



Evaluation of Early Rice (*Oryza sativa* L.) Genotypes for Yield and Yield Components in Madhesh Province of Nepal

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ABSTRACT

The research was laid out in a randomized complete block design (RCBD) with two replications and twenty-four genotypes (two check varieties Hardinath-1 and Hardinath-3) in College of Natural Resource Management, Bardibas, Mahottari, Nepal. Geographically, it is situated at an altitude of 26.9431097° North, longitude 85.8910975° East; approximately 160 m asl. The transplanting distance between the rice plants was 20cmx20cm with plant plot size: 4.5 m² (3.0mx1.5m) and the spacing between two consecutive plots were maintained at 0.5 m. Key agronomic traits of growth, yield and yield components were recorded. Data was entered and tabulated using MS-Excel and analyzed using Gen-Stat ver. 2015. Mean separation was done by DMRT at 5 % level of significance. The results revealed that the highest yield (6.87 t/ha) was achieved by the genotype IR-18-A-2294, followed by IR-19-A-5000 (6.51 t/ha), NS-314 (6.24 t/ha), NS-278 (6.26 t/ha), Hardinath-3 (6.24 t/ha) and least by NS-232 (3.91 t/ha). Hardinath-1 (86.5 DAT) had early maturity followed by NS-201 (91 DAT), Hardinath-3 (94 DAT), IR-19-A-5000 (96 DAT), and IR-132084-B-1191-1-2-B-12 (96 DAT) whereas late maturity was observed in NS-313 (104 DAT) and yields were 5.24 t/ha, 5.14 t/ha, 6.24 t/ha, 6.51 t/ha, 4.87 t/ha, and 5.98 t/ha respectively. In terms of earliness and yield potential, IR-18-A-2294 and IR-19-A-5000 were found to be superior, indicating their potential for further advancement and recommendation in rice production systems and suggesting their usefulness for farmers in areas where early maturity along with high production is desirable to fit into multiple cropping systems or to avoid climatic risks such as terminal drought or flooding. These results provide valuable insights into the selection and development of rice varieties adapted to the specific agro-ecological conditions of Nepal.

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Introduction

Rice (*Oryza sativa* L., $2n=2x=24$) is essential to nutrition, livelihoods, and cultural activities, supporting more than half of the world's population and contributing significantly to global food security (Fukagawa & Ziska, 2019). Rice is the major staple food crop in Nepal, ranking first in both production and area cultivated (AITC, 2024; MoALD, 2024). Rice supplies nearly 20.0 % of the economic to its agricultural GDP, and 7.0 % of its overall GDP comes from rice, making it a vital crop in Nepal (Devkota et al., 2018). It is cultivated in an area of 1,447,789 ha, yielding an average of 3.7 t/ha, where Mahottari District shares 3.00 % production of the national production, located in Terai. It is one of the productive locations for high rice production due to its suitable agro-climatic conditions (AITC, 2024; MoALD, 2024).

Rice production in Nepal is often limited by inconsistent yields caused by water scarcity, poor soil conditions, and susceptibility to insect pests. A weak seed production and distribution system in Nepal limits farmers' access to quality rice seeds (Prasad et al., 2017). Insufficient research on early rice compatibility with farmer needs. This has made it necessary to concentrate on increasing productivity through agronomic development and genetic enhancement. Developing high-yielding, early-maturing rice varieties is necessary to address Nepal's food security concerns, particularly in the Terai region, which serves as the country's agricultural hub (Dhungana et al., 2022). The prevention of terminal drought and the ability to plant successive crops on schedule are two major advantages of early-maturing genotypes for cropping intensity optimization. Sustainable production is hampered by the lack of cultivars appropriate for

Nepal's agro ecological conditions (B. B. Adhikari et al., 2018). Till now, only three early varieties were released by NARC (Nepal Agriculture Research Council) i.e., Hardinath hybrid-3 (F1) in 2020, Hardinath-4 in 2022, and Ghaiya-3 in 2022 (AITC, 2024). The annual average rice productivity of Nepal is relatively low (3.78 t/ha in 2023) as compared to other neighboring countries. Grain yield is a complicated trait impacted by genotype-environment interactions, and finding improved genotypes for it requires a thorough assessment of yield-related traits (Liang et al., 2015).

