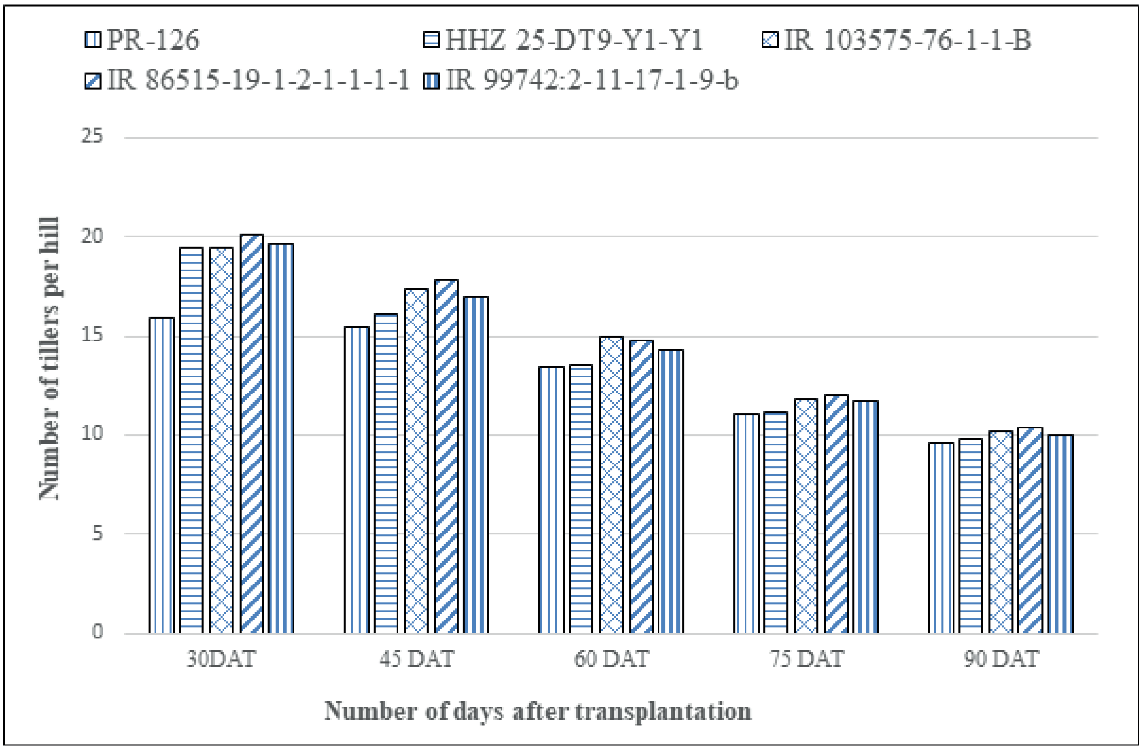

Figure 2. Number of tillers per hill of different genotypes of spring rice studied at different days after transplanting (DAT).

variations among several pipeline genotypes of rice, aligning with our findings (Table 2).

Yield attributing characters

Number of effective tillers per square meter

The number of effective tillers per square meter was found to be highest in PR-126 (247.13), followed by IR 86515-19-1-2-1-1-1-1 (208.91). Conversely, the lowest number of effective tillers per square meter was observed with IR 99742:2-11-17-1-9-B genotypes (150.73), followed by HHZ 25-DT9-Y1-Y1 (174.55), and IR 103575-76-1-1-B (167.73). The variation in the number of effective tillers per plant can be attributed to differences in the genetic makeup of the variety. This finding aligns with the results reported by Ramasamy et al. (1987), who similarly observed that the number of effective tillers varied due to varietal differences. The number of tillers per square meter shows variation across varieties, depending on their ability to compete with other plants and weeds. This observation aligns with the findings of several previous studies, such as those conducted by Choi et al. (2000), Dutta et al. (2002), Hussain et al. (2014) and Ren et al. (2021), which also emphasized the significance of the number of tillers per square meter as a critical varietal characteristic in evaluating rice genotypes (Table 3).

