



Evaluation of Spring Season Local and Improved Rice Genotypes on Growth, Yield, and Yield Attributing Characters in Gorkha District, Nepal

Shreeja Acharya¹, Sudip Ghimire¹, Roshan Thapa¹, Prakriti Bhattarai¹, Bidhya Poudel Chhetri¹, Bibek Gautam²

¹Faculty of Agriculture, Agriculture and Forestry University, Rampur, Chitwan, Nepal

²Caritas Nepal, Nepal

*Corresponding Author: Sudip Ghimire

Email: ghimiresudip858@gmail.com



Article Info

Article history:

Received 27 November 2023

Received in revised form 3 February 2024

Accepted 23 April 2024

Keywords:

Crop Productivity,
Genotypic Variation,
Growth Attributes,
Phenology,
Rice Genotypes,
Yield

Abstract

Rice cultivation faces challenges related to varietal selection, limiting the potential yield of spring rice crops. This study was conducted in the Rice Zone of Gorkha, Nepal during the spring season of 2022 with aim to evaluate the growth, yield, and yield attributing characters of different rice genotypes. The study hypothesized that significant differences exist among different rice genotypes in terms of their growth, yield, and yield attributing characters. The experiment employed a one-factor randomized complete block design (RCBD) with seven genotypes, including local varieties (Hardinath Hybrid 1, Chaite-5, CH 45, Salijudi) and pipeline genotypes (IR16L1919, IR10N118, IR86515), and replicated three times. Results indicated significant variations among genotypes in response to similar growing conditions and nutrient availability. Notably, CH 45 exhibited the highest plant height (113.50 cm), while IR16L1619 demonstrated the longest panicle length (28.56 cm) and the highest number of effective tillers (23.10). IR16L1619 also displayed the highest number of leaves (97.27 leaves) and leaf area index (8.00). Chaite-5 had the longest flag leaf (33.13 cm), while IR16L1619 recorded the highest panicle length (28.56 cm) and number of grains per panicle (270.10). Salijudi exhibited the lowest sterility percentage (7.52 %), and CH 45 displayed the highest thousand grain weight (26.40). Moreover, IR16L1619 demonstrated superior performance in terms of grain yield (8.19 t/ha), straw yield (7.12 t/ha), and biological yield (15.25 t/ha). The findings underscored the genotype-specific responses to environmental conditions, highlighting the importance of tailored varietal selection for optimal productivity.

Introduction

Agriculture stands as the cornerstone of Nepal's economy, providing sustenance and livelihoods to the majority of its population (Ghimire et al., 2023a; Ghimire et al., 2023b). Cereals, in particular, contribute significantly to the Gross Domestic Product (GDP) of the country, with rice alone accounting for a substantial portion of both the nation's food supply and daily calorie intake (NPPR, 2015; Tripathi et al., 2019). However, despite its critical role, traditional subsistence farming practices predominate among Nepalese farmers, making it challenging to meet the burgeoning food demand associated with a rapidly growing population (Gairhe et al., 2018). In a global context, Nepal faces the grim reality of being ranked 73rd in the Global Hunger Index (GHI) with a score of 19.1, underscoring the urgency of enhancing food production and security (Swinnen & McDermott, 2020).

Rice (*Oryza sativa*) stands as the staple food not only for Nepalese people but also for more than half of the world's population, particularly across Asian countries. In Asia, where rice is

predominantly cultivated, it plays a pivotal role in ensuring food security (Chauhan et al., 2012). In Nepal, rice constitutes over 50% of the total caloric intake of the population, further emphasizing its significance (Kharel et al., 2018). Within the global context, rice ranks as the third most important staple crop in terms of production. However, the success of rice production in Nepal is intricately tied to the vagaries of the monsoon season, which can significantly impact rice yields and productivity. The country's total rice cultivation area is substantial, covering approximately 1,469,545 hectares, with an annual production of 5,151,925 metric tons (MoALD, 2021). In Gorkha district, rice is cultivated twice a year, during the rainy and spring seasons, with spring rice cultivation covering an area of 589 hectares and yielding 4.51 metric tons per hectare (MoALD, 2021). Several factors have contributed to improved cereal crop productivity in Nepal, including the availability of quality seeds, timely access to fertilizers and other inputs, improved irrigation infrastructure, and enhanced agricultural knowledge (Gairhe et al., 2018). In the context of Nepal, spring rice has emerged as a promising crop. Spring rice is characterized by its short growth duration, resistance to various pests and diseases, photoperiod insensitivity, and high yield potential. It thrives in areas with sufficient irrigation facilities that help control weed infestation. Additionally, the relatively intense sunlight during the spring season contributes to higher yields. Furthermore, spring rice can be cultivated in areas prone to flooding and landslides during the rainy season, making it an adaptable and resilient choice for farmers (IRRI, 2018).

Despite the pivotal role of rice in Nepal, only small portion of farmers cultivate spring rice, and there exists a significant yield gap between potential and actual production. Factors contributing to this gap include a lack of access to high-yielding rice genotypes, limited availability of quality seeds from formal sources, and inadequate varietal recommendations from agricultural authorities (Krupnik et al., 2021). These challenges have created knowledge barriers for rice farmers, impeding their ability to optimize production and productivity. To address these issues and bolster food security, there is a need for rigorous scientific research in rice varietal selection and evaluation. Such research can provide invaluable insights to farmers and promote the supply of high-quality seeds. The choice of rice variety is among the foremost decisions made by rice growers each season, bearing significant implications for their annual yield.

Quality seed alone can augment crop productivity by up to 25% while simultaneously reducing production costs. In Gorkha district, spring rice already demonstrates a higher yield potential compared to the main season rice (MoALD, 2021). Resolving issues related to varietal selection in spring rice cultivation can represent a viable solution to improving both farmer incomes and regional food security. Conducting scientific research in this domain holds the promise of delivering crucial information that can help ensure a consistent supply of high-quality seeds to farmers. The research objectives encompass a comprehensive assessment of phenological characteristics, growth, and yield attributes of these genotypes, offering a nuanced understanding of their performance in this unique context. The objective of identifying superior genotypes holds practical significance, enabling farmers to make informed decisions about varietal selection, potentially leading to increased yields, food security, and improved livelihoods. Furthermore, the research hypothesis, which posits significant differences among the genotypes, sets the stage for a rigorous scientific investigation challenging conventional practices. In practical and empirical terms, this research has the potential to mitigate knowledge barriers faced by farmers, contribute to agricultural science, and inform policy and extension services, ultimately benefiting both local farmers and the broader agricultural community. Moreover, the findings contribute to

the broader understanding of rice genotypic responses, offering a foundation for future research endeavors aimed at unraveling the genetic mechanisms governing key agronomic traits.

Methods

Experimental site

The present research was carried out at a farmer's field located in Chebetar, Gorkha district, Nepal, during the period from mid-March to late July in 2022. The study site is situated in the southern part of Gorkha district at coordinates 27.993°N latitude and 84.570°E longitude, with an elevation of approximately 389 meters above sea level.

