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ESTIMATING VARIABILITY, HERITABILITY, AND GENETIC ADVANCE OF RICE GENOTYPES IN MID-HILLS OF NEPAL

Estimasi Variabilitas, Heritabilitas, dan Kemajuan Genetik Genotipe Padi di Dataran Menengah Nepal

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ABSTRACT

Rice is an essential staple food in Nepal but researches and varietal improvement programs are rarely carried out due to inadequate variability study. The field study was carried to diagnose the influence of genetic and environmental factors on yield traits to aid future rice breeding programs. Twelve genotypes were arranged in randomized complete block design with three replications from July to November 2019 at the research field of the Institute of Agriculture and Animal Science, Tribhuvan University, in the hilly area of Nepal. Analysis of variance showed significant difference for days to 50% booting, days to 50% flowering, plant height, panicle length, flag leaf area, filled grains per panicle, unfilled grains per panicle, fertility percentage, effective tillers m^{-2}, straw yield, grain yield, 1000-grain weight, and harvesting index indicating the presence of variation in genotypes. LPN BR-1615 was the most promising genotype in grain yield. The values of Phenotypic Coefficient of Variation (PCV) were higher than Genotypic Coefficient of Variation (GCV) for each trait and low difference between them was found for days to 50% booting, days to 50% flowering, plant height, panicle length, grain yield, thousand-grain weight, fertility percentage, and harvesting index. Plant height, effective tillers m^{-2}, and grain yield showed high heritability (i.e. 93.2%, 60.5% and 92.6%, respectively) and higher genetic advance as percentage of mean (i.e. 46.5, 34.6 and 50.1, respectively) . Thus, the experiment revealed that selections favoring plant height, effective tillers m^{-2}, and grain yield would help in effective breeding programs of rice in future.

[Keywords: Genetic advance, grain yield, heritability, rice, variability]

ABSTRAK

Beras merupakan makanan pokok penting di Nepal, tetapi penelitian dan program perbaikan varietas jarang dilakukan karena studi variabilitas yang tidak memadai. Penelitian dilakukan untuk mendiagnosis pengaruh faktor genetik dan lingkungan terhadap sifat hasil untuk membantu program pemuliaan padi pada masa depan. Dua belas genotipe disusun dalam rancangan acak kelompok lengkap dengan tiga ulangan dari Juli hingga November 2019 di kebun percobaan Institute of Agriculture and Animal Science, Tribhuvan University, di daerah perbukitan Nepal. Analisis ragam menunjukkan perbedaan nyata pada umur 50% booting, umur 50% berbunga, tinggi tanaman, panjang malai, luas daun bendera, gabah isi per malai, gabah hampa per malai, persentase kesuburan, anakan efektif per m^2, hasil jerami, hasil gabah, bobot 1.000 butir gabah, dan indeks panen, yang menunjukkan adanya variasi genotipe. LPN BR-1615 merupakan genotipe harapan untuk hasil gabah. Nilai koefisien variasi fenotipe lebih tinggi daripada koefisien variasi genotipe untuk setiap sifat dan perbedaan yang rendah ditemukan untuk umur 50% booting, umur 50% berbunga, tinggi tanaman, panjang malai, hasil gabah, bobot 1.000 butir gabah, persentase kesuburan, dan indeks panen. Tinggi tanaman, anakan efektif per m^2, dan hasil gabah menunjukkan heritabilitas yang tinggi (masing-masing 93,2%, 60,5%, dan 92,6%) dan kemajuan genetik sebagai persentase rata-rata yang tinggi (masing-masing 46,5, 34,6, dan 50,1). Dengan demikian, penelitian mengungkap bahwa seleksi terhadap tinggi tanaman, anakan efektif per m^2, dan hasil gabah akan membantu program pemuliaan padi yang efektif pada masa depan.

[Kata kunci: Kemajuan genetik, hasil gabah, heritabilitas, padi, keragaman]

INTRODUCTION

Rice (*Oryza sativa* L.) is a crop of the Gramineae family. It is a crop from an ancient civilization. The genus *Oryza* includes 22 species, with two of them being cultivated species, and the remaining ones are wild. The subspecies *indica* are tropical and subtropical varieties which is grown around Indian subcontinents in South Asia (CDD and ASoN 2017). Nepal is also reported as one of the centers of rice diversity (Joshi 2005). About 2000 rice landraces are registered in Nepal, growing from 60 m to

3050 m altitude (Mallick 1981). The variety *japonica* is a temperate crop cultivated in Japan, China, and Korea, while *javanica* are mostly cultivated in Indonesia (CDD and ASoN 2017).