Length of panicle (cm)

The study showed significant variations in panicle length among the studied genotypes. The highest panicle length was observed in PR-126 (24.43 cm), which is statistically similar to IR 86515-19-1-2-1-1-1-1 (23.94 cm) and followed by IR 103575-76-1-1-B (20.00 cm), HHZ 25-DT9-

Table 2. Tiller count per hill for different rice genotypes at various days after transplantation, evaluated at Bagdula, Pyuthan, 2021

Genotypes	Number of tillers				
	30 DAT	45DAT	60DAT	75DAT	90DAT
PR-126	15.9	15.45	13.45	11.0	9.65
HHZ 25-DT9-Y1-Y1	19.4	16.10	13.50	11.1	9.80
IR 103575-76-1-1-B	19.4	17.30	14.95	11.8	10.20
IR 86515-19-1-2-1-1-1-1	20.1	17.80	14.75	12.0	10.40
IR 99742:2-11-17-1-9-B	19.6[a]	17.00	14.25	11.7	9.95
SEM (±)	0.651	0.400	0.299	0.267	0.161
$LSD_{0.05}$	NS	NS	NS	NS	NS
CV %	14.199	9.232	5.801	7.193	6.973
F Value	1.590	1.499	2.834	1.147	0.750
Grand Mean	**18.88**	**16.73**	**14.18**	**11.52**	**10.00**

DAT: Days after transplantation, CV: Coefficient of Variation, NS: Non-significant, LSD: Least Significant Difference, SEM (±): Standard Error of Mean. Letters a, b, c, d represent the ranking of treatment according to Duncan Multiple Range Test (DMRT) at 0.05 level of significance.

Table 3. Effect of evaluated rice genotypes on various yield-attributing characters at Bagdula, Pyuthan, 2021

Genotypes	Number of effective tillers *per square meter*	Length of panicle (cm)	Number of grains per panicle	Thousand grain weight (gm)
PR-126	247.13[a]	24.43[a]	206.35[a]	25.90[a]
HHZ 25-DT9-Y1-Y1	174.55[c]	19.82[b]	165.20[c]	23.99[b]
IR 103575-76-1-1-B	167.73[c]	20.00[b]	177.40[b]	23.20[c]
IR 86515-19-1-2-1-1-1-1	208.91[b]	23.94[a]	200.95[b]	25.49[a]
IR 99742:2-11-17-1-9-B	150.73[d]	18.51[c]	158.30[c]	22.53[d]
SEM (±)	8.28	0.55	4.543	0.30
$LSD_{0.05}$	15.07	0.58	9.718	0.48
CV %	5.15	1.77	3.472	1.29
F Value	***	***	***	***
Grand Mean	**189.81**	**21.34**	**181.64**	**24.22**

DAT: Days after transplantation, CV: Coefficient of Variation, LSD: Least Significant Difference, SEM (±): Standard Error of Mean. Letters a, b, c, d represent the ranking of treatment according to Duncan Multiple Range Test (DMRT) at 0.05 level of significance, *represents significance at 5 % level, ** represents significance at 1 % level, *** represents significance at 0.1 %.

Y1-Y1 (19.82 cm), and genotypes IR 99742:2-11-17-1-9-B had the lowest panicle length (18.511 cm), respectively (Table 3). In line with the findings of Akondo et al. (2020), our study highlights the significance of panicle length as a crucial varietal character in rice. This aligns with the broader understanding that different rice varieties exhibit distinct panicle lengths, a factor that can have substantial implications for crop management and productivity. Hussain et al. (2014) also reported panicle length variation in rice as a varietal character. Similarly, Sharma (2002) and Yang et al. (2007) observed differences in panicle length among different tested genotypes as varietal characters. In a field experiment with various Boro rice varieties, Roy et al. (2014) also found a significant difference in panicle length as a varietal character.