The environment has a significant impact on rice grain production, which is a quantitative polygenic characteristic. When selecting germplasm based on the genetic variation available, it is important to consider the extent and significance of the relationship between yield and its components (Aditya & Bhartiya, 2013; B. N. Adhikari et al., 2018). The success of breeding programs depends on the population's level of genetic variability as well as the heritability of the targeted features. With new plant type attributes linked to crop productivity, several morphological features are crucial for increased rice production. The phenological traits of rice are also linked to the yield potential of the many rice varieties to choose the best variations for further rice breeding (Aditya & Bhartiya, 2013). A thousand rice varieties that are well suited to the regional conditions have been developed through selection from the cultivated material many years ago under biotic and abiotic stress conditions, several of those rice varieties have higher yield potential and superior quality traits (Amirova et al., 2024). Considering the above challenges, this study was undertaken to address the gap by identifying high-yielding and early-maturing rice genotypes suitable for the Terai region and by evaluating multiple genotypes for their yield potential and associated yield attributes.

Materials and Methods

Description of the Experimental Site

The study was conducted during the 2024 monsoon season (June-October) at College of Natural Resources Management, Bardibas, Mahottari District of Madhesh Province, which is situated in the inner Terai of Nepal. Geographically, it is situated at an altitude 26.9431097°N and , longitude 85.8910975°E; approximately 160 m above sea level. The region receives an average annual rainfall of (1200-1400) mm. The soil texture was found to be silty clay loam (alluvial deposits), pH was slightly acidic (5.6-6.2) and nutrient status was low organic carbon (0.8-1.2)

%, moderate nitrogen (0.10-0.15) %, deficient available phosphorus (<20) kg ha⁻¹, and high K content.

Experimental Design and Field Trial Management

The research was laid out in randomized complete block design (RCBD) with two replications and 24 genotypes including 2 check varieties; Hardinath-1 and Hardinath-3 at College of Natural Resource Management, Bardibas, Mahottari. The transplanting distance between the rice plants was 20cmx20cm with a plot size: 4.5 m² (3.0mx1.5m) and the spacing between 2 consecutive plots were maintained at 0.5 m. The land preparation of the experimental plots was carried out by one deep ploughing using MB plough and 2-3 harrowing and seedbed was prepared by dry method (Cheng, 2018). The nursery seedlings of 21 days old were transplanted in June 2024.

The plot size was 4.5 m². The fertilizers were applied as urea, diammonium phosphate (DAP), and muriate of potash (MOP) at a rate of 120:40:40 kg N:P₂O₅:K₂O [nitrogen (N), phosphorus (P₂O₅), and potassium (K₂O)] ha⁻¹ (AITC, 2024). The full doses of P₂O₅ and K₂O, along with half of the dose of N, were applied as the basal dose, and the remaining 50% of the nitrogenous fertilizer was applied in 2 split doses. The first one was used during tillering, and the second one was used after panicle initiation. Every other intercultural operation and mandatory practice package was completed as needed and in compliance with the recommended practices.

Treatments

The experiment included twenty-two rice genotypes obtained from the National Rice Research Program in Hardinath, Dhanusha, Nepal, which were used as treatments. The rice genotypes were obtained from the National Rice Research Program, Hardinath, Dhanusha, Nepal. The list of rice genotypes used in this experiment is given in Table 1.

Data Collection and Statistical analysis

The different yield and yield attributing parameters were recorded during the experiment. Such as; Heading Stage(80%), days to maturity, plant height (cm), test weight (g), filled grain per panicle (number of grains), sterility percentage (%), biomass yield (t/ha), and harvest index (%) were recorded.

