



## Agro-morphological and Genotypic Diversity among Rice Germplasms under Rainfed Lowland Condition

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### ABSTRACT

The present study was performed in a randomized complete block design with three replications to identify higher yielding genotypes and putative traits for grain yield improvement under a rainfed environment. Genotypes recorded highly significant variation for most of the observed agro-morphological traits except the number of effective tillers/m<sup>2</sup>. IR102774-31-21-2-4-7 (5.40 t/ha) followed by IR99739: 2-1-1-2-1 (5.22 t/ha), and IR103587-23-2-1-B (5.05 t/ha) respectively were the higher grain yielders. These high yielders were among the sets of early flowering (85-96 days) and maturing (120-130 days) genotypes. Plant height (PHT- 86.62% and 25.69%), harvest index (HI- 87.17% and 44.66%), and thousand-grain weight (TGW- 71.06% and 30.05%) recorded high heritability values coupled with higher genetic advance as a percentage of the mean (GAM). IR102774-31-21-2-4-7 produced superior agro-morphological character for several traits like grain yield, thousand-grain weight, biological yield, plant height, and days to flowering and maturity. Plant height, biological yield, harvest index, days to flowering, and maturity were highly associated with grain yield and had medium to high heritability and GAM values. Therefore, these traits might be of importance for selection in grain yield improvement of rice under rainfed lowland conditions.

### INTRODUCTION

Rice (*Oryza sativa* L.,  $2n = 2x = 24$ ) is the premier cereal crop dominating Nepal's production and food culture. It is cultivated in a 1.46 million hectare area with 5.55 million tons production and 3.80 t/ha productivity (MoALD, 2021). The country boasts more than 1700 rice landraces with diverse adaptation from 60 – 3050 m altitude and is considered one of the important centers for rice genetic resources (CDD, 2015; Mallick, 1981). Currently, the National agriculture genetic resources center conserves about 2605 accessions of rice as orthodox seeds (Genebank, 2020). Additionally, several released and registered rice varieties, including hybrids, are 130, recommended for different agro-ecological domains of Nepal (AITC,

2021). Rice is mainly grown in two major production environments, rainfed and irrigated, from Terai to Mountainous regions of Nepal (MoALD, 2017).

Rainfed rice is an integral component of the rice ecosystem, covering an almost equal area to irrigated rice in the mountains, followed by 40% in hills, 25% in terai, and 30% area coverage in the country (MoALD, 2017). Worldwide, the rainfed environment contributes about 19% from about 52 million hectares of land (GRiSP, 2013). In the present scenario of abnormal climatic conditions, drought has been a significant factor limiting rice production in rainfed environments. Several researchers from different countries reported yield loss in rice from 23 to 69% under a varied degree of drought compared to attainable yield under normal

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conditions (Torres & Henry, 2018; Yang, Wang, Chen, Li, & Cao, 2019). In Nepal, rice yield under a rainfed environment is almost 34% lower than that of the irrigated environment (MoALD, 2017). This suggests the need for improvement in existing varieties or development of new varieties with a higher degree of drought tolerance.

Researchers had reported a pattern of decrease in the area with a reduction in grain yield; a higher reduction was observed in rainfed districts of the eastern, central, and mid-western regions of Nepal (Gumma, Gauchan, Nelson, Pandey, & Rala, 2011). Among several mechanisms, drought escape may be effective in areas where predictive drought occurs. Rice cultivation in the mid-western river basin area usually suffers from drought at the reproductive stage. In such regions, early maturing rice genotypes were found beneficial as they complete or expose minimal to drought during a critical stage of their crop cycle (Dhakal et al., 2020; Panda, Mishra, & Behera, 2021; Tripathi, Adhikari, Pokhrel, & Adhikari, 2019). The primary focus in rice breeding, particularly for Nepal, is to develop high-yielding and stress-tolerant rice genotypes with desirable grain qualities (Tripathi, Bhandari, & Ladha, 2019).

Modern plant breeding identifies “creation of variation” to be the first step in crop improvement programs. The more the variation exhibited within the population, the more chances are there for desirable improvements in the traits. Genetic variability study is significantly vital for breeders as the information of genotypic and phenotypic variation, heritability, and genetic advance provides critical decisions while selecting traits for crop improvement. A highly heritable trait with a higher genetic advance is always preferred. In addition to the genetic parameters, association study between dependent and independent traits assists in the improvement of some quantitative traits. For traits like grain yield, direct selection is less effective as it is controlled by polygenes. In such a case, selecting traits that directly or indirectly contribute to it are the prime targets. Association study assists breeders in identifying traits with a higher value from the lesser important ones, which eventually contributes to the success of designed breeding program.

The present study focuses on identifying high-yielding genotypes that could be cultivated as alternatives to existing lower-yielding varieties.

In addition, genetic parameters; genotypic and phenotypic variation, heritability, and genetic advance along with character association analysis were performed to identify putative traits for future grain yield improvement program under rainfed lowland condition.