The global rice production was around 755.5 million tons in 2019, which is the second-largest rice production recorded in a year. However, the yield was decreased by about 1% from 2018 (Food and Agriculture Organization of the United Nation 2021). In Nepal, the rice production was around 5.61 million metric tons for the year 2018. However, rice production decreased by about 1% in 2019, which was approximately 5.55 million tons (Department of Agriculture Ministry of Agriculture and Livestock Development 2020). Of the total produced paddy, spring season rice contributed to 0.56 million tons, and the main season rice contributed 4.98 million tons. The productivity of rice in Nepal is 3.8 tons per hectare which is very low compared to global rice productivity (Department of Agriculture Ministry of Agriculture and Livestock Development 2020). The contribution of the agriculture sector to GDP of Nepal is around 26.98% for the Fiscal Year (FY) 2018-19 (Department of Customs Ministry of Finance Nepal 2020).

In Nepal, rice is cultivated up to the altitude of 3050 m as lowland and upland rice. At uplands, rice is grown only once a year due to the longer growing period and 'Ghaiya' is the most popular variety. However, rice is grown twice a year at lowlands due to low growth period and abundant irrigation. Rice – wheat – maize is the major sequential cropping system in Nepal (Gadal et al. 2019). There are around 2500 landraces reported in Nepal out of which only 157 are being cultivated (Bajracharya et al. 2010). This large number of landraces makes Nepal an epicenter for genetic resources. The use of several genetic markers to exploit available genetic resources helps in further rice breeding in Nepal. In addition, thousands of genotypes are brought annually from IRRI for evaluation.

The global agricultural crop demand is expected to double by the year 2050. However, there was only an increase of 28% from 1985 to 2005. This recent yield improvement trend falls short of the expected production. At present, around the globe, yields stagnation is seen throughout 35% of rice harvested areas. Major rice growing countries China, India, and Indonesia face yield stagnation across 79%, 36%, and 81% of rice harvested areas, respectively (Ray et al. 2012). Similarly, food security of Nepal is threatened by the stagnating yield of staple crops, especially rice (Marahatta 2018). This problem can be addressed by prioritizing genetic basis of selection and developing cultivars suited to the specific environmental condition. However, there are few researchers to access genetic variability and associations between yield attributing parameters of rice in Nepal. Rice breeding programs are carried out in Nepal by utilizing foreign rice cultivars because of limited research on the variability of available landraces. The modern breeding program embraces creating genetic variability, selection, and using variation found in selected genotypes to generate new breeding materials (Tiwari et al. 2019). Identifying variability among existing genotypes aids in the development of new cultivars through selection.

Nuruzzaman et al. (2002) reported that to achieve improvement of crops, there has to be variability available in breeding materials so that selection can be effective. Yield is governed by various factors and is a very complex trait. Improving variability in existing genotypes and eventually selection efficiency via breeding programs is immensely important to increase the rice productivity surmounting the yield plateau to a higher level. Knowledge of heritability indicates the extent of transmissibility of particular targeted breeding characters to future generations. So, estimation of heritability is essential for selection based varietal improvement of crops (Sabesan et al. 2009). This study aims to identify the extent of environmental or genotypic influence in yield and its attributing traits to aid in selection for effective breeding program. Further, the specific objective of the research was to identify genetic makeup, heritability, and variability of quantitative traits for assisting future breeding programs.

MATERIALS AND METHODS

Experimental Site and Planting Material

The research was carried out in the field experimental station of Institute of Agriculture and Animal Science (IAAS), Lamjung, Nepal, in coordination with the National Agriculture Research Center (NARC). The field is located at the latitude of 28°7' to 28°10' N, and longitude of 84°24' to 84°28' E and the altitude of 725 m above sea level (m asl). The treatments in the experiment comprises of 12 rice genotypes, including 11 genotypes obtained from NARC. 'Ram Dhan' is used as a check variety because the variety is widely cultivated and promising in the experimental locality (Table 1).

Experimental Design

The research was laid out in Randomized Complete Block Design (RCBD) with the 12 treatments replicated three times and performed from June to November 2019. The field experiment was started on 20th June with the preparation of a raised nursery bed of size 1 m x 1 m for each genotype. The 25 days old seedlings were

Table 1. List of rice genotypes used in the experiment and their source of collection.

