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Evaluation of Early Rice Genotypes for Yield and Yield Attributing Characters in Madhesh Province of Nepal

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Abstract

Rice plays crucial role in sustaining nutrition and sustaining livelihoods nutritional and livelihood globally but lack of high yielding and early maturing varieties cause problem in sustainable production. Thus, the study was conducted to evaluate the performance of early rice genotypes in Madhesh province, focusing on yield and yield attributing characters. The research was laid in randomized complete block design (RCBD) with two replications and twenty-four genotypes (2 check varieties Hardinath-1 & Hardinath-3) in CNRM Bardibas. Geographically, it is suited at altitude 26˚52’0’’8North, longitude 85˚49’96’’ East; 78 m above sea level, AFU. The planting distance between the rice plant was 20*20 cm with plant plot size:1.5x3=4.5 and the spacing between two plots consecutive plots was maintained 0.5 m. Key agronomic traits of growth, yield and yield attributes characters 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 highest yield (6.87 t/ha) was achieved by the genotypes IR-18-A-2294, followed by IR-19-A-5000 (6.516 t/ha), NS-314(6.24 t/h), NS-278(6.26 t/h), Hardinath-3(6.24t/h) and least by NS-232(3.91t/h). Hardinath-1 (86.5 DAT) had early maturity followed by NS-201 (91 DAT), Hardinath-3 (94 DAT), IR-132T799(96DAT) & 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/h, 5.14 t/h, 6.24 m/t, 5.37 t/h, 4.87 t/h & 5.98t/h respectively. Based on grain quality and yield, IR-19-A-5000, IR-18-A-2294 were found as high yielding genotypes respectively, while based on earliness and yield potential Hardinath-1, IR-132T799 and Hardinath-3 were found superior among tested. These results provide valuable insights into the selection and development of rice varieties adapted to the specific agro-ecological conditions of Nepal.

Keywords: *Earliness, Rice, Genotypes, Yield, Yield Attributes.*

Introductıon

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 a major staple food crop and ranks first in position in terms of production and productivity in Nepal(AITC, 2024; MoALD, 2024). Rice supplies nearly 20% of the economic to its agricultural GDP, and 7% 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 1447789 hectares, yielding an average of 3.7 t/ha. where Mahottari District shares 3.00 % production of national production, located in Terai,is one of the productive locations for high rice production due to its suitable agro-climatic condition(AITC, 2024; MoALD, 2024).

Inconsistent yield due to poor soil, water scarcity, and pest susceptibility, raises concerns about its stability. 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 agroecological conditions(B. B. Adhikari et al., 2018). 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(B. N. Adhikari et al., 2018; Aditya & Bhartiya, 2013). 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 phonological traits of rice that are also linked to the yield potential of the many rice varieties in order to choose the best variations for further rice breeding(Aditya & Bhartiya, 2013). 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).Keeping in view in the above fact, present evaluation was done with objectives to determine appropriate high-yielding rice genotypes and earliness under the conditions of the Terai region and assess several rice genotypes for yield and yield characteristics.

Materials And Methods

Experimental site

The study was conducted during the 2024 monsoon season (June-October) at College of Natural Resources Management Bardibas (CNRMB) experimental farm in Bardibas, Mahottari District, Nepal, which is suited in the inner terai of Nepal. Geographically, it is suited at altitude 26˚52’0’’8North, longitude 85˚49’96’’ East; 78 m above sea level. The region receives an average annual rainfall 1200-1400 mm. The soil texture was found 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 potassium content.