## MATERIALS AND METHODS

### Experimental Site and Setup

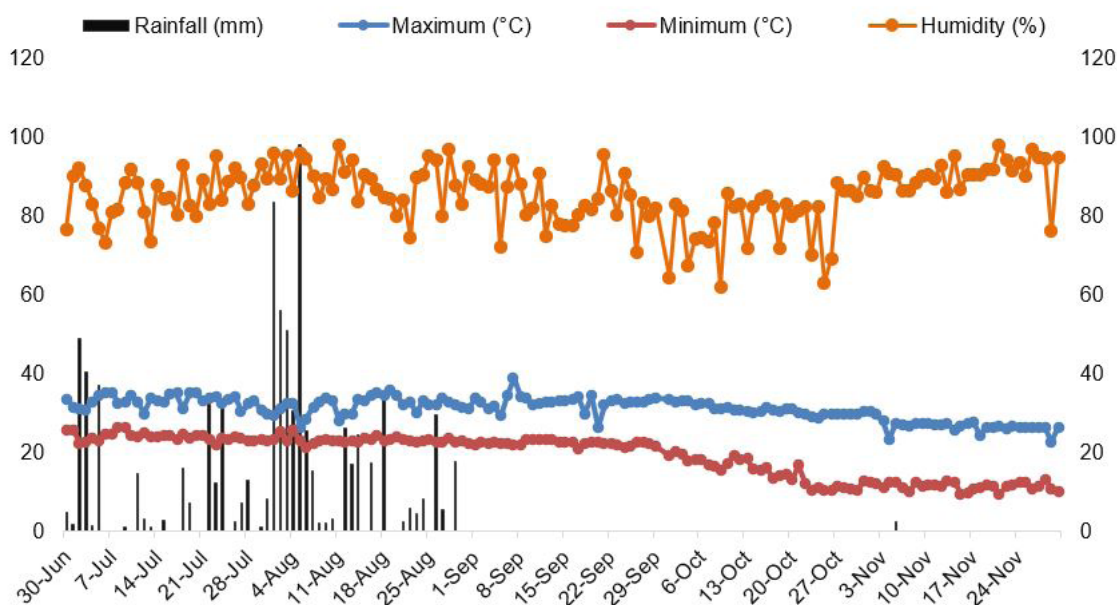
The field experiment was conducted at the Directorate of Agricultural Research, Karnali Province, Dasharathpur, Surkhet (28°30' northern latitude, 81°47' eastern longitude, and 490 meters above mean sea level) from June to November 2018 under rainfed lowland condition. Soil of research site was slightly acidic (pH = 6.1) with medium soil organic matter (1.98%), Nitrogen (0.0964%), and Potassium content (102.51 mg/kg), high Phosphorous (30.038 mg/kg) and sandy loam soil texture. The average maximum and minimum temperatures during the study periods were 31.88°C and 20.03°C, respectively. June was the hottest month (35.5°C), followed by July (33°C). The minimum temperature followed a similar trend with values of 24.2°C and 24°C for June and July, respectively. The experimental block received a total rainfall of 1016.4 mm during sowing to harvesting time, with an average rainfall of 169.4 mm per month. However, very little or no rainfall was recorded for September, October, and November (Fig. 1).

Nineteen rice germplasms obtained from National Rice Research Program (NRRP) were deployed in a Randomized Complete Block Design (RCBD) with three replications. Those genotypes consisted of lines developed by International Rice Research Institute (IRRI) and a variety released from NRRP (Table 1). For the field study, seedlings were raised from available rice germplasms and transplanted in the main field when it attained 30 days of age (July 29, 2018). Transplantation was slightly delayed due to the late onset of the monsoon. Within the field, replications were spaced a meter, and plots, a half. The individual plot size was 8 m<sup>2</sup> (4m × 2m) with ten rows and twenty hills in a crop geometry of 20cm × 20cm. As when it was required, all other cultural practices were performed following recommended practices of the Nepal Agricultural Research Council. The net plot was 6.84 m<sup>2</sup> (3.8m × 1.8m), an outer border excluded during crop harvesting.

**Table 1.** Details of the rice germplasms used in the study

Entry	Designation	Source	Entry	Designation	Source
1	NR2181- 139- 1- 3- 1- 1-1-1	NRRP	11	IR10281- 10- 227- 1- 2- 9	IRRI
2	IR103587- 23- 2- 1- B	IRRI	12	IR99739: 2- 1- 1- 2 -1	IRRI
3	IR15L 1745	IRRI	13	IR98785- 10- 1- 1- 3	IRRI
4	IR15L1735	IRRI	14	IR13F228	IRRI
5	NR2168- 44- 2- 1- 1- 1- 2- 1- 1	NRRP	15	IR13F402	IRRI
6	NR2179- 82- 2- 4- 1- 1- 1- 1	NRRP	16	NR2169- 10- 1- 1- 6- 2- 1- 3- 1	NRRP
7	IR106529- 20- 40- 3- 2- B	IRRI	17	IR16D1058	IRRI
8	IR102774- 31- 21- 2- 4- 7	IRRI	18	IR15D1031	IRRI
9	IR95784- 21- 1- 1- 2	IRRI	19	RADHA- 13	NRRP
10	IR99784- 255- 78- 2- 3- 1- 2	IRRI			

Remarks: IRRI: International Rice Research Institute, NRRP: National Rice Research Program



**Fig. 1.** Agrometeorological parameters recorded during field experimentation of rice germplasms under rainfed lowland conditions. Rainfall (bar graph) is represented by primary vertical axis, maximum, minimum temperature and humidity is represented in secondary vertical axis. Data source: Department of Hydrology and Meteorology, Mid & Far Western Regional Climate Office, Surkhet, Nepal (Mehelkuna site)

**Data Recording and Analysis**

Five random plants were selected from central rows in each plot for recording plant height (PHT- cm) and panicle length (PL- cm). The distance from ground level to the tip of the panicle, excluding awn and panicle base to the end, was recorded as plant height and panicle length, respectively. Recording of days to flowering (DTF) and maturity (DTM) followed population observation of 50% and 85%, respectively, in each plot. The number of fertile

tillers within a square meter area were counted to determine effective tillers/m<sup>2</sup> (ET). Grain yield and yield attributing traits, Straw (SY), biomass (BY), were converted to tons per hectare (t/ha) for the analysis. Biological yield and harvest index were calculated by adding straw and grain yield and grain to biological yield ratio. All field and post-harvest data recording followed the protocol of International Rice Research Institute (IRRI, 2013).

We performed data entry and processing in Microsoft Office Excel 2016, analysis of variance and comparisons of means ( $P < 0.05$ ) using R- Program 3.5.2 (R Core Team, 2019) and Crop Stat 7.2. Correlation analysis was performed using “ggcorrplot” package in R- program 3.5.2. Phenotypic, genotypic components, and Heritability estimation followed the methods of Falconer & Mackay (1996).