Genotypes	Type of genotypes	Source of collection
LPN BR 1628	Promising line	NARC
LPN BR 1615	Promising line	NARC
LPN BR 1641	Promising line	NARC
LPN BR 1621	Promising line	NARC
LPN BR 1618	Promising line	NARC
LPN BR 1632	Promising line	NARC
NR-11319-B-B-5	Promising line	NARC
NR-11374-B-B-23	Promising line	NARC
NR-11372-B-B-11	Promising line	NARC
NR-11361-B-B-7	Promising line	NARC
Khumal-4	Improved variety	NARC
Ram Dhan	Local cultivar (check)	Local farmers of Lamjung

transplanted in the main field plots with row to row and plant to plant spacing of 20 cm. The spacing between each plot within the replications was 50 cm and the blocks (replications) were placed at 75 cm spacing from one another. The size of each plot was 3 m x 2 m.

Fertilizer at the rate of 100:60:30 kg NPK was applied. Urea, Diammonium Phosphate (DAP), and Muriate of Potash (MoP) were used as the source of macronutrients. DAP and MoP were used entirely on the first day of sowing. However, urea was used in the basal dose and two split doses. Half amount of urea was applied in basal dose, a quarter of the amount in first split dose at 35 days after transplanting and remaining quarter in second split dose at 50 days after transplanting. Standard agronomical practices were also adopted for proper crop establishment.

Data Collection and Recording

Randomly five plants were selected from each plot in each replication and their means were used for statistical analysis. Data of different traits were collected, neglecting all the border plants. To evaluate variability, heritability, and relationship among yield attributing traits, 13 quantitative characters were recorded by following the method of Bioversity International, IRRI and WARDA (2007). The detailed description along with their evaluation stage is as listed in Table 2. Besides, several qualitative traits were also taken understudy. The detailed description of the list is presented in Table 3

Statistical Analysis

The mean values of measurement data described in Table 2 were taken from five random plant samples. The observed data of each parameter's quantitative characters were determined using variance analysis (ANOVA) in RCBD for significance of difference between treatments.

Ms Excel Program was used for data collection, ANOVA, and mean comparison among treatments was performed using R-Studio 3.5.1 and IBM SPSS Statistics 23. The following genetic estimates were then calculated.

Variance

The genotypic and phenotypic variances were calculated according to the procedure of Johnson et al. (1955).

Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

where, MSG = mean sum of square for genotypes, MSE = mean sum of square for error and r = number of replications

Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

where, $\delta^2 g$ = genotypic variance = mean square of error, $\delta^2 e$ = environmental variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per Burton (1951).

Genotypic coefficient of variation = $\frac{\delta g}{m} \times 100$

where, δg = genotypic standard deviation, *m* = population mean

Phenotypic coefficient of variation = $\frac{\delta p}{m} \times 100$

where, δp = phenotypic standard deviation, *m* = population mean

According to Sivasubramanian and Madhavamenon (1973), the value of GCV and PCV were ranked as; low = 0–10%, intermediate = 10–20% and high = greater than 20%.

Genetic Advance and Genetic Advance as Percentage of Mean

The improvement of selected lines over the original population is called genetic advance. The expected genetic advance was evaluated with respect to the formula given by Allard (1960).

Genetic advance (GA) = $\frac{\delta^2 g}{\delta^2 p} \times K.\delta p$

where, $\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance, δp = phenotypic standard deviation

K = selection differential at 5% selection intensity = 2.06

Genetic advance as percentage of mean (GAM) was calculated by using the following formula:

Genetic advance as percentage of mean (GAM) = $\frac{GA}{X} * 100$

Table 2. List of traits measured for evaluation, their procedure of collection and evaluation stage (Bioversity International, IRRI & WARDA 2007).