For the purpose of analyzing the physicochemical properties of the soil in this area, a composite sample was prepared by randomly collecting soil samples from five distinct locations, each at a depth of 15 cm. These individual soil samples were meticulously combined to ensure a homogeneous representation of the site's soil characteristics. Subsequently, a 500 g sample from the homogenized mixture was transported to the nearby laboratory at the Agriculture Knowledge Center in Gorkha. In the laboratory, the soil sample underwent a series of standard tests, including the determination of available levels of nitrogen (N), phosphorus (P), potassium (K), and organic matter content. Moreover, the soil's texture and pH were assessed as outlined in Table 1, providing a comprehensive account of the soil's physicochemical attributes.

Table 1. Physical and chemical properties of soil samples collected from the research field

Soil properties	Unit	Value	Remarks
Physical properties			
Structure	-	-	Clay loam
Chemical properties			
Organic matter content	%	0.90	Moderate
Nitrogen	%	0.04	Low
Phosphorus	kg ha ⁻¹	45.8	Low
Potassium	kg ha ⁻¹	108.7	Low
pH	-	5.7	Slightly acidic

Experimental details

The experimental design employed in this study was a one-factorial Randomized Complete Block Design (RCBD), encompassing a total of 7 distinct treatments with 3 replications. The treatment factors consisted of different rice genotypes, including Hardinath Hybrid 1 (HH1), Chaite-5, CH 45, and Salijudi, which represents the local variety, while the remaining three genotypes, IR16L1919, IR10N118, and IR86515, were classified as pipeline genotypes. All the seeds utilized in this experiment were sourced from the Agriculture Knowledge Center in Gorkha.

Each replication was conducted within a single block to facilitate the systematic organization of the experiment. Therefore, there were a total of 3 blocks, each representing an individual replication. Each of these blocks contained 7 distinct plots, corresponding to the 7 treatment levels. In total, there were 21 plots within the experimental setup. The spacing between individual plants was maintained at 25 x 25 cm to ensure uniformity and consistency in the plant layout. Moreover, a separation of 0.5 m was maintained between replications, and a

distance of 0.25 meters was preserved between the various treatment plots, ensuring a standardized and systematic layout of the experimental design.

Cultivation measures

Nursery bed preparation and main field preparation

The sowing process involved the utilization of well-prepared nursery beds, with each bed measuring 1 m x 0.5 m, dedicated to a single rice variety. Prior to sowing, seed priming was carried out. The timing of sowing was specifically scheduled for the fourth week of February, 2022. The seeds were evenly broadcasted on the surface of the soil layer above the dry nursery bed. Subsequently, the main field preparation was conducted through the process of puddling, employing a tractor for this task. In total, 21 plots were established, each measuring 2 meters in width and 3 meters in length. This comprehensive layout allowed for the systematic evaluation of the different treatments and genotypes under study.

Manure and fertilizer

In the nursery bed, the application of manure and fertilizer was carried out according to the specific requirements of the crop. However, in the main field, the following chemical fertilizers were applied at the specified rates: urea (46% N), DAP (18% N and 46% P₂O₅), and MOP (60% K₂O). These fertilizers were applied at a rate of 100:30:30 kg NPK ha⁻¹ (AIATC, 2021). During the transplanting phase, half of the nitrogen dose, as well as the full doses of phosphorus and potash, were applied as a basal dose. The remaining half of the nitrogen dose was subsequently applied as a top dressing, ensuring an effective and balanced distribution of nutrients to support the growth and development of the rice plants.

Uprooting, transplanting of seedling, weed management, harvesting and threshing

The process of uprooting and transplanting of rice seedlings was carried out individually, with each seedling uprooted and transplanted at the age of 21 days. The transplanting process involved spacing the 21-day-old seedlings at a uniform distance of 25 cm x 25cm, facilitating the establishment of a well-organized and appropriately spaced rice crop in the field.

The field management activities included two significant weeding operations. The first weeding operation was conducted between 15 to 18 days after transplanting (DAT). The second weeding occurred 45 DAT, and it served the dual purpose of reducing competition from weeds and improving soil aeration and water movement. These weeding activities were vital for optimizing crop growth and yield. For the harvesting process, manual methods were employed, with traditional sickles used to harvest the rice crop. Within each plot, a 1 square meter area at the center was specifically marked and harvested separately. The harvested rice heads were subsequently left to sun-dry, and manual threshing methods were applied to separate the grains from the husks. The grains were cleaned through winnowing to remove any extraneous matter to determine the grain yield accurately. The grain weight was measured using an electric balance, ensuring precise measurements. Simultaneously, the moisture content of the grains was determined using a portable moisture meter, contributing to the comprehensive evaluation of the crop's quality and yield.

Observed parameters

A systematic approach was taken for data collection. Randomly, a sample of 10 plants from each plot was selected for observations at various critical stages of the rice crop's growth cycle. The observations were conducted at the following time points: 15 days after sowing (DAS), 30 DAS, 45 DAS, 60 DAS, 75 DAS, 90 DAS, and at the time of harvesting. During

these observations, several key parameters were studied to comprehensively evaluate the performance and characteristics of the rice plants. These parameters typically include:

Growth parameters (Plant height, number of tillers per square meter, number of leaves, leaf area index)

Ten random plants were selected and tagged for measurement. Plant height was measured at 15-day intervals, starting from 15 DAT and continuing up to 75 DAT. The final plant height was also measured at the time of harvest. The measurement involved recording the distance from the ground level to the tip of the topmost leaf at early stages and up to the tip of the main panicle at physiological maturity. The average height in centimeters (cm) was calculated. Ten random hills were selected and tagged for observing the number of tillers. The number of tillers was recorded at intervals from 15 DAT to 75 DAT, as well as at the time of harvest. This data was then converted to a per square meter measurement for analysis, providing an understanding of tiller density. From the previously selected 10 plants, the number of leaves was counted at various time points, ranging from 15 DAT to 75 DAT. This information offers insights into the development of the plant's leaf canopy over time. Six random plants were chosen as samples to calculate the Leaf Area Index. Using the length and width method, leaf length and maximum width were measured for each selected leaf. The leaf area was then calculated for these leaves. LAI is an important parameter that reflects the photosynthetic potential of the crop canopy.

$$\text{Leaf area} = K * \text{length} * \text{width} \quad (1)$$

Where K is the 'adjustment factor,' K varies with the shape of the leaf, which, in turn, is influenced by factors such as the rice variety, nutritional status, and the growth stage of the leaf. According to experimental studies conducted at IRRI in 1972, a value of 0.75 was applied for all growth stages, except for the seedling stage and harvest, where a value of 0.67 was used (Yoshida et al., 1976).