$$\text{Grain yield (ton/ha)} = \frac{\text{yield (kg/ha)}}{\text{plot area (m}^2\text{)}} \times \frac{(100-RM)}{(100-AM)} \times \frac{10000}{1000} \quad 1)$$

$$Vg = \frac{(TrMS-ErMS)}{r} \quad \dots\dots\dots 2)$$

$$Vp = \frac{TrMS-ErMS}{r} + ErMS \quad \dots\dots\dots 3)$$

$$Ve = Vp - Vg \quad \dots\dots\dots 4)$$

$$PCV = \frac{\sqrt{Vp}}{x} \quad \dots\dots\dots 5)$$

$$GCV = \frac{\sqrt{Vg}}{x} \quad \dots\dots\dots 6)$$

$$\text{Broad sense heritability (H)} = \frac{Vg}{Vp} \quad \dots\dots\dots 7)$$

$$GA = K \times \sigma p \times H \quad \dots\dots\dots 8)$$

$$GAM = \left(\frac{GA}{x}\right) \times 100 \quad \dots\dots\dots 9)$$

Where, RM: recorded moisture, AM: adjusted moisture (12.5%), ha: hectare, Vg: genotypic variance, TrMS: treatment mean sum of squares for the trait, ErMS: error mean sum of squares, r: number of replications, Vp: Phenotypic variance, Ve: Environmental variance, PCV: Phenotypic coefficient of variation, x: grand mean of the trait, GCV: Genotypic coefficient of variation, GA: Genetic advance, K: selection intensity (5% - 2.06), : phenotypic standard deviation, GAM: Genetic advance as a percentage of the mean.

Estimated heritability was categorized into low (0-30%), medium (30-65%), and high (>65%) by slight modification as described by Robinson, Comstock, & Harvey (1949). As a modification, upper-class value for medium and lower class value of high category increased by 5%. Genetic advance (GA) and Genetic advance as a percentage of the mean (GAM) were calculated by using a formula as suggested by Johnson, Robinson, & Comstock (1955). GAM was categorized as low (0-10%), medium (10-20%), and high (greater or equal to 20%) as given by Falconer & Mackay (1996) and Johnson, Robinson, & Comstock (1955). UPGMA clustering was performed based on the method of Ward Jr (1963) using Minitab 19 software.

## RESULTS AND DISCUSSION

### Analysis of the Variance

Variation is the first requirement for the improvement of any trait. When there is high variation among genotypes for the concerned trait, there lies ample opportunity for advancement. This study found highly significant ( $P < 0.01$ ) differences for days to 50% flowering (DTF), days to 85% maturity (DTM), panicle length (PL), plant height (PH), biological yield (BY), harvest index (HI), thousand-grain weight (TGW), grain yield (GY) and the non-significant effect was observed for effective tillers per meter square (ET) (Table 2). As in the present study, significant variation among evaluated rice genotypes was reported by several researchers (Abebe, Alamerew, & Tulu, 2017; Adhikari, Joshi, Shrestha, & Bhatta, 2018; Lipi et al., 2021; Tiwari, Tripathi, Tripathi, Khatri, & Bastola, 2019). In line with our results, Adhikari, Mehera, & Haefele (2018) also reported non-significant variation among genotypes for effective tillers per meter square.

### Agro-morphological Variation among Genotypes

DTF and DTM range recorded among the genotypes were 85-111 and 116-148 days, respectively. Among the nineteen genotypes, five genotypes recorded 15 days early flowering in comparison to the check genotype. Similar was the trend with DTM, where the early maturing set of genotypes had 15 days early maturation compared to the check genotype (Radha- 13) (Table 2). Genotypes IR99784- 255- 78- 2- 3- 1- 2 and IR99739: 2- 1- 1- 2 -1 took 85.33 days for flowering whereas IR98785- 10- 1- 1- 3, IR15L 1745, and Radha- 13 (check) took 86.67, 87, and 103.67 days respectively. Earliest DTM was recorded from IR99784- 255- 78- 2- 3- 1- 2 (116 days) followed by IR99739: 2- 1- 1- 2 -1 (121 days), IR98785- 10- 1- 1- 3 (124 days) and IR15L1735 (125.33 days) respectively while Radha- 13 had 142.33 days of maturity duration. We observed that early maturing genotypes had higher grain yield patterns except a few (Table 2). This might be attributed to differences in genotypic potential. Genotypes with earliness are favored under likely conditions of terminal drought as they could complete the life cycle before its commencement (Fukai, 1999). The possibility of terminal drought under the rainfed condition of the experimental site is depicted in Fig. 1, where rainfall during the last half period of the season was recorded none or very low. This indicated that most genotypes

with a longer maturity duration experienced moisture stress during pollen development and grain filling.

The association study (Table 3) also depicted significant negative relation of maturity duration and flowering with grain yield of genotypes. In previous reports, high-yielding genotypes had maturity below

122 days under similar study conditions (Adhikari, Mehera, & Haefele, 2018; Dhakal et al., 2020). Tripathi, Adhikari, Pokhrel, & Adhikari (2019) also reported a higher yield of genotype with early flowering nature under rainfed lowland conditions at Surkhet, Nepal.