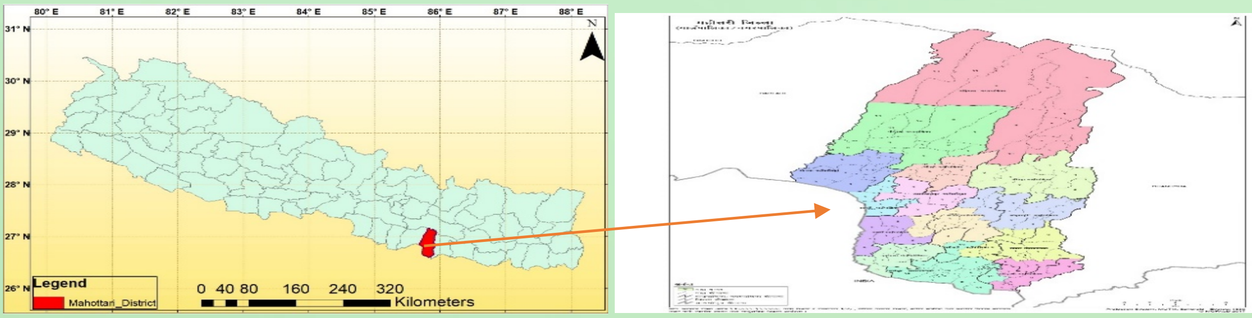

Figure 1: A map showing experimental site

Experimental design and crop management

The research was laid out in one factorial randomized complete block design (RCBD) with two replications and twenty-four genotypes (2 check varieties Hardinath-1 & Hardinath-3) in CNRM Bardibas, AFU. The planting distance between the rice plant was 20*20 cm with plant plot size:1.5x3=4.5 and the spacing between two plots consecutive plots was maintained 0.5 m. The experimental plots and dry seed bed were leveled and prepared using traditional practices. A raised nursery bed was conducted using the dry method of preparing nursery beds. The nursery seedlings of 21 days old were transplanted in June 2024.

The plot size was 4.5 m^2. The fertilizer were applied using urea diammonium phosphate (DAP),and muriate of potash (MOP) at rate of 120:40:40 $N:P_2O_5: K_2O$ [nitrogen (N), phosphorus (P2O5), and potassium 67 68 (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 into two 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.

Plant materials

The rice genotypes were obtained from 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

Panicle initiation 80%, days to maturity, plant height, test weight, filled grain per panicle, sterility percentage, biomass yield, harvest index, effective tillers were recorded. 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 attributes characters were processed to Analysis of Variance (ANOVA). The significant of the differences among the treatments of the rice varieties was estimated with the help of Duncan’s Multiple Range Test (DMRT)at a 5% level of probability.

Results And Dıscussıon

Phenological characteristics

Panicle initiation 80%

the panicle emergence was highly varied with the genotypes at 1% level of significance (Table2).The result depicts that IR-132084-B-1191-1-3-B-5, IR-19-A-3197,NS-224 and NS-313 were found delayed in panicle initiation while in 71 (DAT). Hardinath-1 and NS-201showed earlines in panicle emergence. The days to panicle initiation may be influenced by factors such as water and soil conditions, planting and sowing techniques, and its early maturing genetic ability and translation time(Ashfaq, 2012; Hussain et al., 2005).

Table 1. List of24 rice genotypes used in the experiment at CNRM Bardibas, Nepal in 2024

Treatments	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

Table 2. Phenological Characters affected by of 24 rice genotypes in CNRM Bardibas, Mahottari, Nepal in 2024.

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

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.

Genotype genetic diversity may be one of the cause of the variation in panicle initiation(Khalil et al., 2009).Similarly, genetic composition of the foreign lines and genotypic environmental interaction may be the cause of the variation in days to panicle initiation(Marwat, 2002).

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-313had the highest number of days to maturity 104 (DAT), followed by NS-188in 102 (DAT). The Hardinath-1 genotype was showed earlier in maturity (86 DAT),followed byNS-201(91 DAT).Variation in marturity depend upon the panicle emergence and availability of resource at that time. Maturity of different genotypes may varied due to genetic and environment interaction(Karim et al., 2007).

Plant Height (cm)

The plant height was significantly influenced by genotypic variation at 1% level of significance. (Table 2). IR-18-A-2294 had highest plant height of 147.7 cm followed by NS-313 (141.6cm). The shortest plant height was observed in IR-13C121 (94 cm). followed by IR-19-A-5000 (108.1cm).It has been determined that the climatic requirements of each genotype of rice are distinct, which may account for the variance in plant height among these genotypes(Rabbani et al., 2010).