Number of grains per panicle

Rice varieties were found to significantly influence grain yields per panicle. The highest number of grains per panicle were recorded with PR-126 (206.35), followed by IR 86515-19-1-2-1-1-1-1 (200.95), and IR 103575-76-1-1-B (177.40), as shown in Table 3. Conversely, the lowest grain per panicle was obtained with IR 99742:2-11-17-1-9-B (158.30) and HHZ 25-DT9-Y1-Y1 (165.20), respectively. This observation aligns with the findings of Hussain et al. (2014), who also reported differences in the number of grains per panicle as varietal characteristics of rice.

Thousand grain weight (g)

Thousand grain weight (TGW) was found to be highly influenced by rice varieties (p > 0.001). PR-126 resulted in the highest thousand grain weight (25.90 g), which was statistically similar to IR 86515-19-1-2-1-1-1-1-1 (25.49 g), followed by HHZ 25-DT9-Y1-Y1 (23.99 g), IR 103575-76-1-1-B (23.20 g), and genotypes IR 99742:2-11-17-1-9-B (22.53 g) (Table 3). This observation aligns with the findings of Khatun et al. (2020) and Akondo et al. (2020), who, from their experiment on different rice genotypes, observed variance in thousand grain weight among different rice genotypes as a varietal character.

Phonological parameter

Days to Maturity

Days to maturity were found to be significantly influenced by rice varieties at p > 0.01. Among different genotypes, PR-126 had the longest days to maturity (127.85 days), which was statistically similar to genotypes HHZ 25-DT9-Y1-Y1 (126.95 days) and IR 86515-19-1-2-1-1-1-1 (123.35 days). Following these, IR 99742:2-11-17-1-9-B recorded an average of 120 days, and IR 103575-76-1-1-B had 116.85 days to maturity, respectively. These results indicate that IR 103575-76-1-1-B is an early-maturing genotype, while PR-126 is a late-maturing one. Ashrafuzzaman et al. (2009) also observed a significant difference in days to maturity among different aromatic rice varieties as a varietal character of rice, consistent with our findings (Table 4).

Table 4. Effect of evaluated rice genotypes on days to maturity at Bagdula, Pyuthan, 2021

Genotypes	Days to maturity
PR-126	127.85^{a}
HHZ 25-DT9-Y1-Y1	126.95^{a}
IR 103575-76-1-1-B	116.85^{c}
IR 86515-19-1-2-1-1-1-1	123.35^{ab}
IR 99742:2-11-17-1-9-B	120.00^{bc}
SEM (±)	1.154
$LSD_{0.05}$	4.97
CV %	2.624
F-Value	**
Grand Mean	**123**

Coefficient of Variation, NS: Non-significant, LSD: Least Significant Difference, SEM (±): Standard Error of Mean. Letters a, b, c, d represent the ranking of treatment according to Duncan Multiple Range Test (DMRT) at 0.05 level of significance, *represents significance at 5 % level, ** represents significance at 1 % level, *** represents significance at 0.1 %.

Measurement of yield

Grain Yield

Statistically, the highest grain yield was recorded with PR-126 (6.63 $t.ha^{-1}$), followed by IR 86515-19-1-2-1-1-1-1 (5.432 $t.ha^{-1}$), IR 103575-76-1-1-B (4.55 $t.ha^{-1}$), HHZ 25-DT9-Y1-Y1 (3.15 $t.ha^{-1}$), and genotype IR 99742-2-11-17-1-9-B with the lowest grain yield (2.84 $t.ha^{-1}$). PR-126 resulted in the highest number of effective tillers and panicle length, contributing to its superior grain yield. This variation in grain yield may be attributed to genetic and environmental factors and their interactions (Mhapatra, 1993). Adhikari et al. (2015) also observed a significant variation in grain yield among different rice genotypes, a finding that aligns with the results supported by Khatun et al. (2020). Patel et al. (2019) emphasized the pivotal role of sowing dates in achieving optimum rice yield. Shrestha et al. (2020) similarly concluded that differences in grain yield among various varieties were influenced by varietal characteristics and interactions between their genotype and environment.