**Table 2.** Agro- morphological performance of nineteen rice genotypes under rainfed lowland condition

Genotypes	DTF	DTM	PL (cm)	PHT (cm)	ET	BY (t/ha)	HI	TGW (g)
NR2181- 139- 1- 3- 1- 1-1-1	100.33 <sup>e</sup>	142.00 <sup>b</sup>	25.63 <sup>cdefg</sup>	106.40 <sup>cd</sup>	255.00	12.69 <sup>abcd</sup>	0.26 <sup>hij</sup>	20.80 <sup>efg</sup>
IR103587- 23- 2- 1- B	91.00 <sup>h</sup>	127.67 <sup>d</sup>	23.47 <sup>hi</sup>	102.87 <sup>d</sup>	206.00	10.53 <sup>cde</sup>	0.42 <sup>ab</sup>	26.97 <sup>cd</sup>
IR15L 1745	87.00 <sup>ij</sup>	127.67 <sup>d</sup>	26.33 <sup>bcd</sup>	105.20 <sup>cd</sup>	229.00	10.18 <sup>cde</sup>	0.37 <sup>cd</sup>	20.40 <sup>fg</sup>
IR15L1735	91.67 <sup>h</sup>	125.33 <sup>de</sup>	25.00 <sup>efghi</sup>	100.00 <sup>de</sup>	188.00	10.35 <sup>cde</sup>	0.27 <sup>hi</sup>	35.17 <sup>a</sup>
NR2168- 44- 2- 1- 1- 1- 2- 1- 1	98.00 <sup>f</sup>	135.67 <sup>c</sup>	27.23 <sup>bcd</sup>	92.17 <sup>e</sup>	258.67	6.68 <sup>f</sup>	0.25 <sup>hij</sup>	25.43 <sup>de</sup>
NR2179- 82- 2- 4- 1- 1- 1- 1	110.33 <sup>ab</sup>	146.67 <sup>ab</sup>	23.00 <sup>i</sup>	97.53 <sup>de</sup>	198.33	11.87 <sup>bcde</sup>	0.20 <sup>k</sup>	23.53 <sup>defg</sup>
IR106529- 20- 40- 3- 2- B	102.00 <sup>de</sup>	143.00 <sup>b</sup>	25.27 <sup>defgh</sup>	98.27 <sup>de</sup>	275.00	12.46 <sup>abcd</sup>	0.29 <sup>fgh</sup>	24.27 <sup>def</sup>
IR102774- 31- 21- 2- 4- 7	87.67 <sup>i</sup>	125.67 <sup>de</sup>	26.70 <sup>bcde</sup>	142.00 <sup>a</sup>	227.33	14.63 <sup>ab</sup>	0.32 <sup>efg</sup>	35.27 <sup>a</sup>
IR95784- 21- 1- 1- 2	101.67 <sup>de</sup>	136.67 <sup>c</sup>	27.20 <sup>bcd</sup>	99.13 <sup>de</sup>	225.67	9.89 <sup>cdef</sup>	0.22 <sup>jk</sup>	23.93 <sup>defg</sup>
IR99784- 255- 78- 2- 3- 1- 2	85.33 <sup>j</sup>	116.00 <sup>f</sup>	24.47 <sup>fghi</sup>	105.93 <sup>cd</sup>	202.00	11.40 <sup>cde</sup>	0.32 <sup>defg</sup>	32.50 <sup>a</sup>
IR10281- 10- 227- 1- 2- 9	95.00 <sup>g</sup>	134.00 <sup>c</sup>	26.40 <sup>bcd</sup>	123.40 <sup>b</sup>	218.33	12.42 <sup>abcd</sup>	0.35 <sup>de</sup>	19.30 <sup>g</sup>
IR99739- 2- 1- 1- 2 -1	85.33 <sup>j</sup>	121.33 <sup>e</sup>	28.13 <sup>b</sup>	112.73 <sup>c</sup>	252.33	12.97 <sup>abc</sup>	0.35 <sup>cde</sup>	27.53 <sup>bcd</sup>
IR98785- 10- 1- 1- 3	86.67 <sup>ij</sup>	124.67 <sup>de</sup>	31.20 <sup>a</sup>	98.53 <sup>de</sup>	208.33	8.71 <sup>ef</sup>	0.45 <sup>a</sup>	30.47 <sup>abc</sup>
IR13F228	95.33 <sup>g</sup>	136.67 <sup>c</sup>	26.73 <sup>bcde</sup>	101.53 <sup>d</sup>	236.00	12.19 <sup>bcd</sup>	0.33 <sup>def</sup>	27.10 <sup>bcd</sup>
IR13F402	111.00 <sup>a</sup>	148.00 <sup>a</sup>	25.47 <sup>cdefgh</sup>	99.07 <sup>de</sup>	259.00	14.61 <sup>ab</sup>	0.25 <sup>hij</sup>	31.83 <sup>ab</sup>
NR2169- 10- 1- 1- 6- 2- 1- 3- 1	104.67 <sup>c</sup>	146.33 <sup>ab</sup>	26.60 <sup>bcd</sup>	99.13 <sup>de</sup>	239.33	12.67 <sup>abcd</sup>	0.23 <sup>ijk</sup>	21.57 <sup>efg</sup>
IR16D1058	90.33 <sup>h</sup>	126.67 <sup>d</sup>	27.10 <sup>bcde</sup>	98.13 <sup>de</sup>	221.67	9.49 <sup>def</sup>	0.40 <sup>bc</sup>	25.47 <sup>de</sup>
IR15D1031	108.67 <sup>b</sup>	144.67 <sup>ab</sup>	27.47 <sup>bc</sup>	103.47 <sup>cd</sup>	223.33	11.44 <sup>bcde</sup>	0.28 <sup>gh</sup>	27.07 <sup>bcd</sup>
RADHA- 13	103.67 <sup>cd</sup>	142.33 <sup>b</sup>	24.33 <sup>ghi</sup>	146.00 <sup>a</sup>	213.33	15.43 <sup>a</sup>	0.21 <sup>k</sup>	21.77 <sup>efg</sup>
Grand Mean	96.61	134.26	26.20	106.92	228.25	11.61	0.30	26.34
F- test	**	**	**	**	ns	**	**	**
SEM	0.81	1.66	0.74	3.25	19.40	1.12	0.02	1.68
LSD (5%)	2.33	4.75	2.13	9.32	-	3.21	0.04	4.81
CV (%)	1.50	2.10	4.90	5.30	14.70	16.70	8.90	11.00

Remarks: DTF: days to 50% flowering, DTM: days to 85% maturity, PL: panicle length, PHT: plant height, ET: number of effective tillers per meter square, BY: biological yield, HI: harvest index, TGW: thousand-grain weight, SEM: standard error of the mean, LSD: least significant difference, CV: coefficient of variation, \* significant at P <0.05, \*\* significant at P <0.01, mean values with similar letters within the column denotes non-significant effect at P ≤ 0.05.

**Table 3.** Pearson's correlation coefficient among grain yield and yield attributing traits of nineteen rice genotypes studied under rainfed lowland conditions.

Traits	DTF	DTM	PL (cm)	PHT (cm)	ET	BY (t/ha)	HI	TGW (g)	GY (t/ha)
<b>DTF</b>	1.000								
<b>DTM</b>	0.936**	1.000							
<b>PL (cm)</b>	-0.264*	-0.152	1.000						
<b>PHT (cm)</b>	-0.138	-0.085	0.006	1.000					
<b>ET</b>	0.188	0.319*	0.180	-0.059	1.000				
<b>BY (t/ha)</b>	0.254	0.305*	-0.140	0.634**	0.224	1.000			
<b>HI</b>	-0.706**	-0.614**	0.341**	-0.077	-0.212	-0.314*	1.000		
<b>TGW (g)</b>	-0.262*	-0.388**	0.098	0.001	-0.055	0.019	0.145	1.000	
<b>GY (t/ha)</b>	-0.414**	-0.288*	0.184	0.470**	0.093	0.590**	0.557**	0.162	1.000

Remarks: DTF: days to 50% flowering, DTM: days to 85% maturity, PL: panicle length, PHT: plant height, ET: number of effective tillers per meter square, BY: biological yield, HI: harvest index, TGW: thousand-grain weight, GY: grain yield, \* significant at  $P < 0.05$ , \*\* significant at  $P < 0.01$ .