Yield and Yield Attributing Characteristics:

1000 grain weight (gram)

Difference in 1000 grain weight was significant to various genotypes (Table 3).Thousand grain weight of tested ranged from (20.75-29.24).IR-18-A-2294 shown the highest grain weight of 29.24gm, followed by IR-127153-2-3-5-1-B-B (28.57 gm). And lowest was shown in NR-2312-59-1-3-1-1 (20.75 gm) followed by Hardinath-1 (21.24 gm).Several traits showed highly significant variance, and these attributes were controlled by genotypic differences across the tested genotypes(Tahir et al., 2002).

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 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). Different rice genotypes may differ in their genetic composition, which could account for the variance in panicle length(Sultana et al., 2014). The genetic variability for several traits in ten rice genotypes, and he found that these traits were controlled by genetics and could be used to choose a desired characteristic of rice(Cha-um et al., n.d.; Tahir et al., 2002).

Filled Grain per Panicle

The number of filled grain per panicle of different genotypes of rice was shown significantly difference 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). The variance was shown due to panicle length, days to maturity and traits among genotypes(Karim et al., 2014). The length of the panicles and the configuration of their spikelets determine the amount of grain per panicle(Balasubramanian et al., 2006; Zhao et al., 2020).

Sterility percentage

Analysis of various genotypes indicates that the differences in sterility percentages amongst the genotypes are statically 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 at14.20%. The component of variation for Sterility percentage was due to A lack of boron, which is essential for the growth of pollen tubes, varies by genotype, and drought stress interferes with the uptake of nutrients and water, which impacts spikelet development.(Ali et al., 2013).

Biomass Yield (ton ha^{-1})

The biomass production of the several rice genotype was non-significant (Table 4). The maximum biomass production 32.44 t/ha, was obtained by the genotype NR-2312-59-1-3-1-1, followed by IR-18-A-2294 which yielded 30.01 t/ha. Conversely, And lowest production 21.28 t/ha, was obtained by the genotype IR-132084-B-1191-1-2-B-12, followed by Hardinath-1 which yield 21.82 28 t/ha).These differences suggest that both genetic factors and breeding history contribute to biomass yield variations among rice genotypes(Chen et al., 2008; Jahn et al., 2011).

Harvesting Index

The research revealed that the harvesting index of different genotypes of rice significant difference relation among them (Table 4). The mean harvesting index of different rice genotypes was highest in IR-19-A-5000 (28.40), followed by IR-19-A-4494 (25.11). And lowest was IR-12C170 (13.5), followed by NS-232 (15.14). The variation in harvesting index could be attributed to genetic background plays a significant role in determining harvesting index.(Cui et al., 2000)

Table 3. Yield and Yield Attributing Characters affected by 24 rice genotypes in CNRM Bardibas, Mahottari, Nepal in 2024.

Genotypes	**Test Weight (gm)**	**Panicle Length(cm)**	**Filled Grain/Panicle**	**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^{bcdefg}
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^{bcdef}	38.67^{abcd}
IR-116713-B-B-34-3-B-B	$23.69^{defghij}$	29.25^{abc}	123.1^{abc}	26.89^{bcdefg}
NS-232	26.86^{abcd}	25.70^{abcde}	103.1^{abcde}	27.22^{bcdefg}
NS-314	25.44^{bcde}	28.24^{abcde}	102.2^{abcdef}	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^{bcdefg}
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^{bcdef}	31.57^{abcde}
IR-13C121	25.65^{bcde}	25.49^{abcde}	82^{def}	30.67^{abcdef}
IR-132084-B-1191-1-2-B-12	27.35^{abc}	24.93^{abcdef}	76.1^{ef}	$28.74^{abcdefg}$
IR-132T799	21.29^{ij}	24.69^{bcdef}	131.3^{ab}	24.76^{cdefg}
IR-127152-1-6-7-1-B-B	24.86^{cdefg}	25.24^{abcde}	97^{cdef}	$28.73^{abcdefg}$
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.

Table 4. Yield and Yield Attributing Characters affected by 24 rice genotypes in CNRM Bardibas, Mahottari, Nepal in 2024.