Quantitative trait	Procedure	Evaluation stage
Days to 50% booting	Recorded when 50% of plants show thickening at stem in a plot.	Vegetative
Days to 50% flowering	Recorded when 50% of plants show anthesis within a plot.	Maturity
Plant height (cm)	Measured from surface of soil to base of the panicle.	Maturity
Panicle length (cm)	Measured from basal node to tip of main panicle.	Maturity
Flag leaf area (cm^2)	Breadth was taken at base, middle and tip of leaf and average of it were multiplied by the length of each leaf.	Maturity
Effective tillers per m^2	Total numbers of tillers bearing panicle were counted from 1 m^2 of each plot.	Maturity
Filled grains per panicle	Total numbers of grains containing endosperm were counted from the main panicle.	After harvesting
Unfilled grains per panicle	Total numbers of grains that lacked endosperm were counted from the main panicle	After harvesting
Grain yield (t ha^{-1})	Weighed through precision balance which was taken after proper harvesting, threshing, winnowing, and drying.	After harvesting
Straw yield (t ha^{-1})	Taken with the help of precision balance after harvesting, threshing, and drying.	After harvesting
Fertility percentage	Calculated with the help of the following formula and expressed in percentage. $Spikelet\ fertility = \frac{Filled\ grains}{Total\ grains} \times 100$	After harvesting
Thousand grain weight	1000 grains were counted and their weight was taken.	After harvesting
Harvesting index	Calculated by using the following formula and expressed in percentage. $Harvesting\ Index = \frac{Grain\ Yield}{Grain\ Yield + Straw\ Yield} \times 100$	After harvesting

Table 3. List of qualitative traits studied along with their labels and evaluation stages.

Qualitative traits	Labels	Evaluation stage
Basal leaf sheath color	Green, green with a purple line, light purple, purple	Late vegetative
Ligule color	Absent whitish, yellowish green, purple, light purple, purple lines	Late vegetative
Ligule shape	Absent, truncate, acute to acuminate, two cleft	Late vegetative
Collar color	Absent, green, light green, purple, purple lines	Late vegetative
Auricle color	Absent, whitish, yellowish green, purple, light purple, purple lines	Late vegetative
Leaf blade anthocyanin coloration	Absent, purple, light purple, purple lines	After flowering
Culm: lodging resistance	Very weak, weak, intermediate, strong, very strong	At maturity
Flag leaf attitude	Erect, Semi-erect (intermediate), horizontal, descending	Early reproductive stage
Panicle shattering	Very low, low, moderate, high, very high	At maturity
Leaf blade pubescence	Glabrous, intermediate, pubescent	Late vegetation
Lemma and palea color	White, straw, gold and gold furrows, brown (tawny), brown spots, brown furrows, purple, reddish to light purple, purple spots, purple furrows, black	At maturity
Spikelet: fertility	Completely sterile, highly sterile, partly sterile, fertile, highly fertile	At maturity

where, GA= genetic advance, X = population mean where selection is performed

Johnson *et al*. (1955) suggested that the genetic advance as percentage of mean can be classified as; low = less than 10%, intermediate = 10-20%, and high = more than 20%.

Heritability in Broad Sense

It is the proportion of phenotypic variability that is due to genetic reasons. It was computed by using the formula given by Allard (1960).

$$H^2\ (\%) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

where, H^2 = broad sense heritability, $\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance

As suggested by Johnson et al. (1955), heritability in broad sense can be categorized as; low ,= 0-30%, intermediate (medium) = 30-60% and high = above 60%.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

The ANOVA revealed significant differences at $p< 0.05$ for flag leaf area, filled grains per panicle, unfilled grains per panicle, and straw yield per hectare, significant different at $p< 0.01$ for fertility percentage, and highly significant difference at $p<0.001$ for all other tested traits (Table 4). These results indicate an inherent genetic difference among the genotypes for the traits under

Table 4. Analysis of variance results of 13 observed traits derived from 12 rice genotypes grown at Lamjung, Nepal, June-November 2019.

Traits	Mean sum of squares of source of variation		
	Replication (df= 2)	Treatment (df=11)-	Error (df= 22)
B	0.083	84.909 ***	1.811
F	7.194	121.3 ***	1.194
PH	43.41	1697.9 ***	40.09
PL	5.0040	9.3410 ***	1.4447
FLA	189.673	124.98 *	46.002
ET	732.86	2592.26 ***	463.8
FG	5379.9	3090.6 *	1202.7
UnFG	36.028	82.505 *	31.21
FP	4.0717	29.2116 **	6.3949
SY	1.8898	1.963 *	0.8467
GY	0.317	4.26 ***	0.111
TW	0.459	15.980 ***	0.7347
HI	17.497	119.500 ***	19.841

* = significant at 5%, ** = significant at 1%, *** =significant at 0.1%; df = degree of freedom; B = days to 50% booting, F = days to 50% flowering, PH = plant height, PL = panicle length, FLA = flag leaf area, ET = effective tillers m^{-2}, SY = straw yield, GY = grain yield per plot, FG = filled grains per panicle, UnFG = unfilled grains per panicle, FP = fertility percentage, TW = thousand grain weight, and HI = harvesting index.

study. This signifies that the parents of the genotypes which were selected for our study were of diverse origin and that these characters may be undertaken for further selection Akbar et al.(2021). Similarly, Fentie et al. (2014) and Dhanwani et al. (2013) performed genetic variability and diversity with grain yield in different rice genotypes and found that there were significant differences among different traits taken under study. The tabulation of ANOVA obtained for other qualitative traits is done in Table 4.