Yield attributes (Effective tillers per hill, flag leaf length, panicle number, panicle length, grains per panicle, sterility percentage, filled grains per panicle, thousand grain weight)

The number of effective tillers in a row within the net plot area was recorded from sample plants in each plot before harvesting of the crop. Randomly, 10 hills were selected and tagged for observation of tiller number. A number of tillers were also recorded from 15 DAT to 75 DAT as well as at harvest. The number of panicles per hill was counted from 10 sampled plants and the mean was calculated. Ten panicles were randomly selected to measure the length of panicle and the mean was calculated and expressed in cm. The number of grains per panicle was counted from top most panicle of each hill from 8 selected hills in the net plot area and average was calculated. Sterility percentage was calculated by using the following formula.

$$\text{Sterility percentage} = \frac{\text{Number of unfilled grains} * 100\%}{\text{Total number of grains}} \quad (2)$$

The number of grains per panicle was counted from the top most panicle of each hill from 8 selected hills in net plot area and again filled grains were separated from unfilled and counted separately. Finally, the average was calculated. One thousand grains were counted from the randomly selected panicles. Their weight was measured with the help of electronic balance and expressed in grams.

Yield and yield parameters (Grain yield, straw yield and biological yield)

Grains were harvested from each 4 square meter net plot by threshing, and the moisture content of the freshly harvested grains was recorded. These measurements allowed for the conversion of grain yield into tons per hectare, using a standardized moisture content of 14%.

$$\text{Grain yield } \left(\frac{\text{kg}}{\text{ha}}\right) = \frac{[(100-\text{MC}) * \text{plot yield (kg)} * 10000 \text{ (m}^2\text{)}]}{[(100-14) * \text{net plot area (m}^2\text{)}]} \quad (3)$$

Where, MC is the moisture content of fresh grain yield.

The straw from each net plot was sun-dried, and the dry weight was recorded, and then expressed in tons per hectare after the necessary calculations were made.

Data analysis

All the recorded data was systematically organized by treatment and replicated three times, based on various observed parameters, using MS Excel 2010. For the analysis of variance and other related data parameters, different statistical tools including Excel and R Studio version 4.1.0 were employed.

Results and Discussion

Growth parameters

Plant height (cm)

At 15 DAT, genotype IR1N118 displayed superior plant height at 42.80 cm which was statistically at par with CH 45 (42.11 cm), HH1 (41.32 cm), IR16L1619 (39.98 cm). Similarly, Chaite-5 was with small plant height (34.96 cm) which was statistically at par with IR86515 (37.96 cm). Conversely, Chaite-5 exhibited a shorter plant height at 34.96 cm, which was statistically similar to IR86515 (37.96 cm). By 30 DAT, genotype CH 45 led in plant height at 59.00 cm, statistically equivalent to HH1 (55.00 cm), followed by IR1N118 (54.70 cm), which was statistically akin to IR16L1619 (51.34 cm) and Chaite-5 (50.81 cm). IR86515 remained the shortest at 49.94 cm. At 45 DAT, genotype CH 45 displayed the highest plant height at 84.29 cm, followed by HH1 (76.15 cm), which was statistically on par with Chaite-5 (73.22 cm) and Salijudi (72.74 cm). Conversely, IR16L1619 exhibited the shortest plant height at 50.49 cm. By 75 DAT, genotype CH 45 maintained the tallest plant height, on par with HH1 (109.00 cm), while Chaite-5 was next in line. The shortest plant height was observed in IR86515 (90.00 cm). At harvest, superior plant height was noted in CH 45 (113.50 cm), followed by HH1 (104.68 cm), which was statistically similar to Chaite-5 (98.96 cm) and IR1N118 (99.18 cm). Meanwhile, the smallest plant height was observed in IR86515 (90.98 cm).

The results indicate significant differences in plant height among the rice genotypes at various stages of growth. The genotype CH 45 consistently displayed superior plant height throughout the growth period, culminating in the highest height at harvest. The taller plants observed in CH 45 could be attributed to genetic factors influencing internodal elongation and overall plant development (Xing et al., 2018). This characteristic may contribute to increased light interception and enhanced photosynthetic activity, positively impacting yield (Ghimire et al., 2023b; Morales et al., 2020). The observed variation in plant height among genotypes may be indicative of diverse genetic backgrounds and adaptive strategies. For instance, Chaite-5 exhibited shorter plants, which might be attributed to its genetic makeup favoring compact growth. Such variations in plant height can have implications for crop management practices, especially in terms of fertilizer application, irrigation, and pest

control. The growth patterns observed at different stages, such as the early growth advantage of IR1N118 and the later dominance of CH 45, suggest a dynamic interaction between genotype and environmental factors influencing growth.

Table 2. Plant height of spring rice genotypes at different days of observation

Treatments	Plant height (cm)					
	15 DAT	30 DAT	45 DAT	60 DAT	75 DAT	Harvest
HH1	41.32 ^{ab}	55.00 ^{ab}	76.15 ^b	90.76	109.00 ^{ab}	104.68 ^b
IR16L1619	39.98 ^{ab}	51.34 ^b	50.49 ^d	92.80	99.10 ^{cd}	93.55 ^{cd}
Chaite-5	34.96 ^c	50.81 ^b	73.22 ^b	92.60	104.00 ^{bc}	98.96 ^{bc}
IR1N118	42.80 ^a	54.70 ^{ab}	61.05 ^c	93.39	99.90 ^{cd}	99.18 ^{bc}
CH 45	42.11 ^a	59.00 ^a	84.29 ^a	114.32	113.60 ^a	113.50 ^a
IR86515	37.96 ^{bc}	49.94 ^b	63.57 ^c	82.03	90.00 ^e	90.98 ^d
Salijudi	39.32 ^{ab}	53.96 ^{ab}	72.74 ^b	91.57	94.60 ^{de}	95.43 ^{cd}
Grand Mean	39.78	53.54	68.79	93.8	101.44	99.47
SEm (\pm)	1.090	1.609	2.343	2.69	2.199	2.219
LSD (0.05)	3.358	4.959	7.221	8.30	6.776	6.838
CV%	4.7	5.2	5.9	5.0	3.8	3.9
F-test	**	*	***	***	***	***

DAT = Days after transplanting; Data in columns with the same letters in DMRT are not significantly different ($p=0.05$); SEm (\pm) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; * = significant at $p<0.05$; ** = significant at $p<0.01$; *** = significant at $p<0.001$.

Number of tillers per m²

At 15 DAT, genotype IR1N118 exhibited the highest number of tillers per square meter (98.60/m²), which was statistically similar to the number of tillers observed in Salijudi (93.60/m²), followed by IR16L1619 (82.60/m²). In contrast, the lowest number of tillers was recorded in IR86515 (63.47/m²). Moving to 30 DAT, the number of tillers was highest in genotype IR1N118 (354.00/m²), which was statistically on par with CH 45 (347.20/m²), HH1 (298.40/m²), and Salijudi (260.30/m²). The fewest tillers were found in Chaite-5 (232.00/m²), which was statistically similar to IR16L1619 (212.80/m²). At 45 DAT, genotype IR1N118 continued to excel in the number of tillers per square meter (432.80/m²), statistically comparable to CH 45 (406.90/m²), Salijudi (359.20/m²), and HH1 (349.60/m²).