Straw yield

The highest straw yield was recorded with IR 86515-19-1-2-1-1-1-1 (5.78 $t.ha^{-1}$), which was similar to IR 103575-76-1-1-B (5.67 $t.ha^{-1}$) and HHZ 25-DT9-Y1-Y1 (5.30 $t.ha^{-1}$), followed by PR-126 (4.40 $t.ha^{-1}$) and genotypes IR 99742:2-11-17-1-9-B (3.19 $t.ha^{-1}$). Subudhi et al. (2020) also observed differences in the straw yield of different rice varieties as a result of varietal characteristics.

Biological yield

The highest biological yield was recorded with PR-126 (11.04 $t.ha^{-1}$), while the lowest was numerically recorded with IR 99742:2-11-17-1-9-B (6.04 $t.ha^{-1}$). The lack of a genotype effect on biological yield could be attributed to similarities in morphological aspects of vegetative growth among aerobic rice cultivars, such as time to heading initiation and grain heading duration. For instance, biomass accumulation in the form of stem biomass reached its peak at heading and declined during grain filling, which finally affected yield output. Islam et al. (2013) also observed differences in total biological yield among different rice varieties in their experiment, highlighting the varietal character of different rice cultivars.

Harvest index

The harvest index of PR-126 was found to be superior (60.14 %), followed by IR 86515-19-1-2-1-1-1-1 (48.42 %), IR 99742:2-11-17-1-9-B (47.24 %), IR103575-76-1-1-B (44.55 %), and HHZ 25-DT9-Y1-Y1 (37.4 %) (Table 5).

Conclusion

In conclusion, considering all parameters, PR-126 emerges as the most suitable genotype for spring rice in Bagdula, Pyuthan, Nepal. It is followed by IR 86515-19-1-2-1-1-1-1 and IR 103575-76-1-1-B genotypes. Therefore, it is advisable to cultivate PR-126, IR 86515-19-1-2-1-1-1-1, and IR 103575-76-1-1-B in Bagdula and similar agro-ecological conditions. Moreover, it is essential to acknowledge the research constraints of this particular experiment, and further consideration should be given to conducting numerous multi-location yield trials with these genotypes in the future. This will help establish their unbiased geographic performances and determine their

Table 5. Effect of evaluated rice genotypes on different yield parameters at Bagdula, Pyuthan, 2021

Genotypes	Yield			
	Grain Yield ($t.ha^{-1}$)	Straw Yield ($t.ha^{-1}$)	Biological yield ($t.ha^{-1}$)	Harvest Index (%)
PR-126	6.630^{a}	4.40^{b}	11.04	60.14^{a}
HHZ25-DT9-Y1-Y1	3.155^{d}	5.30^{a}	8.455	37.4^{c}
IR103575-76-1-1-B	4.555^{c}	5.67^{a}	10.225	44.55^{bc}
IR86515-19-1-2-1-1-1-1	5.432^{b}	5.78^{a}	11.212	48.42^{b}
IR99742:2-11-17-1-9-B	2.847^{d}	3.19^{c}	6.038	47.24^{b}
SEM (±)	0.327	0.56	1.03	1.02
$LSD_{0.05}$	0.377	0.54	NS	5.33
CV %	5.414	14.34	8.6	6.04
F value	***	*	NS	**
Grand Mean	**4.524**	**4.86**	**9.4**	**47.55**

Coefficient of Variation, NS: Non-significant, LSD: Least Significant Difference, SEM (±): Standard Error of Mean. Letters a, b, c, d represent the ranking of treatment according to Duncan Multiple Range Test (DMRT) at 0.05 level of significance, *represents significance at 5 % level, ** represents significance at 1 % level, *** represents significance at 0.1 %.

appropriateness for cultivation in farmers' fields.

Author contributions

Elaboration and execution, development of methodology, conception and design; editing of articles and supervision of the study have involved all authors.

Conflicts of Interest

Signing authors of this research work declare that they have no potential conflict of personal or economic interest with other people or organizations that could unduly influence this manuscript.

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