Mean Performance

The mean performance of 12 genotypes for different traits is presented in Table 5. Out of 12 varieties tested, five showed higher grain yield in comparison to check variety. LPN BR 1615 (5.97 t ha^{-1}), LPN BR 1618 (5.96 t ha^{-1}), LPN BR 1621 (5.94 t ha^{-1}), LPN BR 1628 (5.74 t ha^{-1}) and LPN BR 1641 (5.39 t ha^{-1}) showed higher yield than check variety Ram Dhan (4.96 t ha^{-1}) (Table 5). The lowest grain yield was given by NR-11372-B-B-11 (2.61 t ha^{-1}).

Genotype LPN BR 1615 (5.97 t ha^{-1}) showed the highest grain yield among the 12 rice genotypes tested. So, this genotype can be used over local check variety, i.e., ‘Ram Dhan’ to obtain higher rice yield. NR-11372-B-B-11 was the earliest to complete flowering in 59 days and, this genotype can be used as a donor in hybridization program to develop early maturing varieties (Pratap et. al 2013).

The Estimate of Genetic Parameters

Phenotypic and Genotypic Coefficient of Variation

Phenotypic Coefficient of Variation (PCV) was recorded to be highest for effective tillers m^{-2} (27.8) followed by grain yield (26.27), plant height (24.22), straw yield (23.58), and unfilled grains per panicle (21.20) (Table 6). PCV was seen to be the lowest for fertility percentage (4.3). However, intermediate to low PCV was shown by filled grains per panicle (18.92), flag leaf area (18.11), harvesting index (14.68), thousand grain weight (10.04), days for 50% flowering (9.69), days to 50% booting (9.05), and panicle length (8.01) (Table 6).

Similarly, the Genotypic Coefficient of Variation (GCV) was highest for grain yield (25.28) followed by plant height (23.38), and effective tillers m^{-2} (21.62). The lowest GCV was shown by fertility percentage (3.17). Intermediate to low GCV was shown by straw yield (13.03), unfilled grains per panicle (12.61), harvesting index (11.62), filled grains per panicle (11.09), flag leaf area (10.93), days to 50% flowering (9.54), thousand grain weight (9.39), days to 50% booting (8.77), and panicle length (6.44) (Table 6).

Similar findings were recorded by Augustina et al. (2013) for effective tillers per m^{2}; Ogunbayo et al. (2014) for days to 50% flowering; Kole et al. (2010) for harvesting index, fertility percentage and panicle length; Sadeghi et al. (2011) for plant height and grain yield; Yadav et al. (2017) for flag leaf area, and Hossain et al. (2015) for filled grains per panicle. Hossain et al. (2018) found a similar result for thousand grain weight. Bhandari et al. (2019) found a higher value of PCV and moderate value for GCV in case of straw yield. Abebe et al. (2017) found high PCV in the case of unfilled grains per panicle and they also noticed the higher difference between PCV and GCV for this trait.

The studied traits exhibited a wide range of phenotypic and genotypic coefficient of variation. In general, it was seen PCV was higher than GCV (Table 6).

The magnitude of genotypic and phenotypic variance for all traits was different. Genotypic variance measures the extent of genetic variability present in the trait whereas phenotypic variance is variability due to both genetic and environmental factors. The value of phenotypic variance was higher than the corresponding genotypic variance, indicating that environmental factors influenced these traits. This finding corresponds to that made by Singh et al. (2011).

Table 5. Trait mean performances of 12 rice genotypes grown at Lamjung, Nepal, June-November 2019.