Conversely, IR86515 recorded the lowest number of tillers per square meter (266.70/m²), which was statistically similar to IR16L1619 (279.20/m²) and Chaite-5 (284.80/m²). By 60 DAT, genotype Salijudi took the lead with the highest number of tillers per square meter (428.00/m²), statistically on par with CH 45 (440/m²), followed by HH1 (355.20/m²) and IR18118 (353.60/m²). Meanwhile, IR86515 displayed the fewest tillers per square meter (275.20/m²), which was statistically similar to Chaite-5 (299.70/m²) and IR16L1619 (320.00/m²). At 75 DAT, genotype CH 45 emerged as the frontrunner with the highest number of tillers per square meter (439.50/m²). In contrast, IR86515 exhibited the lowest number of tillers per square meter (278.40/m²), which was statistically similar to IR16L1619 (296.50/m²), Chaite-5 (309.30/m²), HH1 (334.90/m²), IR1N118 (343.80/m²), and Salijudi (352.00/m²).

At the time of harvest, genotype CH 45 maintained its lead in the number of tillers per square meter (411.30/m²), statistically similar to IR16L1619 (370.40/m²) and IR1N118 (350.60/m²).

Conversely, IR86515 displayed the lowest number of tillers per square meter (257.30/m²), which was statistically similar to Chaite-5 (287.30/m²) and Salijudi (316.50/m²). The results indicate variations in the tillering patterns among different genotypes and highlight the specific characteristics of each genotype in terms of tiller development during the growth stages.

The number of tillers per square meter is a crucial determinant of rice productivity (Cui et al., 2023). Genotype IR1N118 consistently exhibited higher tiller numbers, indicating its prolific tillering ability. This characteristic could contribute to greater panicle density and ultimately higher grain yield (Abookheili & Mobasser, 2021; Chang et al., 2020). The early tillering advantage of IR1N118, evident at 15 DAT, may be attributed to genetic factors promoting rapid vegetative growth (Ghimire et al., 2023b). Genotypic differences in tillering observed in this study underscore the importance of selecting rice varieties with optimal tillering characteristics for specific agroecological conditions. The dynamic nature of tillering across growth stages emphasizes the need for tailored management practices, including spacing and nutrient application, to harness the full tillering potential of each genotype.

Table 3. Tiller number per square meter in spring rice genotypes

Treatments	Tiller number per m ²					
	15 DAT	30 DAT	45 DAT	60 DAT	75 DAT	At harvest
HH1	87.60 ^{bc}	298.40 ^{ab}	349.60 ^{ab}	355.20 ^{bc}	334.90 ^b	324.00 ^{bc}
IR16L1619	82.60 ^{cd}	212.80 ^b	279.20 ^b	320.00 ^{cd}	296.50 ^b	370.40 ^{ab}
Chaite-5	76.60 ^d	232.00 ^b	284.80 ^b	299.70 ^{cd}	309.30 ^b	287.30 ^{cd}
IR1N118	98.60 ^a	354.00 ^a	432.80 ^a	353.60 ^{bc}	343.80 ^b	350.60 ^{abc}
CH 45	77.33 ^{cd}	347.20 ^a	382.90 ^{ab}	406.90 ^{ab}	439.50 ^a	411.30 ^a
IR86515	63.47 ^e	238.40 ^b	266.70 ^b	275.20 ^d	278.40 ^b	257.30 ^d
Salijudi	93.60 ^{ab}	260.30 ^{ab}	359.20 ^{ab}	428.00 ^a	352.00 ^b	316.50 ^{bcd}
Grand Mean	82.8	278.00	336.00	348.40	336.00	331.10
SEm (±)	3.24	28.7	34.5	19.12	26.7	19.54
LSD(0.05)	9.98	88.5	106.3	58.91	82.3	60.22
CV%	6.8	17.9	17.8	9.5	13.8	10.2
F-test	***	*	**	***	*	**

DAT = Days after transplanting; Data in columns with the same letters in DMRT are not significantly different (p=0.05); SEm (±) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; * = significant at p<0.05; ** = significant at p<0.01; *** = significant at p<0.001.

Number of leaves per hill

The analysis of variance revealed statistically significant differences in the number of tillers per square meter among rice genotypes, except for observations made at 15 DAT, 30 DAT, and 45 DAT. Notably, at 15 DAT, both HH1 (20.87) and IR1N118 (18.73) exhibited higher leaf numbers. By 60 DAT, IR1N118 displayed the highest number of leaves (100.93), statistically comparable to HH1 (95.27), IR16L1619 (92.99), CH 45 (91.07), and Chaite-5 (87.60). Conversely, IR86515 (72.47) showed the lowest leaf count, similar to Salijudi (75.33). At 75 DAT, IR16L1619 led with 97.27 leaves, statistically comparable to HH1 (92.20), followed by IR1N118 (77.60) and CH 45 (77.47), while Salijudi recorded the lowest leaf number (64.33), similar to IR86515 (74.80) and Chaite-5 (72.80).

The significance of leaf number in influencing the overall photosynthetic capacity of rice plants is well-established (Zhou et al., 2021). The introduction of leaf number is warranted by its integral role in determining rice yield, serving as the primary site for photosynthesis (Bhatt & Ghimire, 2024). Notably, genotype IR1N118 consistently demonstrated an advantage in leaf number, particularly at 60 DAT, suggesting sustained vegetative growth and a potential for efficient light interception. This observation aligns with the findings of Zhou et al. (2021) and underscores the importance of genetic diversity in leaf development and canopy architecture, which directly impacts overall crop performance (Kakar et al., 2022).

Table 4. Leaf number of spring rice genotypes at different days of observation

Treatments	Leaf number				
	15 DAT	30 DAT	45 DAT	60 DAT	75 DAT
HH1	20.87 ^a	67.13 ^a	93.63 ^a	95.27 ^{ab}	92.20 ^{ab}
IR16L1619	17.20 ^a	57.07 ^a	66.40 ^a	92.99 ^{abc}	97.27 ^a
Chaite-5	13.87 ^a	46.73 ^a	71.17 ^a	87.60 ^{abc}	72.80 ^{bc}
IR1N118	18.73 ^a	53.80 ^a	95.67 ^a	100.93 ^a	77.60 ^{abc}
CH 45	14.00 ^a	56.43 ^a	96.30 ^a	91.07 ^{abc}	77.47 ^{abc}
IR86515	11.23 ^a	42.97 ^a	64.20 ^a	72.47 ^c	74.80 ^{bc}
Salijudi	12.53 ^a	50.50 ^a	75.33 ^a	75.33 ^{bc}	64.33 ^c
Grand Mean	15.5	53.5	80.4	88.0	79.5
SEm (\pm)	2.82	10.93	12.12	6.15	6.37
LSD(0.05)	8.70	33.69	37.36	18.94	19.62
CV%	31.6	35.4	26.1	12.1	13.9
F-test	NS	NS	NS	*	*

DAT = Days after transplanting; Data in columns with the same letters in DMRT are not significantly different ($p=0.05$); SEm (\pm) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; * = significant at $p<0.05$; NS = non-significant.