Genotypes recorded plant height, panicle length, and effective tillers per meter square within the range of 92-146 cm, 23-31.20 cm, and 188-275, respectively. Tallest plant height was recorded in RADHA- 13 (146 cm) followed by IR102774-31- 21- 2- 4- 7 (142 cm), IR10281- 10- 227- 1- 2- 9 (123.40 cm), IR99739: 2- 1- 1- 2- -1 (112.73 cm), and IR99784- 255- 78- 2- 3- 1- 2 (105.93 cm) respectively (Table 2). Plant height plays a vital role in grain yield produced by a genotype or a variety. This research found that grain yield and plant height had a highly significant positive correlation (Table 3), suggesting that grain yield increased with increased plant height. Increasing plant height is an appropriate way of increasing grain yield (Zhang et al., 2017). In accord with this finding, Zhao et al. (2020) also reported a significant and positive association of grain yield with plant height. Similarly, a positive effect of plant height on grain yield was disseminated based on several years of study (Li, Li, Ashraf, Liu, & Zhang, 2019). IR98785- 10- 1- 1- 3 had longest panicle (31.20 cm) corresponded by IR99739: 2- 1- 1- 2- -1 (18.13 cm), IR 15D 1031 (27.47 cm), NR2168- 44- 2- 1- 1- 1- 2- 1- 1 (27.20 cm), and RADHA- 13 (24.33 cm) respectively. A longer panicle with more filled grains directly contributes to the grain yield, but while the number of filled grains is less in ratio to unfilled grains, the case might be different. In our study, a non-significant positive association was found between panicle length and grain yield of genotypes. The result indicated a trend of increased grain yield with an increase in panicle length. Panicle length, additionally, had a significant negative relation with

days to maturity (Table 3). In late flowering genotypes, panicle exertion was poor in the field, contributing highly to determining filled grains per panicle and the overall grain yield of genotypes. Adhikari, Joshi, Shrestha, & Bhatta (2018), corroborating our current finding, forwarded a positive relation of panicle length with grain yield from their study.

In contrast, some studies reported genotypes with shorter panicle lengths also had higher grain yield under rainfed lowland conditions. Earliness enabled such genotypes to depart more dry matter than in the case of late-maturing genotypes with longer panicles (Dhakal et al., 2020). In accord with our study, Allah, Ammar, & Badawi (2010), under moisture stress conditions, disseminated a low positive association of panicle length with grain yield.

Number of effective tillers per meter square was recorded highest in IR106529- 20- 40- 3- 2- B (275) which was followed by IR13F402 (259), NR2168- 44- 2- 1- 1- 1- 2- 1- 1 (258.67), and RADHA- 13 (213.33) (Table 2). In general, the more effective tillers recorded per plot, the more grain yield production is possible. Under the rainfed condition, not all the effective tillers bear a higher number of filled grains as water stress limits them. Earlier genotypes could take advantage of available moisture in the field and depart more dry matter, while late maturing genotypes suffer badly from moisture stress (Kumar et al., 2006). In the present study, effective tillers per meter square had a low positive correlation to grain yield (Table 3). This suggested that a higher number of effective tillers were advantageous in grain yield, but their contribution was not large. Some

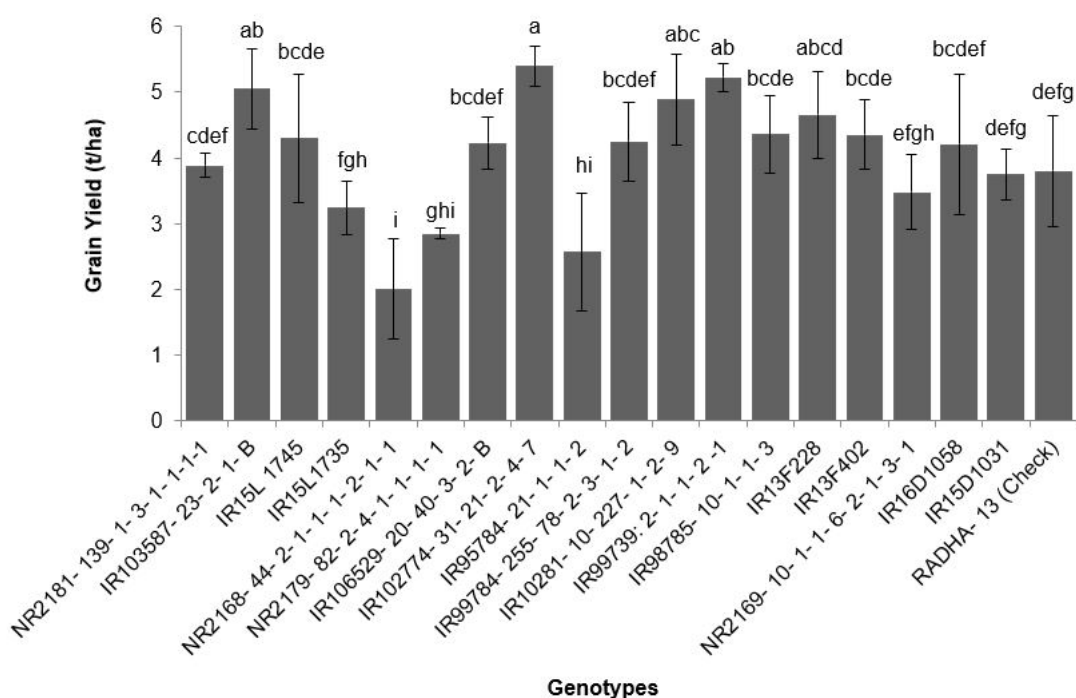
researchers forwarded a medium number of tillers to be much effective under rainfed lowland conditions. A higher number of tillers would fail to extract sufficient moisture during the grain filling period from the moisture-stressed soil (Akbar, Purwoko, Dewi, Suwarno, & Sugiyanta, 2019; Dhakal et al., 2020).