The methods of data collection of various above mentioned parameters were discussed below.

- **Heading Stage (80%):** days of 80% heading stage were recorded by visual observation.

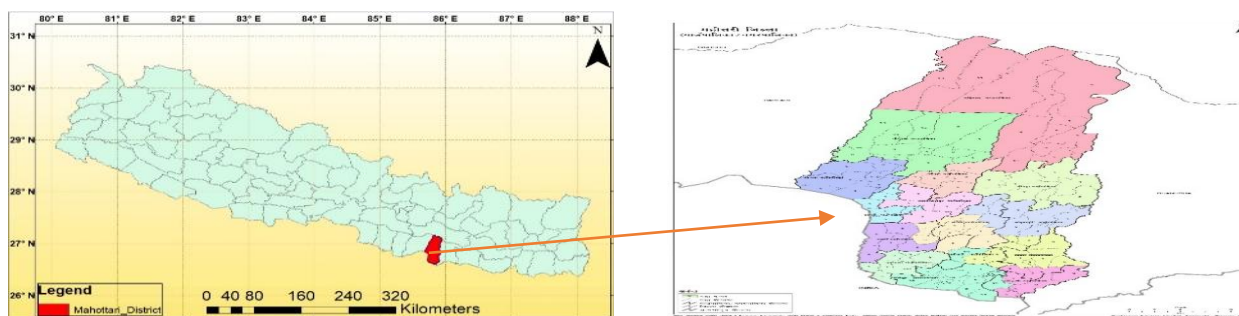


Figure 1. A map showing the experimental site

Table 1. List of 24 rice genotypes used in the experiment at CNRM, Bardibas, Mahottari, Nepal (2024).

Treatments	Rice Genotypes	Source
T1	IR-127153-2-3-5-1-B-B	IRRI
T2	Hardinath-3*	NRRP
T3	IR-12C170	IRRI
T4	IR-97205-73-1-2-2	IRRI
T5	IR-116713-B-B-34-3-B-B	IRRI
T6	NS-232	IRRI
T7	NS-314	IRRI
T8	IR-18-A-2294	IRRI
T9	NS-278	IRRI
T10	NS-224	IRRI
T11	IR-19-A-4494	IRRI
T12	IR-19-A-5000	IRRI
T13	NS-188	IRRI
T14	NS-313	IRRI
T15	Hardinath-1*	NRRP
T16	NS-201	IRRI
T17	IR-19-A-3197	IRRI
T18	IR-132084-B-1191-1-3-B-5	IRRI
T19	IR-132084-B-628-1-1-B-9	IRRI
T20	IR-13C121	IRRI
T21	IR-132084-B-1191-1-2-B-12	IRRI
T22	IR-132T799	IRRI
T23	IR-127152-1-6-7-1-B-B	IRRI
T24	NR-2312-59-1-3-1-1	NRRP

Note: * means the standard check variety

- *Days to Maturity*: total days required to attain full maturity of crop were recorded.
- *Plant height (cm)*: 5 representative plants height were measured using rural and their average were interpreted and plotted in excel file for further analysis.
- *Test weight (g)*: It is the weight of 1000 grains in gram.
- *Filled grain per panicle (number of grains)*: 5 random mature panicles were harvested from each experimental unit and filled grains per panicle were recorded and their average was taken as final representative data.
- $SP\% = \frac{\text{Total Unfilled Grains per panicle}}{\text{Total Grains per panicle}} \times 100$
SP: Sterility percentage (%)

- *Biomass yield (t/ha)*: total yield i.e., grain yield + straw yield during harvest.

- $\text{Harvest index (\%)} = \frac{\text{Grain yield at 12\% moisture}}{\text{Biomass Yield}} \times 100$

The grain yield at 12% moisture was calculated using the formula adopted (Shrestha et al., 2021). Data was entered and tabulated using MS-Excel and analyzed using Gen-stat ver. 2015. Key agronomic traits of growth, yield and yield components were processed for Analysis of Variance (ANOVA). To evaluate the effect of treatments on rice genotypes, we applied Duncan's Multiple Range Test (DMRT) at the 5 % significance level.