Genotypes	B	F	PH (cm)	PL (cm)	FLA (cm^2)	ET	UnFG	FG	SY (t ha^{-1})	GY (t ha^{-1})	FP (%)	TW (g)	HI (%)
LPN BR 1628	56.33 ^{e}	64.00 ^{cd}	83.72 ^{de}	25.05 ^{bcd}	50.78 ^{bc}	127 ^{cd}	26.67 ^{cd}	257.33 ^{ab}	4.27 ^{bc}	5.75 ^{ab}	90.71 ^{ab}	23.94 ^{cd}	57.48 ^{ab}
LPN BR 1615	56.67^{e}	63.67 ^{cd}	90.62 ^{d}	23.45 ^{de}	46.58 ^{bc}	136.67 ^{bc}	23 ^{d}	278 ^{a}	5.48 ^{ab}	5.97 ^{a}	92.39 ^{a}	26.99 ^{a}	52.73 ^{abc}
LPN BR 1641	58 ^{cde}	65.33 ^{c}	84.47 ^{de}	22.58 ^{e}	45.96 ^{bc}	113.67 ^{cde}	36.67 ^{ab}	233.33 ^{ab}	5.05 ^{abc}	5.39 ^{bc}	86.35 ^{cde}	26.04 ^{ab}	51.59 ^{bc}
LPN BR 1621	60 ^{c}	65.33 ^{c}	84.77 ^{de}	24.39 ^{cde}	48.82 ^{bc}	107 ^{cde}	34.33 ^{abc}	225.33^{abcd}	4.11 ^{bc}	5.94 ^{ab}	86.7 ^{bcde}	26.92 ^{a}	59.33 ^{a}
LPN BR 1618	59 ^{cd}	63.67 ^{cd}	81.60 ^{de}	26.72 ^{b}	45.83 ^{bc}	121.67 ^{cde}	29 ^{bcd}	237 ^{abc}	4.18 ^{bc}	5.96 ^{a}	88.99 ^{abcd}	22.15 ^{e}	58.81 ^{ab}
LPN BR 1632	57.67 ^{de}	64 ^{cd}	77.93 ^{e}	23.61 ^{de}	40.94 ^{c}	134.33 ^{c}	28.67 ^{bcd}	261.67 ^{ab}	4.41 ^{abc}	4.21 ^{ef}	90.16 ^{abc}	22.13 ^{e}	49.21 ^{cd}
NR-11319-B-B-5	66 ^{b}	71.33 ^{b}	137.80 ^{a}	25.70 ^{bc}	62.87 ^{a}	105.67 ^{cde}	35 ^{abc}	209.67 ^{bcd}	5.399 ^{ab}	3.87 ^{fg}	84.67 ^{ef}	25.26 ^{bc}	42.79 ^{de}
NR-11374-B-B-23	57 ^{de}	61.67 ^{e}	103.23 ^{c}	24.38 ^{cde}	41.47 ^{c}	94 ^{de}	35.67 ^{abc}	210 ^{bcd}	3.73 ^{c}	3.10 ^{hi}	84.89 ^{def}	21.51 ^{e}	45.48 ^{cde}
NR-11372-B-B-11	53.67 ^{f}	59 ^{f}	121.68 ^{b}	29.27 ^{a}	40.96 ^{c}	88.33 ^{e}	37.67 ^{ab}	168.67 ^{d}	3.63 ^{c}	2.61 ^{i}	81.61 ^{f}	24.63 ^{bc}	41.60 ^{e}
NR-11361-B-B-7	57.33 ^{de}	63 ^{de}	128.53 ^{ab}	26.20 ^{bc}	53.75 ^{ab}	97 ^{de}	41 ^{a}	212.67 ^{bcd}	4.20 ^{bc}	3.50 ^{gh}	83.93 ^{ef}	25.96 ^{ab}	46.46 ^{cde}
Khumal-4	66.33 ^{b}	71.67 ^{b}	135.83 ^{a}	25.77 ^{bc}	43.05 ^{bc}	171.67 ^{ab}	35.67 ^{abc}	239.67 ^{bc}	5.88 ^{a}	4.59 ^{de}	86.98 ^{bcde}	19.92 ^{f}	43.94 ^{de}
Ram Dhan	72 ^{a}	83 ^{a}	76.15 ^{e}	25.24 ^{bcd}	42.39 ^{bc}	181.67 ^{a}	30 ^{bcd}	181 ^{cd}	5.87 ^{a}	4.96 ^{cd}	85.71 ^{def}	22.84 ^{de}	45.92 ^{cde}
Mean	60	66.31	100.53	25.2	46.95	123.22	32.8	226.2	4.68	4.65	86.92	24.02	49.61
CV%	2.24	1.65	6.3	4.77	14.4	17.47	3.57	17.04	19.65	7.16	2.9	3.57	9
LSD (0.05)	2.28	1.85	10.72	2.04	11.48	36.47	1.45	9.46	1.55	0.56	4.28	1.45	7.54