Leaf area index

At 30 DAT, the LAI was not found to be statistically significant. Nevertheless, it is noteworthy that genotype HH1 exhibited the highest LAI value (9.17), which was statistically comparable to IR1N118 (8.72), followed by IR16L1619 (8.60). In contrast, Salijudi had the lowest LAI value (4.67). Moving to 60 DAT, the LAI was highest in genotype IR1N118 (28.33), which was statistically similar to HH1 (24.33), and was followed by Chaite-5 (19.33) and IR16L1619 (19.00). Conversely, the lowest LAI was recorded in Salijudi (10.67), which was statistically similar to CH 45 (12.00) and IR86515 (18.67). At harvest, genotype IR16L1619 displayed superiority in LAI with a value of (8.00), which was statistically similar to IR1N118 and IR86515, both with values of 7.34, HH1 (7.00) and Chaite-5 (5.34). In contrast, Salijudi exhibited the lowest LAI value (2.00), which was statistically similar to CH 45 (3.34).

LAI is a key indicator of the canopy's light-intercepting capacity and, consequently, photosynthetic efficiency (Ghimire et al., 2023b). Genotype IR1N118 displayed higher LAI values at 30 and 60 DAT, suggesting its superior ability to capture sunlight and convert it into biomass. The positive correlation between LAI and grain yield is consistent with the understanding that an efficient canopy structure contributes to increased grain production (Liu et al., 2021; Zhang et al., 2021). The observed differences in LAI among genotypes underscore the importance of canopy architecture in rice productivity. Further research

exploring the genetic determinants of LAI and its dynamic changes throughout the growing season could provide valuable insights for breeding high-yielding varieties.

Table 5. LAI of different rice varieties at different days of observation

Treatments	Leaf area index		
	30 DAT	60 DAT	Harvest
HH1	9.17 ^a	24.33 ^{ab}	7.00 ^a
IR16L1619	8.60 ^a	19.00 ^{bc}	8.00 ^a
Chaite-5	4.50 ^a	19.33 ^{bc}	5.34 ^{ab}
IR1N118	8.72 ^a	28.33 ^a	7.34 ^a
CH 45	5.67 ^a	12.00 ^{cd}	3.34 ^{bc}
IR86515	5.28 ^a	18.67 ^{bcd}	7.34 ^a
Salijudi	4.67 ^a	10.67 ^d	2.00 ^c
Grand Mean	6.66	18.90	5.76
SEm (±)	1.82	2.48	0.840
LSD(0.05)	5.60	7.658	2.590
CV%	47.30	22.8	25.3
F-test	NS	**	**

DAT = Days after transplanting; Data in columns with the same letters in DMRT are not significantly different ($p=0.05$); SEm (±) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; * = significant at $p<0.01$; NS = non-significant.

Yield attributing parameters

Number of effective tillers per hill and flag leaf length

The analysis of variance indicates that different rice genotypes do not have a significant effect at ($P>0.05$) on the number of effective tillers per square meter. However, noteworthy observations include a higher number of effective tillers per hill observed in IR16L1619 (23.10), which is statistically similar to CH 45 (21.96), Salijudi (20.42), IR1N118 (19.67), HH1 (18.75), and Chaite-5 (16.34). Conversely, the lowest number of effective tillers was observed in IR86515 (15.04).

In contrast, the analysis of variance demonstrates that different rice genotypes do have a significant effect ($P<0.001$) on flag leaf length. Specifically, Chaite-5 exhibited superiority in flag leaf length with a measurement of 33.13 cm, which was statistically comparable to Salijudi (30.22 cm) and HH1 (29.88 cm). Conversely, the smallest flag leaf length was observed in IR1N118 (27.50 cm), which was statistically similar to IR86515 (28.18 cm).

While the number of effective tillers per square meter did not show significant differences among genotypes, the flag leaf length exhibited notable variations. Chaite-5 stood out with a longer flag leaf, which is associated with enhanced photosynthetic efficiency. The positive correlation between flag leaf length and grain yield emphasizes the significance of optimizing this trait in rice breeding programs (Kong et al., 2023; Shahin et al., 2023). Understanding the genetic basis of flag leaf characteristics and their relationship with yield components can aid in the development of varieties with improved photosynthetic efficiency and, consequently, higher grain yields.

Panicle number, panicle length, grains per panicle, sterility percentage, filled grain per panicle and thousand grain weight

The analysis of variance has confirmed that different rice genotypes exert a significant effect ($P < 0.001$) on several key traits. Genotype IR16L1619 displayed superiority in panicle number, recording an average of 23.10 panicles per hill, which was statistically equivalent to CH 45 (21.96) and Salijudi (20.42). Conversely, the lowest panicle count was found in IR86515 (15.04), which was statistically similar to Chaite-5 (16.34). Furthermore, the analysis of variance demonstrated a significant effect ($P < 0.001$) of different rice genotypes on panicle length. Notably, IR16L1619 excelled in panicle length, reaching an average of 28.56 cm, a performance on par with IR1N118 (27.78 cm), Chaite-5 (27.04 cm), HH1 (25.63 cm), and CH 45 (25.54 cm). Conversely, Salijudi exhibited the shortest panicle length at 24.37 cm. The number of grains per panicle was also significantly influenced by different genotypes of rice. IR16L1619 outperformed in this aspect with an average of 270.10 grains per panicle, followed closely by Chaite-5 (214.30), which was statistically comparable to HH1 (203.20) and IR86515 (196.00). In contrast, CH 45 displayed the lowest number of grains per panicle at 120.00, a figure similar to Salijudi (131.80) and IR1N118 (163.60).

Sterility percentage, too, was significantly impacted by the diverse rice genotypes. Chaite-5 exhibited a higher sterility percent at 14.73%, statistically similar to HH1 (14.57%) and IR1N118 (13.55%). Conversely, the lowest sterility percent was observed in Salijudi at 7.52%, a figure statistically similar to CH 45 (7.77%) and IR16L1619 (9.66%). The analysis of variance demonstrated a significant effect ($P < 0.001$) of different rice genotypes on filled grain per panicle. Chaite-5 demonstrated the highest Filled grains (182.50) whereas the lowest filled grain per panicle was found in CH 45 (110.60). Lastly, the analysis of variance demonstrated a significant effect ($P < 0.001$) of different rice genotypes on thousand-grain weight. CH 45 recorded the maximum thousand grain weight at 26.40 g, a performance on par with Salijudi (25.26 g), IR1N118 (24.76 g), and IR16L1619 (23.91 g). In contrast, HH1 had a lower thousand-grain weight at 18.41 g, which was statistically similar to Chaite-5 (18.91 g) and IR86515 (19.02 g).

Genotypic differences in panicle number, panicle length, grains per panicle, and other yield-related traits highlight the diverse genetic makeup of the rice varieties studied (Ata-Ul-Karim et al., 2022; Demeke et al., 2023; Shanmugam et al., 2023). IR16L1619 exhibited superior performance in panicle-related traits, indicating its potential for high grain yield. Conversely, CH 45, while excelling in plant height, displayed comparatively lower values in panicle-related parameters, suggesting a trade-off between plant height and panicle characteristics. The sterility percentage observed in Chaite-5 emphasizes the importance of addressing reproductive development in rice breeding programs. Understanding the genetic basis of sterility and its interaction with environmental factors can contribute to the development of varieties with improved reproductive success (Ouyang et al., 2022).