Results

Phenological characteristics

Heading Stage (80%)

The heading stage was highly varied with the genotypes at 1% level of significance (Table 2). The result indicate that IR-132084-B-1191-1-3-B-5 and IR-19-A-3197 were

found delayed in heading stage in 71 (DAT) and followed by NS-224, and NS-313 in 70.5 (DAT). Hardinath-1 and NS-201 showed earliness in panicle emergence in 55 (DAT) and 58 (DAT) respectively.

Plant Height (cm)

The plant height was significantly influenced by genotypic variation at 1% level of significance. (Table. 2). IR-18-A-2294 had the highest plant height of 147.7 cm followed by NS-313 (141.6 cm). The shortest plant height was observed in IR-13C121 (94 cm) followed by IR-19-A-5000 (108.1 cm).

Days to maturity

The days to maturity of the examined rice genotypes varied significantly at 1% level of significance (Table 2). The results indicated that NS-313 had the highest number of days to maturity 104 (DAT), followed by NS-188 in 102 (DAT). The Hardinath-1 genotype was shown earlier in maturity (86 DAT), followed by NS-201 (91 DAT).

Yield and Yield Components

1000 grain weight (g)

Difference in 1000-grain weight was significant for various genotypes (Table 3). Thousand-grain weight of tested ranged from (20.75g-29.24 g). IR-18-A-2294 showed the highest grain weight of 29.24g, followed by IR-127153-2-3-5-1-B-B (28.57 g). And lowest was shown in NR-2312-59-1-3-1-1 (20.75 g), followed by Hardinath-1 (21.24 g).

Panicle length (cm)

The panicle length was observed significant difference in the panicle length among the observed genotypes (Table 3). Longest panicle length was observed on NS-313 (30.19 cm), followed by IR-18-A-2294 (30.01 cm) and the shortest panicle length was observed on NR-2312-59-1-3-1-1 (19.85 cm), followed by R-19-A-5000 (23.12 cm).

Table 2. Phenological Characters affected by 24 rice genotypes at CNRM, Bardibas, Mahottari, Nepal (2024).

Genotypes	Heading Stage 80% (DAT)	Plant Height (cm)	Days to Maturity (DAT)
IR-127153-2-3-5-1-B-B	64 ^{de}	121 ^{cde}	98 ^{efg}
Hardinath-3	62.50 ^{ef}	135.6 ^{abc}	94 ^h
IR-12C170	68 ^{bc}	115.7 ^{de}	97.5 ^{fg}
IR-97205-73-1-2-2	64 ^{de}	118.9 ^{cde}	97.5 ^{fg}
IR-116713-B-B-34-3-B-B	64 ^{de}	124 ^{bcd}	99 ^{cdef}
NS-232	63 ^{ef}	128.5 ^{bcd}	96 ^{gh}
NS-314	63 ^{ef}	126.2 ^{bcd}	97.5 ^{fg}
IR-18-A-2294	68.5 ^{abc}	147.7 ^a	99 ^{cdef}
NS-278	68.5 ^{abc}	124.7 ^{bcd}	99 ^{cdef}
NS-224	70.5 ^{ab}	130.1 ^{bcd}	98.5 ^{def}
IR-19-A-4494	63 ^{ef}	112.3 ^{de}	96 ^{gh}
IR-19-A-5000	61 ^f	108.1 ^{ef}	96 ^{gh}
NS-188	68.5 ^{abc}	113.1 ^{de}	102 ^b
NS-313	70.5 ^{ab}	141.6 ^{ab}	104 ^a
Hardinath-1	55 ^h	113.2 ^{de}	86.5 ^k
NS-201	58 ^g	134.2 ^{abc}	91 ^j
IR-19-A-3197	71 ^a	123.8 ^{cde}	100 ^{bcd}
IR-132084-B-1191-1-3-B-5	71 ^a	113.9 ^{de}	101 ^{bc}
IR-132084-B-628-1-1-B-9	66.5 ^{cd}	127.1 ^{bcd}	100 ^{bcd}
IR-13C121	68.5 ^{abc}	94.5 ^f	100.5 ^{bcd}
IR-132084-B-1191-1-2-B-12	68.5 ^{abc}	108.7 ^{ef}	96 ^{gh}
IR-132T799	68.5 ^{abc}	123.7 ^{cde}	96 ^{ghi}
IR-127152-1-6-7-1-B-B	67 ^c	114.4 ^{de}	99 ^{cdef}
NR-2312-59-1-3-1-1	66.5 ^{cd}	118.6 ^{cde}	99 ^{cdef}
F-test	<0.001(***)	<0.001(***)	<0.001(***)
CV%	1.8	6.1	0.9
LSD (0.05)	2.508	15.44	1.913
Grand Mean	65.94	121.5	97.62