Genotypes	Biomass Yield (ton ha^{-1})	Harvesting Index	Grain Yield (ton ha^{-1})
IR-127153-2-3-5-1-B-B	27.48^{abcd}	19.01^{defghi}	5.21^{bcdef}
Hardinath-3	28.37^{abcd}	22.11^{bcdef}	6.24^{abc}
IR-12C170	29.48^{abc}	13.50^{j}	3.983^{ef}
IR-97205-73-1-2-2	26.34^{abcd}	18.43^{efghi}	4.83^{cdef}
IR-116713-B-B-34-3-B-B	24.62^{bcd}	21.96^{bcdef}	5.40^{abcdef}
NS-232	26.12^{bcd}	15.14^{ij}	3.91^{f}
NS-314	28.51^{abcd}	22.26^{bcde}	6.34^{abc}
IR-18-A-2294	30.01^{ab}	23.10^{bcd}	6.87^{a}
NS-278	28.30^{abcd}	22.15^{bcdef}	6.26^{abc}
NS-224	28.97^{abcd}	16.98^{hij}	4.29^{cdef}
IR-19-A-4494	24.21^{bcd}	25.11^{ab}	6.07^{abcd}
IR-19-A-5000	22.94^{bcd}	28.40^{a}	6.51^{ab}
NS-188	$25.^{72abcd}$	21.14^{bcdefg}	5.47^{abcde}
NS-313	24.91^{abcd}	24.04^{b}	5.98^{abcd}
Hardinath-1	21.82^{cd}	24.04^{b}	5.24^{bcdef}
NS-201	24.83^{abcd}	$21^{bcdefgh}$	5.14^{bcdef}
IR-19-A-3197	25.41^{abcd}	19.25^{cdefgh}	4.89^{cdef}
IR-132084-B-1191-1-3-B-5	25.13^{abcd}	18^{fghi}	4.58^{def}
IR-132084-B-628-1-1-B-9	25.84^{abcd}	17.23^{ghij}	4.45^{ef}
IR-13C121	22.63^{bcd}	19.43^{cdefgh}	4.41^{ef}
IR-132084-B-1191-1-2-B-12	21.28^{d}	22.72^{bcd}	$4.^{87cdef}$
IR-132T799	23.06^{bcd}	23.21^{bc}	5.37^{bcdef}
IR-127152-1-6-7-1-B-B	22.27^{cd}	$21.04^{bcdefgh}$	4.66^{def}
NR-2312-59-1-3-1-1	32.44^{a}	16.92^{hij}	5.48^{abcde}
F-test	0.111 (NS)	<0.001(***)	0.003(**)
CV%	12.1	8.4	11.8
LSD (0.05)	6.484	3.573	1.2888
Grand Mean	25.86	20.67	5.3

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.

PHOTOS

(A) (B)

(C)

Figure 2: A Panicle initiation stage of rice B. Maturity stage of rice C. Layout of rice experiment conducted in CNRM Bardibas

Grain Yield (ton ha^{-1})

When evaluating the grain yield of the tested rice genotypes against the standard (2 check varieties (Hardinath-1 & Hardinath-3), the majority of them were found to be better and significant (Table 4). The results revealed that highest yield (6.87 t/ha) was achieved by the genotypes IR-18-A-2294, followed by IR-19-A-5000 (6.516 t/ha), NS-314(6.24 t/h), NS-278(6.26 t/h), Hardinath-3(6.24t/h) respectively and least by NS-232 (3.91 t/h), followed by IR-12C170 (3.983 t/h).As breeding materials for confirmation, these superior rice genotypes over the standard check in terms of grain yield might be examined further.(AITC, 2024; Pervaiz et al., n.d.)

Conclusion

A rice breeding program's main objective is to evaluate the genotypes of rice for a particular region or niche. The finding of this study showed that based on grain quality and yield, IR-19-A-5000, IR-18-A-2294 were found as high yielding genotypes respectively, while based on earliness and yielding potential Hardinath-1, IR-132T799 and Hardinath-3 were found superior among tested.

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Conflict Of Interest

Authors declare no conflict of interest exists.

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