CV% = coefficient of variation, LSD = Least Significant Difference, B = days to 50% booting, F = days to 50% flowering, PH = plant height, PL = panicle length, FLA = flag leaf area, ET = effective tillers m^{-2}, SY = straw yield, GY = grain yield, FG = filled grains per panicle, UnFG = ufilled grains per panicle, FP = fertility percentage, TW = thousand grain weight, and HI = harvesting index).

Grain yield, straw yield, and number of filled grains per panicle gave a higher range of variability, indicating that the parents may be of diverse origins. Abebe et al. (2017) reported that characters with higher variability might be selected for further varietal improvement programs because there is higher scope of variations available for selection. However, the absolute values of genotypic and phenotypic variance cannot be used for comparing the degree of variability present in different traits because the characters differ in the unit of measurement. Hence, the coefficient of variations, i.e. GCV and PCV, are generally used for the comparisons. Higher values of GCV and PCV denote that there is higher variability and *vice versa*.

The difference between PCV and GCV was lower for days to 50% booting, days to 50% flowering, plant height, panicle length, grain yield, thousand grain weight, fertility percentage, and harvesting index. Also, the narrow differences between GCV and PCV indicate a lower role of environment and a higher role of genetic factors in the expression of these traits. However, moderate to high differences were seen in flag leaf area, effective tillers m^{-2}, filled grains per panicle, unfilled grains per panicle, and straw yield. Also, studies revealed that genotypes with high GCV for yield attributing traits are important for yield improvements. It is expected that higher GCV gives variable offsprings in segregating generations (Tiwari et al. 2019). The higher values of PCV and GCV suggests that selection can be done from these traits for improvement and lower value indicates that the variation is very low in these traits and there is a need for creation of variability either by hybridization or by mutation followed by selection in advance generation (Dhakal et al. 2020).

Heritability and Genetic Advance as Percentage of Mean (GAM)

This study revealed that the highest heritability was shown by days to 50% flowering (97.11) followed by days to 50% booting (93.9), plant height (93.24), grain yield (92.57), thousand grain weight (87.37), panicle length (64.56), harvesting index (62.61), effective tillers m^{-2} (60.47), fertility percentage (54.35), flag leaf area (36.40), unfilled grains per panicle (35.39), filled grains per panicle (34.35), and straw yield (30.52). The genetic advance by percentage of mean concerning thirteen characters was estimated to determine the expected response of selection at 5 percentage selection intensity, i.e. K = 2.06. The estimated genetic advance has been presented in Table 7.

Genetic advance as percentage of mean (GAM) was found to be highest for grain yield (50.105) followed by plant height (46.513) and effective tillers m^{-2} (34.628). However, days to 50% flowering (19.375), harvesting index (18.937), thousand grain weight (18.071), days to 50% booting (17.5), unfilled grains per panicle (15.46), straw yield (14.827), flag leaf area (13.583), filled grains per panicle (13.39), and panicle length (10.656) showed moderate genetic advance as percentage of mean.

Table 6. Estimates of GV, PV, PCV, and GCV of quantitative traits in rice genotypes.

Parameters	GV	PV	PCV	GCV
B	27.7	29.5	9.05	8.77
F	40.06	41.25	9.69	9.54
PH	552.61	592.70	24.22	23.38
PL	2.63	4.08	8.01	6.44
FLA	26.33	72.33	18.11	10.93
ET	709.49	1173.29	27.80	21.62
SY	0.3720	1.219	23.58	13.03
GY	1.3846	1.495	26.27	25.28
FG	629.30	1832.00	18.92	11.09
UnFG	17.10	48.31	21.20	12.61
TW	5.08	5.82	10.04	9.39
FP	7.61	14.00	4.30	3.17
HI	33.22	53.06	14.68	11.62

PV = phenotypic variance, GV = genotypic variance, PCV = phenotypic coefficient of variation,GCV = genotypic coefficient of variation, HB% = broad sense heritability, GA = genetic advance, GAM = genetic advance as percentage of mean.