Note- DAT: Days after Transplanting, LSD: Least significant Difference, CV: Coefficient of Variation, *: significant at (P<0.05), **: significant at (P<0.01), ***: significant at (P<0.001), NS: Non-Significant. DAT: Days after transplanting.

Table 3. Yield and Yield Components affected by 24 rice genotypes in CNRM, Bardibas, Mahottari, Nepal (2024).

Genotypes	Test Weight (g)	Panicle Length (cm)	Grain Panicle ⁻¹	Sterility Percentage (%)
IR-127153-2-3-5-1-B-B	28.57 ^{ab}	25.55 ^{abcde}	82.2 ^{def}	41.27 ^{ab}
Hardinath-3	22.04 ^{fghij}	25.90 ^{abcde}	129.9 ^{abc}	26.02 ^{bcd}
IR-12C170	27.03 ^{abc}	27.68 ^{abcde}	74.9 ^{ef}	43.60 ^a
IR-97205-73-1-2-2	26.10 ^{abcd}	28.23 ^{abcde}	98.5 ^{bcd}	38.67 ^{abcd}
IR-116713-B-B-34-3-B-B	23.69 ^{defghij}	29.25 ^{abc}	123.1 ^{abc}	26.89 ^{bcd}
NS-232	26.86 ^{abcd}	25.70 ^{abcde}	103.1 ^{abcde}	27.22 ^{bcd}
NS-314	25.44 ^{bcd}	28.24 ^{abcde}	102.2 ^{abcde}	33.11 ^{abcde}
IR-18-A-2294	29.24 ^a	30.01 ^{ab}	131.6 ^{ab}	19.95 ^{efg}
NS-278	25.13 ^{cdef}	26.25 ^{abcde}	102.5 ^{abcde}	35.07 ^{abcde}
NS-224	26.69 ^{abcd}	23.34 ^{def}	68.9 ^f	31.02 ^{abcde}
IR-19-A-4494	22.53 ^{efghij}	25.33 ^{abcde}	134 ^a	24.32 ^{defg}
IR-19-A-5000	21.84 ^{ghij}	23.12 ^{ef}	114 ^{abcd}	14.66 ^{fg}
NS-188	24.70 ^{cdefgh}	25.96 ^{abcde}	78.2 ^{ef}	41.11 ^{abc}
NS-313	27.16 ^{abc}	30.19 ^a	122.6 ^{abc}	13.9 ^g
Hardinath-1	21.24 ^{ij}	25.53 ^{abcde}	128.1 ^{abc}	25 ^{bcd}
NS-201	24.38 ^{cdefghi}	25.33 ^{abcde}	135.8 ^a	14.20 ^g
IR-19-A-3197	24.90 ^{cdefg}	28.61 ^{abcd}	108.3 ^{abcde}	19.68 ^{efg}
IR-132084-B-1191-1-3-B-5	26.39 ^{abcd}	26.66 ^{abcde}	103.5 ^{abcde}	22.38 ^{defg}
IR-132084-B-628-1-1-B-9	21.66 ^{hij}	24.19 ^{cdef}	99.4 ^{bcd}	31.57 ^{abcde}
IR-13C121	25.65 ^{bcd}	25.49 ^{abcde}	82 ^{def}	30.67 ^{abcde}
IR-132084-B-1191-1-2-B-12	27.35 ^{abc}	24.93 ^{abcde}	76.1 ^{ef}	28.74 ^{abcde}
IR-132T799	21.29 ^{ij}	24.69 ^{bcd}	131.3 ^{ab}	24.76 ^{cdefg}
IR-127152-1-6-7-1-B-B	24.86 ^{cdefg}	25.24 ^{abcde}	97 ^{cdef}	28.73 ^{abcde}
NR-2312-59-1-3-1-1	20.75 ^j	19.85 ^f	119.4 ^{abc}	33.23 ^{abcde}
F-test	<0.001(***)	0.031(*)	<0.001(***)	0.004(**)
CV%	5.4	8.5	13.1	23.8
LSD (0.05)	2.766	4.594	28.82	13.868
Grand Mean	24.81	26.05	106.1	28.16