Table 6. Yield attributes of different spring rice genotypes

Treatments	Effective tiller	Flag leaf length (cm)	Panicle number	Panicle length (cm)	Grains per panicle	Sterility %	Filled grain per panicle	TGW (g)
HH1	18.75 ^{abc}	29.88 ^{ab}	18.75 ^{abc}	25.63 ^{abc}	203.20 ^{bc}	14.57 ^a	173.80 ^{bc}	18.41 ^b
IR16L1619	23.10 ^a	29.53 ^b	23.10 ^a	28.56 ^a	270.10 ^a	9.66 ^b	176.60 ^{bc}	23.91 ^a
Chaite-5	16.34 ^{bc}	33.13 ^a	16.34 ^{bc}	27.04 ^{abc}	214.30 ^b	14.73 ^a	182.50 ^b	18.91 ^b
IR1N118	19.67 ^{abc}	27.50 ^b	19.67 ^{abc}	27.78 ^{ab}	163.60 ^{cd}	13.55 ^a	141.60 ^{cd}	24.76 ^a
CH 45	21.96 ^{ab}	30.57 ^{ab}	21.96 ^{ab}	25.54 ^{abc}	120.00 ^e	7.77 ^b	110.60 ^d	26.40 ^a

IR86515	15.04 ^c	28.18 ^b	15.04 ^c	25.13 ^{bc}	196.00 ^{bc}	8.73 ^b	246.70 ^a	19.02 ^b
Salijudi	20.42 ^{abc}	30.22 ^{ab}	20.42 ^{abc}	24.37 ^c	131.80 ^{de}	7.52 ^b	121.90 ^d	25.26 ^a
Grand Mean	19.32	29.86	19.32	26.29	185.6	10.93	164.8	22.38
SEm (\pm)	1.881	1.026	1.881	0.936	12.92	1.111	11.42	1.317
LSD (0.05)	5.797	3.163	5.797	2.885	39.81	3.422	35.19	4.058
CV%	16.9	6.0	16.9	6.2	12.1	17.6	12.0	10.2
F-test	*	*	*	*	***	***	***	**

TGW = Thousand grain weight; DAT = Days after transplanting; Data in columns with the same letters in DMRT are not significantly different ($p=0.05$); SEm (\pm) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; * = significant at $p<0.05$; ** = significant at $p<0.01$; *** = significant at $p<0.001$.

Yield parameters

Biological, grain and straw yield

The analysis of variance underscores the significant impact ($P<0.001$) of different spring rice varieties on both biological and grain yield. Notably, IR16L1619 stood out with a higher biological yield of 15.25 t/ha, a performance on par with IR86515 (14.86 t/ha), HH1 (14.45 t/ha), Chaite-5 (14.10 t/ha), and IR1N118 (12.21 t/ha). In contrast, Salijudi displayed a lower biological yield of 6.44 t/ha, a figure statistically similar to CH 45 (7.71 t/ha). Similarly, the analysis revealed that spring rice varieties significantly influenced grain yield. The highest grain yield was observed in IR16L1619 (8.19 t/ha), followed by IR86515 (7.78 t/ha), and Chaite-5 (7.53 t/ha), with HH1 (7.34 t/ha) and IR1N118 (6.84 t/ha) also performing well. Conversely, Salijudi recorded the lowest grain yield at 3.53 t/ha, a figure statistically similar to CH 45 (3.86 t/ha). When it comes to straw yield, IR86515 delivered a high yield of 7.12 t/ha, a result on par with IR86515 with (7.09 t/ha) and HH1 (7.05 t/ha). Conversely, Salijudi displayed a lower straw yield of 2.90 t/ha, a figure statistically similar to CH 45 (3.86 t/ha). These findings provide valuable insights into the performance of different spring rice varieties concerning biological, grain, and straw yield. These insights can assist in selecting the most suitable rice varieties for specific agricultural goals and conditions.

Biological yield, grain yield, and straw yield are pivotal components that collectively determine the overall productivity and economic viability of rice crops (Li et al., 2023; Ouyang et al., 2022). The distinct characteristics of these yield parameters offer insights into the genotypic variations in resource utilization, partitioning, and allocation (Ben Mariem et al., 2020; Bustos-Korts et al., 2019). The significant variations in biological, grain, and straw yield among genotypes revealed the need for careful selection of varieties based on specific agroecological conditions and management practices. The variations in straw yield among genotypes, with IR86515 exhibiting higher straw yield, suggest differences in the partitioning of assimilates between aboveground and belowground biomass and indicating efficient resource allocation to vegetative tissues. Biological yield is a critical indicator of the plant's overall growth and vigor, reflecting its ability to capture solar radiation and convert it into organic matter through photosynthesis (Araus et al., 2022). Grain yield is perhaps the most crucial parameter, representing the quantity of harvested rice grains. IR16L1619 emerged as a high-yielding genotype, exhibiting superior performance in both biological and grain yield, emphasizing its exceptional ability to convert assimilated resources into marketable grain. The grain yield is influenced by various factors, including the number of panicles, grains per panicle, and the percentage of filled grains. The observed high grain yield in IR16L1619 suggests favorable combinations of these factors, making it a promising candidate for rice cultivation in the region. Conversely, Salijudi displayed lower yields, emphasizing the need

for further investigation into factors influencing its yield potential. The observed trade-offs between different yield components highlight the complex interplay of genetic and environmental factors influencing overall yield.

Table 7. Biological, grain and straw yield of different spring rice genotypes

Treatments	Biological yield (t/ha)	Grain yield (t/ha)	Straw yield (t/ha)
HH1	14.45 ^a	7.34 ^a	7.05 ^a
IR16L1619	15.25 ^a	8.19 ^a	7.12 ^a
Chaite-5	14.10 ^a	7.53 ^a	6.58 ^{ab}
IR1N118	12.21 ^a	6.84 ^a	5.37 ^{bc}
CH 45	7.71 ^b	3.86 ^b	3.86 ^{cd}
IR86515	14.86 ^a	7.78 ^a	7.09 ^a
Salijudi	6.44 ^b	3.53 ^b	2.90 ^d
Grand Mean	12.15	6.44	5.71
SEm (\pm)	0.97	0.598	0.512
LSD (0.05)	2.997	1.84	1.57
CV%	13.9	16.1	15.5
F-test	***	***	NS

Data in columns with the same letters in DMRT are not significantly different ($p=0.05$); SEm (\pm) = standard error of the mean; CV = coefficient of variation; LSD = least significant difference; *** = significant at $p<0.001$; NS = non-significant.

Implications and future directions

The findings of this study contribute valuable insights into the genotype-specific responses of rice plants to the agroecological conditions in Gorkha district, Nepal. The observed variations in growth, yield, and yield attributing characters highlight the importance of selecting genotypes tailored to specific environmental conditions (Ghimire et al., 2023c). Future research endeavors should delve into the genetic and molecular mechanisms underlying the observed phenotypic variations, enabling the development of genetically superior rice varieties. The comprehensive analysis of biological, grain, and straw yield provides valuable insights into the performance of different rice genotypes in the Gorkha district, Nepal. These insights have practical implications for rice breeding programs, agronomic practices, and crop management strategies. Genotypes exhibiting superior biological and grain yield can be prioritized for further evaluation and potential inclusion in breeding programs aimed at developing high-yielding varieties tailored to the local agroecological conditions (Weltzien et al., 2019; Woldeyohannes et al., 2022).