B = days to 50% booting, F = days to 50% flowering, PH = plant height, PL = panicle length, FLA = flag leaf area, ET = effective tillers m^{-2}, SY = straw yield, GY = grain yield, FG = filled grains per panicle, UnFG = unfilled grains per panicle, FP = fertility percentage, TW = thousand grain weight, and HI = harvesting index.

Table 7. Estimates of HB, GA, and GAM of quantitative traits in Rice genotypes.

Parameters	**HB (%)**	**GA**	**GAM**
B	93.9	10.5	17.5
F	97.11	12.85	19.38
PH	93.24	46.76	46.51
PL	64.56	2.69	10.66
FLA	36.40	6.38	13.58
ET	60.47	42.67	34.63
SY	30.52	0.694	14.83
GY	92.57	2.33	50.10
FG	34.35	30.29	13.39
UnFG	35.39	5.07	15.46
TW	87.37	4.34	18.07
FP	54.35	4.19	4.82
HI	62.61	9.39	18.94

PV = phenotypic variance, GV = genotypic variance, PCV = phenotypic coefficient of variation,GCV = genotypic coefficient of variation, HB% = broad sense heritability, GA = genetic advance, GAM = genetic advance as percentage of mean.

B = days to 50% booting, F = days to 50% flowering, PH = plant height, PL = panicle length, FLA = flag leaf area, ET = effective tillers m^{-2}, SY = straw yield, GY = grain yield, FG = filled grains per panicle, UnFG = unfilled grains per panicle, FP = fertility percentage, TW = thousand grain weight, and HI = harvesting index.

Similarly, fertility percentage (4.819) showed low genetic advance as percentage of mean.

High heritability coupled with higher genetic advance as percentage of mean was shown by plant height, effective tillers m^{-2}, and grain yield. A similar result was recorded by Gangashetty et al. (2013) for plant height and effective tillers m^{-2}. Aditya and Bhartiya (2013) also found a similar result for grain yield and thousand grain weight; Singh et al. (2011) for harvesting index; Sudeepthi et al. (2020) for panicle length; Seyoum et al. (2012) for fertility percentage; Bhandari et al. (2019) for straw yield, Idris and Mohamed (2013) for filled grains per panicle.

Heritability and genetic advance are essential parameters for selection. According to Johnson et al. (1955), heritability estimates along with genetic advance are more helpful in predicting genotypes for selection than heritability alone. Thus, it is essential to consider both of these parameters during selection. Similar conclusions were also given by Bagudam et. al (2018).

Days to 50% booting, days to 50% flowering, plant height, panicle length, grain yield, thousand grain weight, harvesting index, and effective tillers m^{-2} showed high heritability as a result, these traits were less controlled by environmental and random factors. High heritability along with higher genetic advance as percentage of mean was shown by plant height, effective tillers m^{-2} and grain yield, stipulating that additive gene action governs these characters and selection for improvement of these characters might be rewarding through phenotypic selection. Grain yield has both high heritability and GAM. So, selecting this trait will be fruitful in yield improvement and overcoming yield stagnation problem. In the study, high heritability accompanied with moderate GAM was shown by days to 50% booting, days to 50% flowering, panicle length, thousand grains weight, and harvesting index. Such circumstances suggest that these characters were governed by genetic by environmental interaction. Thus, the genotypic selection is not ideal. However, the remaining traits, flag leaf area, straw yield, filled grains per panicle, unfilled grains per panicle, and fertility percentage were influenced by non-additive gene action and heterosis breeding is handy rather than selection for the refinement of those traits because there is the presence of inbreeding depression. Inbreeding depression increases homozygousity and induces the expression of unfavorable recessive alleles. Heterosis breeding or crossing offers an effective measure to control inbreeding depression.

CONCLUSION

The genetic variability among different rice genotypes indicated ample scope of selection from existing variation for different traits among the tested genotypes. Higher value of PCV over GCV demonstrated a certain degree of environmental influence in expression of traits. The presence of high variability in traits revealed that parents may be of diverse origin. Some traits showed higher heritability in combination with high genetic advance as percentage of mean which implies selection of those traits is effective for future crop improvement. Since, rice yield is the most important trait; genotype LPN BR-1615 is promising for mid hills of Nepal. The existence of huge variability among these rice genotypes suggests there is higher scope for utilization of these genotypes in future rice breeding programs. Grain yield showed high heritability along with high genetic advance thus, it should be selected for increasing productivity in future breeding programs.

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