LSD: Least significant Difference, CV: Coefficient of Variation, *: significant at (P<0.05), **: significant at (P<0.01), ***: significant at (P<0.001), NS: Non-Significant. DAT: Days after transplanting.

Filled grain per panicle

The number of filled grains per panicle of different genotypes of rice was showed significant different under this experiment (Table 3). The highest number was observed in NS-201 (135.8), followed by IR-18-A-2294 (131.6). And lowest number was observed by NS-224 (68.9), followed by IR-12C170 (74.9).

Sterility percentage (%)

Analysis of various genotypes indicates that the differences in sterility percentages amongst the genotypes are statistically significant, as presented in Table 3. The genotypes IR-12C170 exhibited the highest sterility percentages at 43.60%, followed by IR-127153-2-3-5-1-B-B at 41.27%. Conversely, the lowest sterility percentage was observed in NS-313 at 13.9%, followed by NS-201 at 14.20%.

Grain Yield (t ha⁻¹)

When evaluating the grain yield of the tested rice genotypes against the standard (two check varieties namely, Hardinath-1 and Hardinath-3), the majority of them were found to be better and significant (Table 4). The result revealed that highest yield (6.87 t/ha) was achieved by the genotypes IR-18-A-2294, followed by IR-19-A-5000 (6.51 t/ha), NS-314 (6.24 t/ha), NS-278 (6.26 t/ha), Hardinath-3 (6.24t/ha) respectively and least by NS-232 (3.91 t/ha), followed by IR-12C170 (3.983 t/ha).

Biomass Yield (ton ha⁻¹)

The biomass production of among the rice genotypes were non-significant (Table 4). Numerically the maximum

biomass production 22.64 t/ha, was obtained by the genotype NR-2312-59-1-3-1-1, followed by IR-18-A-2294, which yielded 20.94 t/ha. Conversely, and lowest production 14.84 t/ha, was obtained by the genotype IR-132084-B-1191-1-2-B-12, followed by Hardinath-1 which yielded 15.22 t/ha.

Harvesting Index (%)

The research revealed that the harvesting index of different genotypes of rice showed a significant difference among them (Table 4). The harvesting index of different rice genotypes ranges from lowest 19.35 % in IR-12C170 to highest 40.71 % in IR-19-A-5000.

Discussion

All the genotypes had shown certain significant variation among them in term of different parameters. The considerable variation in days to heading Stage among the tested rice genotypes underscores the significant genetic diversity within the germplasm. Factors such as soil fertility, water availability, planting techniques, and intrinsic genetic potential collectively influence this trait (Hussain et al., 2005; Ashfaq, 2012). In the present study, this variation highlights the potential of the evaluated genotypes for targeted breeding programs, allowing selection of lines suitable for early or late sowing in the Terai region. Genotype × environment interactions further modulate these differences, corroborating findings from (Khalil et al., 2009).