RADHA- 13 recorded the highest biological yield (15.43 t/ha) among the tested genotypes. Similarly, genotypes IR102774- 31- 21- 2- 4- 7, IR13F402, and IR99739: 2- 1- 1- 2 -1 produced biological yield of 14.63, 14.61, and 12.97 t/ha respectively. Biological yield comprises grain and straw yield in total. We observed the pattern of higher biological yield from the genotypes with earlier flowering and maturity. Early flowering genotypes had the advantage of the utilization of rainfall during the early season. They were exposed less to the moisture stress at their critical growth period due to their early flowering behavior (Panda, Mishra, & Behera, 2021). Moreover, the correlation between biological yield and grain yield was highly significant and positive (Table 3). These results suggested that genotypes with higher biomass also produced higher grain yield. Kumar et al. (2015) had similar findings and reported that genotypes with higher biological yield also produced higher yield advantage among genotypes tested under drought stress conditions. Genotypes IR102774- 31- 21- 2- 4- 7 (35.26 g), IR 15L 1735 (35.17 g), IR99784- 255- 78- 2- 3- 1- 2 (32.50 g) produced higher dry matter in grain, while lowest deposition was recorded in IR10281- 10- 227- 1- 2- 9 (19.30 g). Harvest index was highest for IR98785- 10- 1- 1- 3 (0.45) followed by IR103587- 23- 2- 1- B (0.43), IR 16D 1058 (0.40), and IR15L 1745 (0.37) respectively while RADHA- 13 (check) recorded 0.21.

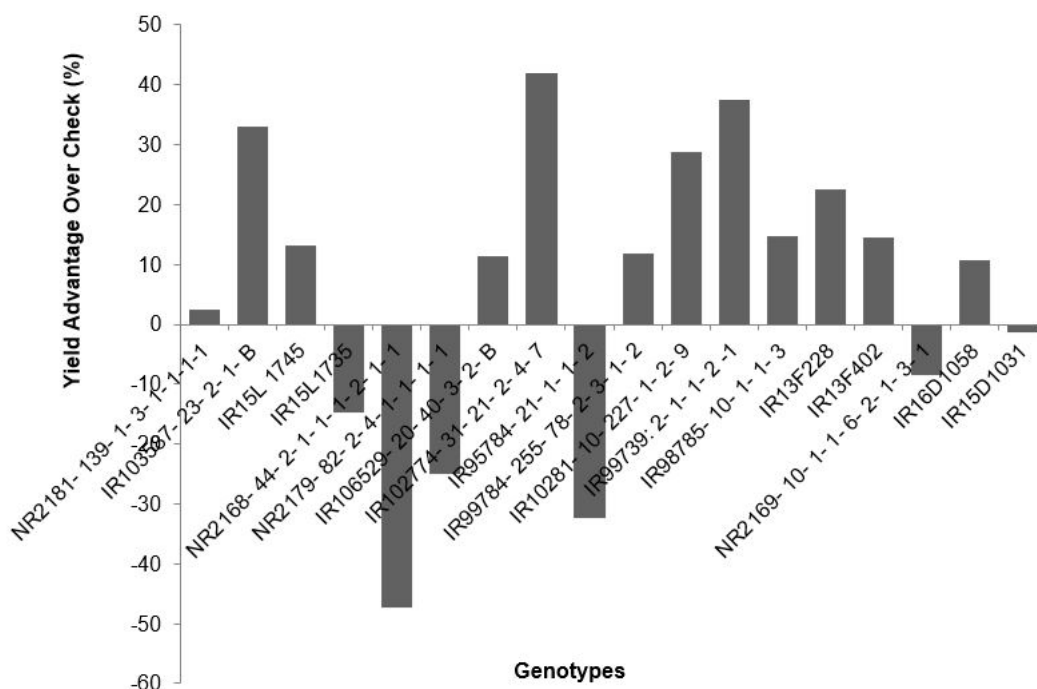
Dry matter deposition into the grains under rainfed conditions depends on the moisture available in the soil during the grain-filling period. Moisture stress at such a critical period would directly affect the boldness of grain. This study observed that thousand-grain weight and harvest index were higher for genotypes with early maturity (Table 2, Table 3). Early maturing genotypes utilized early season rainfall and partitioned more dry matter into the grain during the grain-filling period. The genotypes with the ability to partition dry matter at higher rates during terminal drought are suitable for overcoming late-season moisture stress under rainfed lowland conditions (Kumar et al., 2006).

Additionally, a positive correlation of TGW and a highly significant positive association of harvest index was found with the grain yield (Table 3). Adhikari, Joshi, Shrestha, & Bhatta (2018), Li, Li, Ashraf, Liu, & Zhang (2019) and Zhao et al. (2020) also reported a positive association of TGW with grain yield as in the present finding. Akbar, Purwoko, Dewi, Suwarno, & Sugiyanta (2019) disseminated TGW in the range of 21- 32g from the selected superior genotypes under rainfed lowland conditions. These reports sufficiently support the present findings.