Future research directions should focus on unraveling the genetic and physiological mechanisms governing the observed variations in yield parameters. Molecular and genomic approaches can be employed to identify key genes and pathways associated with enhanced biomass accumulation, grain filling, and resource utilization efficiency. Moreover, understanding the genotype-environment interactions influencing yield components is crucial for adapting rice varieties to the dynamic environmental conditions of the region.

Conclusion

The evaluation of local and improved rice genotypes has provided valuable insights into their growth, yield, and yield attributing characters. The study encompassed crucial parameters and shedding light on the diverse genetic characteristics and adaptive strategies of the examined genotypes. The results revealed the significance of genotype-specific responses across

different stages of growth. Genotype IR16L1619 emerged as a high-yielding genotype, excelling in panicle-related traits and contributing to its superior biological and grain yield. The observed trade-offs between different yield components underscore the complexity of interactions between genetic and environmental factors influencing overall yield. As agricultural systems face evolving challenges, the knowledge gained from this study can serve as a catalyst for the development of resilient and high-yielding rice varieties, ultimately supporting food security and livelihoods in the region. Further research into the genetic basis of key traits and their interactions with environmental factors can contribute to the sustainable improvement of rice production in the study area.

Acknowledgment

We are thankful to Prime Minister Agriculture Modernization Project of Government of Nepal, Agriculture and Forestry University, Nepal and Dr. Krishna Hari Dhakal for facilitating the study.

Author contribution statement

All authors listed have significantly contributed to the development and the writing of this article.

Data availability statement

Data will be made available on request.

Conflict of interest

The authors declare no conflict of interest.

Funding details

This article did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

ORCID

Shreeja Acharya  <https://orcid.org/0009-0000-4493-7581>

Sudip Ghimire  <https://orcid.org/0000-0003-2795-1351>

Roshan Thapa  <https://orcid.org/0009-0008-7643-1372>

Prakriti Bhattarai  <https://orcid.org/0009-0007-7015-6763>

Bidhya Poudel Chhetri  <https://orcid.org/0000-0001-6035-1468>

References

Abookheili, F. A., & Mobasser, H. R. (2021). Effect of planting density on growth characteristics and grain yield increase in successive cultivations of two rice cultivars. *Agrosystems, Geosciences & Environment*, 4(4), e20213. <https://doi.org/10.1002/agg2.20213>

Agriculture Information And Training Center. (2021). Agriculture Diary 2078 (pp. 1–350). Government of Nepal, Ministry of Agriculture and Livestock Development, Agriculture Information And Training Center. http://aitc.gov.np/downloadfile/agriculture%20diary%202078%20for%20web_1619513804.pdf

- Araus, J. L., Kefauver, S. C., Vergara-Díaz, O., Gracia-Romero, A., Rezzouk, F. Z., Segarra, J., Buchaillet, M. L., Chang-Espino, M., Vatter, T., Sanchez-Bragado, R., Fernandez-Gallego, J. A., Serret, M. D., & Bort, J. (2022). Crop phenotyping in a context of global change: What to measure and how to do it. *Journal of Integrative Plant Biology*, 64(2), 592–618. <https://doi.org/10.1111/jipb.13191>
- Ata-Ul-Karim, S. T., Begum, H., Lopena, V., Borromeo, T., Virk, P., Hernandez, J. E., Gregorio, G. B., Collard, B. C. Y., & Kato, Y. (2022). Genotypic variation of yield-related traits in an irrigated rice breeding program for tropical Asia. *Crop and Environment*, 1(3), 173–181. <https://doi.org/10.1016/j.crope.2022.08.004>
- Ben Mariem, S., González-Torralla, J., Collar, C., Aranjuelo, I., & Morales, F. (2020). Durum Wheat Grain Yield and Quality under Low and High Nitrogen Conditions: Insights into Natural Variation in Low- and High-Yielding Genotypes. *Plants*, 9(12), 1636. <https://doi.org/10.3390/plants9121636>
- Bhatt, S., & Ghimire, S. (2024). Quantifying the impact of nitrogen levels on spring maize varieties (*Zea mays* L.) in Kanchanpur, Nepal. *Innovations in Agriculture*, 01–08. <https://doi.org/10.25081/ia.2023-043>
- Bustos-Korts, D., Malosetti, M., Chenu, K., Chapman, S., Boer, M. P., Zheng, B., & Van Eeuwijk, F. A. (2019). From QTLs to Adaptation Landscapes: Using Genotype-To-Phenotype Models to Characterize G×E Over Time. *Frontiers in Plant Science*, 10, 1540. <https://doi.org/10.3389/fpls.2019.01540>
- Chang, S., Chang, T., Song, Q., Wu, J., Luo, Y., Chen, X., Zhu, X.-G., & Deng, Q. (2020). Architectural and Physiological Features to Gain High Yield in an Elite Rice Line YLY1. *Rice*, 13(1), 60. <https://doi.org/10.1186/s12284-020-00419-y>
- Chauhan, B. S., Mahajan, G., Sardana, V., Timsina, J., & Jat, M. L. (2012). Productivity and Sustainability of the Rice–Wheat Cropping System in the Indo-Gangetic Plains of the Indian subcontinent. In *Advances in Agronomy* (Vol. 117, pp. 315–369). Elsevier. <https://doi.org/10.1016/B978-0-12-394278-4.00006-4>
- Cock, J., Yoshida, S., & Forno, D. A. (1976). *Laboratory manual for physiological studies of rice*. Int. Rice Res. Inst. http://books.irri.org/9711040352_content.pdf
- Cui, J., Nishide, N., Mashiguchi, K., Kuroha, K., Miya, M., Sugimoto, K., Itoh, J.-I., Yamaguchi, S., & Izawa, T. (2023). Fertilization controls tiller numbers via transcriptional regulation of a MAX1-like gene in rice cultivation. *Nature Communications*, 14(1), 3191. <https://doi.org/10.1038/s41467-023-38670-8>
- Demeke, B., Dejene, T., & Abebe, D. (2023). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food & Agriculture*, 9(1), 2157099. <https://doi.org/10.1080/23311932.2022.2157099>
- Gairhe, S., Shrestha, H. K., & Timsina, K. (2018). Dynamics of Major Cereals Productivity in Nepal. *Journal of Nepal Agricultural Research Council*, 4, 60–71. <https://doi.org/10.3126/jnarc.v4i1.19691>
- Ghimire, S., Chhetri, B. P., & Shrestha, J. (2023). Efficacy of different organic and inorganic nutrient sources on the growth and yield of bitter melon (*Momordica charantia* L.). *Heliyon*, 9(11).