Table 4. Yield and Yield Components affected by 24 rice genotypes in CNRM, Bardibas, Mahottari, Nepal (2024).

Genotypes	Grain Yield (ton ha ⁻¹)	Biomass Yield (ton ha ⁻¹)	Harvesting Index (%)
IR-127153-2-3-5-1-B-B	5.21 ^{bcdef}	19.17 ^{abcd}	27.25 ^{defghi}
Hardinath-3	6.24 ^{abc}	19.79 ^{abcd}	31.69 ^{bcdef}
IR-12C170	3.983 ^{ef}	20.57 ^{abc}	19.35 ^j
IR-97205-73-1-2-2	4.83 ^{cdef}	18.38 ^{abcd}	26.42 ^{efghi}
IR-116713-B-B-34-3-B-B	5.40 ^{abcdef}	17.18 ^{bcd}	31.47 ^{bcdef}
NS-232	3.91 ^f	18.22 ^{abcd}	21.70 ^{ij}
NS-314	6.34 ^{abc}	19.89 ^{abcd}	31.91 ^{bcde}
IR-18-A-2294	6.87 ^a	20.94 ^{ab}	33.11 ^{bcd}
NS-278	6.26 ^{abc}	19.74 ^{abcd}	31.75 ^{bcdef}
NS-224	4.29 ^{cdef}	20.21 ^{abcd}	24.34 ^{hij}
IR-19-A-4494	6.07 ^{abcd}	16.89 ^{bcd}	35.99 ^{ab}
IR-19-A-5000	6.51 ^{ab}	16.01 ^{bcd}	40.71 ^a
NS-188	5.47 ^{abcde}	17.95 ^{bcd}	30.30 ^{bcdefg}
NS-313	5.98 ^{abcd}	17.38 ^{bcd}	34.45 ^b
Hardinath-1	5.24 ^{bcdef}	15.22 ^{cd}	34.46 ^b
NS-201	5.14 ^{bcdef}	17.33 ^{abcd}	30.10 ^{bcdefgh}
IR-19-A-3197	4.89 ^{cdef}	17.73 ^{abcd}	27.59 ^{cdefgh}
IR-132084-B-1191-1-3-B-5	4.58 ^{def}	17.53 ^{abcd}	25.80 ^{fghi}
IR-132084-B-628-1-1-B-9	4.45 ^{ef}	18.03 ^{abcd}	24.70 ^{ghij}
IR-13C121	4.41 ^{ef}	15.79 ^{bcd}	27.84 ^{cdefgh}
IR-132084-B-1191-1-2-B-12	4.87 ^{cdef}	14.84 ^d	32.57 ^{bcd}
IR-132T799	5.37 ^{bcdef}	16.09 ^{bcd}	33.27 ^{bc}
IR-127152-1-6-7-1-B-B	4.66 ^{def}	15.53 ^{cd}	30.16 ^{bcdefgh}
NR-2312-59-1-3-1-1	5.48 ^{abcde}	22.64 ^a	24.25 ^{hij}
F-test	0.003(**)	0.111 (NS)	<0.001(***)
CV%	11.8	12.1	8.4
LSD (0.05)	1.2888	4.524	5.122
Grand Mean	5.3	18.04	29.63

LSD: Least significant Difference, CV: Coefficient of Variation, *: significant at (P<0.05), **: significant at (P<0.01), ***: significant at (P<0.001), NS: Non-Significant. DAT: Days after transplanting.

Days to maturity varied widely, ranging from 86 to 104 DAT, reflecting a 20-day genetic window. Such diversity is highly valuable: early-maturing genotypes facilitate timely planting of subsequent crops such as wheat and lentil, while late-maturing types may maximize biomass and yield under favorable conditions. This observation aligns with (Karim et al., 2007), who emphasized that maturity is strongly influenced by both genetic constitution and environmental interactions, particularly resource availability during panicle emergence.