Nineteen genotypes produced grain yield within the range of 2.00 to 5.40 t/ha, depicting considerable variability for grain yield (Fig. 2). The reason might be due to differences in the genotypic constitution and their response to the growing environment. Genotypes IR102774- 31- 21- 2- 4- 7 (5.40 t/ha) followed by IR99739: 2- 1- 1- 2 -1 (5.22 t/ha), and IR103587- 23- 2- 1- B (5.05 t/ha) were the higher yielders (Fig. 2). Yield advantage over check was highest for IR102774- 31- 21- 2- 4- 7 (42.02%) followed by IR99739: 2- 1- 1- 2 -1 (37.46%), IR103587- 23- 2- 1- B (32.98%), and IR10281- 10- 227- 1- 2- 9 (28.77%) respectively in comparison to Radha- 13 (Fig. 3). These high yielders were among the sets of early flowering (85- 96 days) and maturing (120- 130 days) genotypes. According to the meteorological reports (Fig. 1), rainfall during the second half of the growing season was recorded as very low or none. Previous work done in the same location reported poor water table and holding capacity of the soil, thus, drought occurrence at the late vegetative stage to grain filling time was quite common due to soil physical properties and reduced rainfall at the reproductive stage (Dhakal et al., 2020). In such conditions, genotypes with the ability to partition dry matter directly to the grains would perform superior in both; yield and attributing traits (Kumar et al., 2006). Drought stress at reproductive stage holds strong influence over rice physiological traits and grain yield. Thus, reduces total dry matter production, and grain yield (Torres & Henry, 2018; Yang, Wang, Chen, Li, & Cao, 2019). The superior performance of early flowering and maturing genotypes might be attributed to earliness that escaped water stress during pollen development and grain filling period (Panda, Mishra, & Behera, 2021). Several researchers reported superior performance of early maturing genotypes under rainfed lowland conditions (Dhakal et al., 2020; Monkham et al., 2015).



**Fig. 2.** Grain yield variation among nineteen rice genotypes studied under rainfed lowland condition. Mean grain yield with similar letter across the genotypes denotes non-significant effect at  $P \leq 0.05$



**Fig. 3.** Grain yield advantage of the tested genotypes over Radha- 13 (Check) under rainfed lowland condition. The inverted bar in the figure indicates negative yield advantage over check.



**Table 4.** Genotypic and phenotypic variance, heritability, and genetic advance of twelve traits from nineteen rice genotypes studied under rainfed lowland condition.

Traits	Range	TrMSS	ErMSS	Vg	Vp	PCV	GCV	H	GA	GAM (%)
DTF	85- 113	225.158	1.985	74.391	76.376	9.046	8.927	97.401	17.535	18.150
DTM	115- 149	283.762	8.227	91.845	100.072	7.451	7.138	91.779	18.913	14.087
PL (cm)	22.20- 33.60	10.224	1.661	2.854	4.515	8.111	6.449	63.217	2.767	10.563
PHT (cm)	88- 158.6	647.305	31.700	205.202	236.902	14.395	13.398	86.619	27.464	25.686
ET	156- 323	1671.180	1128.750	180.810	1309.560	15.854	5.891	13.807	10.293	4.509
BY ( t/ha)	4.22- 17.70	13.959	3.763	3.399	7.162	23.050	15.879	47.454	2.616	22.533
HI	0.18- 0.46	0.016	0.001	0.005	0.006	24.868	23.219	87.172	0.136	44.657
TGW (g)	17.90- 43.60	70.743	8.454	20.763	29.217	20.525	17.303	71.064	7.913	30.047
GY (t/ha)	1.19 - 5.73	2.430	0.380	0.683	1.063	25.586	20.511	64.263	1.365	33.872

Remarks: TrMSS: treatment mean sum of the square, ErMSS: error mean sum of the square, Vg: genotypic variance, Vp: phenotypic variance, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, H: broad-sense heritability, GA: genetic advance, GAM: genetic advance as percentage of mean, DTF: days to 50% flowering, DTM: days to 85% maturity, PL: panicle length, PHT: plant height, ET: number of effective tillers per meter square, BY: biological yield, HI: harvest index, TGW: thousand-grain weight, GY: grain yield.

#### Genetic Parameters

Both phenotypic variance (Vp) and phenotypic coefficient of variation (PCV) were higher than corresponding genotypic variance (Vg) and its coefficient (GCV), indicating that the environment influenced the expression of the traits (Table 4). The highest value of PCV was for grain yield (GY- 25.586%) followed by harvest index (HI- 24.868%) and biological yield (BY- 23.050%), whereas GCV was highest for harvest index (HI- 23.219%) corresponded by grain yield (GY- 20.511%), and biological yield (BY- 15.879%). The differences between the genotypic and phenotypic coefficient of variation were greater for effective tillers/m<sup>2</sup> (ET), biological yield (BY), thousand grain weight (TGW), and grain yield (GY). In contrast, traits like days to flowering (DTF), and maturity (DTM), plant height (PHT), harvest index (HI), and panicle length (PL) had smaller differences, suggesting that effective and reliable improvement can be made on these traits by phenotypic selection. In accord with our findings, grain yield was reported for a higher phenotypic and genotypic coefficient of variation by several researchers. These researchers also find phenotypic components higher over genotypic components of variation in the studied traits (Abebe, Alamerew, & Tulu, 2017; Adhikari, Joshi, Shrestha, & Bhatta, 2018; Govintharaj, Manonmani, & Robin, 2018; Kishore, Srinivas, Nagabhushanam, Pallavi, & Sameera, 2015; Tiwari, Tripathi, Tripathi, Khatri, & Bastola, 2019). Broad sense heritability values were

recorded highest for DTF (97.40%), DTM (91.78%), PHT (86.62%), HI (87.17%), and TGW (71.06%) whereas found moderate for PL (63.22%), BY (47.45%), and GY (64.26%) respectively. Similarly, ET (13.81%) recorded the lowest heritability values among the studied agro- morphological traits (Table 4). Heritability is a phenomenon where traits from parents are transferred to and expressed in the progeny. Genetic improvement in highly heritable traits of the crops would also bring out desirable changes in their progeny for the concerned trait. Heritability, thus, is a great selection tool for plant breeders. From our findings, traits like days to flowering and maturity, harvest index, and thousand-grain weight were recognized as important traits based on their heritability. These findings correspond to the results of Kishore, Srinivas, Nagabhushanam, Pallavi, & Sameera (2015), Lipi et al. (2021), Singh, Nandan, & Singh (2014), and Tiwari, Tripathi, Tripathi, Khatri, & Bastola (2019). Some researchers reported medium heritability for days to flowering and maturity (43- 50%), lower to medium heritability for thousand-grain weight and harvest index (25- 49%) (Abebe, Alamerew, & Tulu, 2017; Adhikari, Joshi, Shrestha, & Bhatta, 2018).