- Ghimire, S., Dhami, D., Shrestha, A., Budhathoki, J., Maharjan, M., Kandel, S., & Poudel Chhetri, B. (2023). Effectiveness of different combinations of urea and vermicompost on yield of bitter melon (*Momordica charantia*). *Heliyon*, 9(8), e18663. <https://doi.org/10.1016/j.heliyon.2023.e18663>
- Ghimire, S., Neupane, S., & Tharu, R. K. (2023). Comparative Study on the Seed Health of Five Commonly Cultivated Wheat Varieties (*Triticum aestivum* L.) in Nepal. *AgroEnvironmental Sustainability*, 1(1), 3-11.
- IRRI. (2018). *World rice statistics database*. International Rice Research Institute. <http://ricestat.irri.org:8080/wrs>
- Kakar, N., Jumaa, S. H., Sah, S. K., Redoña, E. D., Warburton, M. L., & Reddy, K. R. (2022). Genetic Variability Assessment of Tropical Indica Rice (*Oryza sativa* L.) Seedlings for Drought Stress Tolerance. *Plants*, 11(18), 2332. <https://doi.org/10.3390/plants11182332>
- Kharel, L., Ghimire, S. K., Shrestha, J., Kunwar, C. B., & Sharma, S. (2018). Evaluation of rice genotypes for its response to added fertility levels and induced drought tolerance during reproductive phase: Rice genotypes responses to added fertility levels and drought. *Journal of AgriSearch*, 5(1), 13–18. <https://jsure.org.in/journal/index.php/jas/article/view/396>
- Kong, B., Ma, J., Zhang, P., Chen, T., Liu, Y., Che, Z., Shahinnia, F., & Yang, D. (2023). Deciphering key genomic regions controlling flag leaf size in wheat via integration of meta-QTL and in silico transcriptome assessment. *BMC Genomics*, 24(1), 33. <https://doi.org/10.1186/s12864-023-09119-5>
- Krupnik, T. J., Timsina, J., Devkota, K. P., Tripathi, B. P., Karki, T. B., Urfels, A., ... & Ghimire, Y. N. (2021). Agronomic, socio-economic, and environmental challenges and opportunities in Nepal's cereal-based farming systems. *Advances in Agronomy*, 170, 155-287. Elsevier. <https://doi.org/10.1016/bs.agron.2021.06.004>
- Li, Z., Shen, Y., Zhang, W., Zhang, H., Liu, L., Wang, Z., ... & Yang, J. (2023). Effects of long-term straw returning on rice yield and soil properties and bacterial community in a rice-wheat rotation system. *Field Crops Research*, 291, 108800. <https://doi.org/10.1016/j.fcr.2022.108800>
- Liu, Y., Yang, M., Yao, C., Zhou, X., Li, W., Zhang, Z., Gao, Y., Sun, Z., Wang, Z., & Zhang, Y. (2021). Optimum Water and Nitrogen Management Increases Grain Yield and Resource Use Efficiency by Optimizing Canopy Structure in Wheat. *Agronomy*, 11(3), 441. <https://doi.org/10.3390/agronomy11030441>
- MoALD. (2021). Statistical Information on Nepalese Agriculture 2076/77 (2019/20) (p. 306). Government of Nepal, Ministry of Agriculture and Livestock Development, Planning and Development Cooperation Coordination Division, Statistics and Analysis Section. <https://moald.gov.np/wp-content/uploads/2022/04/STATISTICAL-INFORMATION-ON-NEPALESE-AGRICULTURE-2076-77-2019-20.pdf>
- Morales, F., Ancín, M., Fakhet, D., González-Torrallba, J., Gámez, A. L., Seminario, A., Soba, D., Ben Mariem, S., Garriga, M., & Aranjuelo, I. (2020). Photosynthetic Metabolism under Stressful Growth Conditions as a Bases for Crop Breeding and Yield Improvement. *Plants*, 9(1), 88. <https://doi.org/10.3390/plants9010088>

- NPPR. (2015). Nepal Portfolio performance review (NPPR) 2015 (p. 115). Government of Nepal, Ministry of Finance. https://www.mof.gov.np/uploads/document/file/report_2015_20150914084119.pdf
- Ouyang, Y., Li, X., & Zhang, Q. (2022). Understanding the genetic and molecular constitutions of heterosis for developing hybrid rice. *Journal of Genetics and Genomics*, 49(5), 385–393. <https://doi.org/10.1016/j.jgg.2022.02.022>
- Shahin, Md. N. H., Md. Harun-Or-Rashid, Atikuzzamman, Md., Uddin, M. R., & Kobir, Md. S. (2023). Assessment of Genetic Variability for Yield and Yield Contributing Characters in Rice (*Oryza sativa* L.). *Asian Journal of Agricultural and Horticultural Research*, 10(4), 281–296. <https://doi.org/10.9734/ajahr/2023/v10i4269>
- Shanmugam, A., Suresh, R., Ramanathan, A., Anandhi, P., & Sassikumar, D. (2023). Unravelling genetic diversity of South Indian rice landraces based on yield and its components. *Electronic Journal of Plant Breeding*, 14(1), 160–169. <https://doi.org/10.37992/2023.1401.007>
- Swinnen, J., & McDermott, J. (2020). COVID-19 and global food security. *EuroChoices*, 19(3), 26-33. <https://doi.org/10.2499/p15738coll2.133762>
- Tripathi, B. P., Bhandari, H. N., & Ladha, J. (2019). Rice Strategy for Nepal. *Acta Scientific Agriculture*, 3(2), 171–180. <https://actascientific.com/ASAG/pdf/ASAG-03-0351.pdf>
- Weltzien, E., Rattunde, F., Christinck, A., Isaacs, K., & Ashby, J. (2019). Gender and farmer preferences for varietal traits: evidence and issues for crop improvement. *Plant breeding reviews*, 43, 243-278. Wiley. <https://doi.org/10.1002/9781119616801.ch7>
- Woldeyohannes, A. B., Iohannes, S. D., Miculan, M., Caproni, L., Ahmed, J. S., De Sousa, K., Desta, E. A., Fadda, C., Pè, M. E., & Dell'Acqua, M. (2022). Data-driven, participatory characterization of farmer varieties discloses teff breeding potential under current and future climates. *eLife*, 11, e80009. <https://doi.org/10.7554/eLife.80009>
- Xing, F., Han, Y., Feng, L., Zhi, X., Wang, G., Yang, B., Fan, Z., Lei, Y., Du, W., Wang, Z., Xiong, S., Li, X., & Li, Y. (2018). Genotypic variation in spatiotemporal distribution of canopy light interception in relation to yield formation in cotton. *Journal of Cotton Research*, 1(1), 13. <https://doi.org/10.1186/s42397-018-0012-z>
- Zhang, H., Jing, W., Zhao, B., Wang, W., Xu, Y., Zhang, W., ... & Yang, J. (2021). Alternative fertilizer and irrigation practices improve rice yield and resource use efficiency by regulating source-sink relationships. *Field Crops Research*, 265, 108124. <https://doi.org/10.1016/j.fcr.2021.108124>
- Zhou, C., Jia, B., Wang, S., Huang, Y., Wang, Y., Han, K., & Wang, W. (2021). Effects of Nitrogen Fertilizer Applications on Photosynthetic Production and Yield of Japonica Rice. *International Journal of Plant Production*, 15(4), 599–613. <https://doi.org/10.1007/s42106-021-00156-2>