Plant height is a polygenic trait, predominantly regulated by the genetic architecture of the genotype, and is determined by the combined effect of the number and length of internodes (Rahman et al., 2018). Plant height also exhibited marked genotypic differences, reflecting the influence of genetic architecture and climatic adaptability (Rabbani et al., 2010). Maintaining moderate height is crucial in the Terai to minimize lodging risk under high fertility and rainfall conditions, directly impacting yield stability.

Yield components including thousand-grain weight, panicle length, and grains per panicle showed significant variation, demonstrating the strong genetic control of these traits (Tahir et al., 2002; Sultana et al., 2014). Thousand-grain weight, a critical determinant of final yield, varied across genotypes, suggesting differential grain-filling efficiency. Similarly, variation in panicle length and spikelet number directly influenced the potential grain output per panicle (Balasubramanian et al., 2006; Zhao et al., 2020). Sterility percentage was affected by environmental stress and nutrient availability, particularly boron deficiency, which hampers pollen tube growth and spikelet development (Ali et al., 2013).

Grain yield differed substantially among genotypes, with IR-18-A-2294 achieving the highest yield of 6.87 t/ha followed by IR-19-A-5000 (6.51 t/ha), far exceeding the productivity of widely cultivated Terai varieties such as Mansuli, Sabitri, Makwanpur-1, Radha 7, and Hardinath (3.5–4.8 t/ha) (AITC, 2024). This superior performance highlights IR-18-A-2294 and IR-19-A-5000 as a promising candidate for breeding programs aimed at enhancing rice productivity in the Terai. Variations in harvest index further indicate that genetic background significantly influences assimilate partitioning (Cha-um et al., 2007) and resource allocation, confirming observations by (Cui et al., 2000; Chen et al., 2008).

Collectively, the substantial variability observed across phenological, morphological, and yield traits confirm the presence of wide genetic diversity in the studied rice germplasm. This diversity provides a solid foundation for breeding programs targeting high-yielding, early-maturing, and regionally adapted rice varieties. Furthermore, the identification of superior genotypes such as IR-18-A-2294 and IR-19-A-5000 offers new opportunities for developing next-generation cultivars tailored to the specific agro-ecological conditions of the Terai. By integrating these findings into selection strategies, plant breeders can enhance rice productivity and sustainability in the region, bridging the gap between genetic potential and field performance.



(A)



(B)



(C)

Figure 2. A Heading stage of rice, B. Maturity stage of rice, C. Layout of rice experiment conducted in CNRM Bardibas

Conclusion

The present rice breeding program was carried out with the primary objective of evaluating different rice genotypes for their adaptability, earliness, yield potential, and suitability to the target region. The results of the study revealed significant variation among the tested genotypes in terms of yield performance and maturity traits. In terms of earliness and yield potential, IR-18-A-2294 and IR-19-A-5000 were found to be superior, indicating their potential for further advancement and recommendation in rice production systems and suggesting their usefulness for farmers in areas where early maturity along with high production is desirable to fit into multiple cropping systems or to avoid climatic risks such as terminal drought or flooding. These findings emphasize the importance of genotype evaluation in rice breeding programs to identify stable and location-specific cultivars that can contribute to enhanced productivity and food security. The promising genotypes identified in this study should be further

subjected to multi-location trials and farmer-participatory evaluations to validate their performance under diverse agro-ecological conditions.

Declarations

Author Contribution Statement

Vijay Singh: Conducted the Study, Data collection, Analysis, Writing of the manuscript and editing.

Tirth Narayan Yadav: Contributed in conducting the study, data collection, analysis, and editing.

Nitu Kumari Mahato: Contributed to the conduct of the study, data collection and analysis.

Anita Bhandari: Contributed to the conduct of the study, data collection and analysis.

Abhisek Shrestha: Designed experiment, analysis and material collection.

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Conflict of Interest

Authors declare no conflict of interest exists.

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