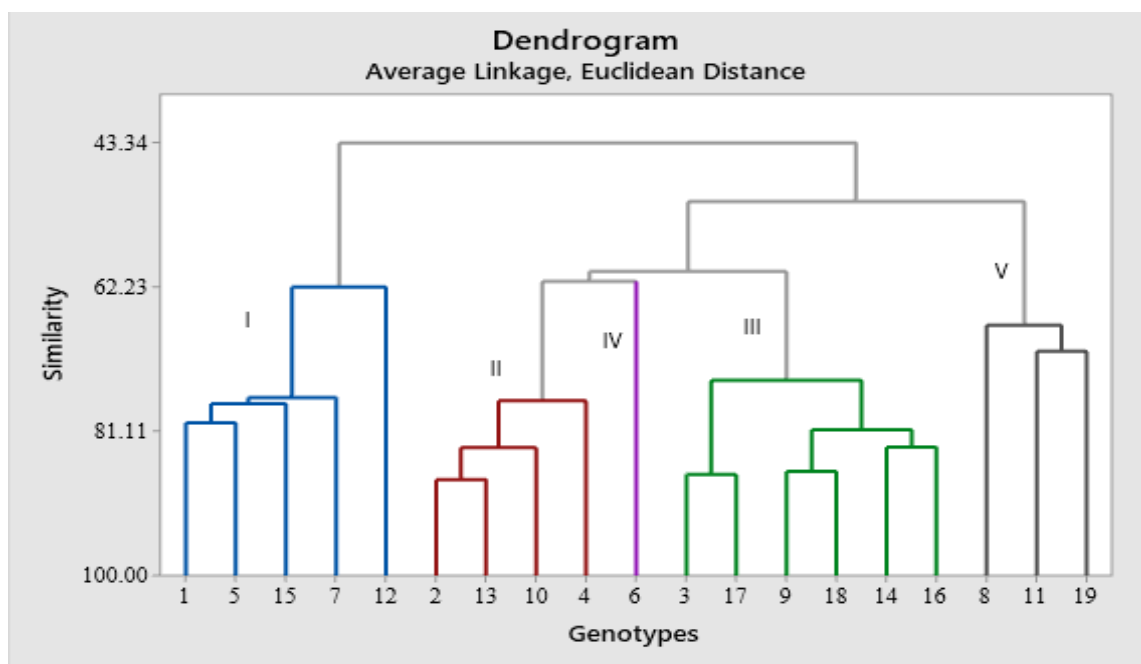
Genetic advance as percentage of mean (GAM) estimate for HI (44.65%) was highest followed by GY (33.87%), TGW (30.05%), PHT (25.68%), and BY (22.53%) respectively (Table 4). Moderate values were obtained for DTF (18.15%), DTM (14.08%), and PL (10.56%), whereas ET (4.51%)

had the lowest value among the traits under study. Among the observed agro- morphological traits, PHT (86.62% and 25.69%), HI (87.17% and 44.66%), and TGW (71.06% and 30.05%) recorded high heritability values coupled with higher GAM values. Similarly, DTF (97.40% and 18.15%), and DTM (91.78% and 14.08%) had higher heritability values with moderate GAM values. PL (63.22% and 10.56%), and BY (47.45% and 22.53%) had moderate heritability values coupled with moderate GAM values, whereas ET (13.81% and 4.51%) had low heritability and GAM values among the traits under study (Table 4). Among the genetic parameters, plant breeder looks for the traits with higher heritability in combination with higher genetic advance as a percentage of the mean (GAM) (Lipi et al., 2021). In our findings, plant height, harvest index, and thousand-grain weight were identified as traits with higher heritability and higher values of GAM. High heritability coupled with high GAM for plant height and thousand-grain weight was reported by Lipi et al. (2021) and Singh, Nandan, & Singh (2014). In addition, Abebe, Alamerew, & Tulu (2017) mentioned a similar result for plant height.

#### UPGMA Clustering

UPGMA (Unweighted Pair Group Method with Arithmetic Mean) clustering (Ward method) separated Nineteen rice genotypes into five different

clusters based on observed agro- morphological traits (Fig. 4). The Dendrogram grouped six genotypes in cluster III, followed by five in cluster I, four in cluster II, three in cluster V, and only one genotype in cluster IV, respectively (Fig. 4). The significant characteristics of genotypes grouped in cluster I were a higher number of effective tillers per meter square, medium to higher biological yield, short to medium plant stature, low to medium thousand-grain weight, and harvest index. Cluster II is characterized as earlier flowering and maturity, shorter panicle length, lower number of effective tillers per meter square, lower to medium biological yield, medium to high harvest index, and thousand-grain weight. Similarly, cluster III was characterized as medium to longer panicle length, short to medium plant stature, medium number of effective tillers per meter square, low to medium biological yield, harvest index, thousand-grain weight, and grain yield. Likewise, genotypes in Cluster IV had late flowering and maturity, shortest panicle length and plant height, lower number of effective tillers per meter square. It also had a lower harvest index, thousand-grain weight, and grain yield. Cluster V grouped genotypes with medium to high grain yield, biological yield, medium number of effective tillers per meter square, taller plant stature, early to medium flowering, and maturity duration.



**Fig. 4.** Clustering of nineteen rice genotypes based on the Euclidean distance estimated from nine agro-morphological traits. The respective name of the genotypes could be extracted from Table 1.

## CONCLUSION

Among studied genotypes, IR102774- 31- 21- 2- 4- 7 (5.40 t/ha) followed by IR99739: 2- 1- 1- 2 -1 (5.22 t/ha), and IR103587- 23- 2- 1- B (5.05 t/ha) respectively were the higher grain yielders. These high yielders were early flowering (85-96 days) and maturing (120-130 days) genotypes. The differences between the genotypic and phenotypic coefficient of variation were found smaller for days to flowering (DTF) and maturity (DTM), plant height (PHT), harvest index (HI), and panicle length (PL). IR102774- 31- 21- 2- 4- 7 produced superior agromorphological character for several traits like grain yield, thousand-grain weight, biological yield, plant height, and days to flowering and maturity. Plant height, biological yield, harvest index, days to flowering, and maturity were highly associated with grain yield and had medium to high heritability and GAM values. Therefore, these traits might be of importance for selection in grain yield improvement of rice under rainfed lowland conditions. Late maturing genotypes had very poor panicle exertion, thus not suitable for cultivation under the rainfed lowlands of the mid-western river basin of Nepal.

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