VARIABILITY AND HERITABILITY ESTIMATE OF 30 RICE LANDRACES OF LAMJUNG AND TANAHUN DISTRICTS, NEPAL

Estimasi Diversitas dan Heritabilitas 30 Padi Lokal di Lamjung dan Tanahun, Nepal

Anup Dhakal[*], Shishir Sharma, Amrit Pokhrel, and Ankur Poudel

[*]*Department of Agronomy, Plant Breeding and Agriculture Statistics,*
Institute of Agriculture and Animal Science, Lamjung Campus, Nepal

Corresponding author: dklanup@gmail.com

ABSTRACT

The variability existing in the rice landraces is the source of variation and offers a substantial opportunity for the development of new varieties. Exploration and understanding diversity and variability in landraces determines the success of rice improvement programs. The objective of the study was to assess diversity, genetic variability, heritability, genetic advance for the yield, and yield contributing traits of 30 landraces of rice. An experiment was carried out in alpha-lattice with two replications in the Agronomy Farm of IAAS, Lamjung Campus, Nepal during June–November, 2018. Shannon and Simpson's indices were calculated for 18 qualitative traits. The value of the Shannon and Simpson index ranged 0.15–1.41 and 0.07–0.75, respectively. All landraces showed significant variations (p <0.001) for all 13 qualitative traits studied. The higher value of the phenotypic coefficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated the influence of the environment. The filled-grain per panicle exhibited a high estimate of PCV and GCV, followed by the effective tiller and filled grain percentage. High heritability, along with a high genetic advance was found in 10 traits, including 1000 grain weight, grain length, and filled grain per panicle indicated the presence of additive gene action. Direct selection of characters of these traits based on phenotypic expression by a simple selection method would be more reliable for yield improvement. The study suggests the existence of the diversity and estimated genetic parameters among landraces of rice that can be exploited in future breeding programs.

[**Keyword**: *Oryza sativa*, Shannon index, Simpson index, variability]

ABSTRAK

*Variabilitas padi lokal (*landrace*) merupakan sumber keragaman genetik dan menawarkan peluang besar untuk pengembangan varietas baru. Eksplorasi dan pemahaman keragaman dan variabilitas genetik padi lokal menentukan keberhasilan program pemuliaan tanaman. Penelitian ini bertujuan untuk menilai indeks keragaman, variabilitas genetik, heritabilitas, kemajuan genetik untuk hasil, dan sifat-sifat yang berkontribusi terhadap hasil pada 30 padi lokal. Percobaan dilakukan di kebun Department of Agronomy, IAAS, Lamjung Campus, Nepal pada Juni–November 2018. Indeks Shannon dan Simpson dianalisis untuk 18 sifat kualitatif. Nilai indeks Shannon dan Simpson masing-masing berkisar 0,15–1,41 dan 0,07–0,75. Semua padi lokal menunjukkan variasi yang signifikan (p <0,001) untuk 13 sifat kualitatif yang dipelajari. Nilai yang lebih tinggi untuk koefisien variasi fenotipik (PCV) dibandingkan dengan koefisien variasi genotipik (GCV) untuk semua sifat yang diteliti menunjukkan adanya pengaruh lingkungan. Gabah isi per malai menunjukkan estimasi yang tinggi untuk PCV dan GCV, diikuti oleh anakan efektif dan persentase gabah isi. Heritabilitas yang tinggi, ditambah dengan kemajuan genetik yang tinggi ditemukan dalam 10 sifat, termasuk 1000 butir gabah, panjang gabah, dan gabah isi per malai yang menunjukkan adanya aksi gen aditif. Seleksi secara langsung terhadap karakter dari sifat-sifat tersebut berdasarkan ekspresi fenotipik dengan metode seleksi sederhana dapat diandalkan untuk perbaikan hasil. Studi ini menunjukkan adanya keragaman dan estimasi parameter genetik padi lokal yang dapat dieksploitasi dalam program pemuliaan padi di masa depan.*

[**Kata kunci**: *Oryza sativa*, indeks Shannon, indeks Simpson, variabilitas]

INTRODUCTION

Rice *(Oryza sativa* L.), 2n=2x=24, a member of Poaceae is among the three most important grain crops in the world, and it has a significant contribution to fulfill the food needs across the globe. The role of the rice crop is inevitable in the current and future global food security (Chauhan et al. 2017). In Nepal, it ranks first in position in terms of production and productivity and contributes significantly to the livelihood of the majority of people (Tiwari et al. 2019). It is grown in 1.55 million hectares and produces 5.2 million tons with a productivity of 3.36 t ha^{-1} (MOAD 2018).

Rice is the most diversified crop species due to its adaption to a wide range of geographical, ecological, and climatic regions. During the process of dispersal during domestication, rice has evolved into a tremendously broad base for genetic diversity, as reflected by a number of landraces existing today (Shivapriya and Hittalmani 2006). Nepal is considered one of the centers of origin

of rice (Upreti 2017) where 2500 landraces are reported (Joshi et al. 2017).

A crop landrace is a result of selection by farmers during the propagation process for desirable characteristics such as a variety that produces more fruit or is more resistant to disease and nature through the effects of local environmental conditions, some of which include climate and soil quality and is traditional locally-adapted crop variety. Therefore, they are more adapted to those conditions and have a higher chance of survival, reproduction and thus passing on their characteristics to the next generation.

The area coverage of landraces of rice decreased from 70% in 1999 (Gauchan 1999) to 10% in 2017 (CDD 2017). Due to the introduction of modern varieties, the landraces lost. The green revolution has remarkably increased crop productivity over the past four decades (Mann 1997). Still, this agricultural transformation has also resulted loss of crop genetic diversity (Tilman 1998). In Nepal, among the 73 released rice varieties, only 12 varieties were developed using only 6 local landraces, among which Pokhreli Masino has been excessively used; however, only three landraces have been released for general cultivation from pure line selection (Upreti 2017). Although we have such a huge diversity in rice, foreign germplasm is commonly used as the parents in rice breeding programs, and Nepal is about 95% dependent on foreign rice germplasm for varietal development (Joshi 2017). Some of the landraces like Rato Masino, Thakali Lahare Marsi, Biramful, and Lekali Marsi from Lamjung and Tanahun districts were found to be promising landraces for yield and yield attributing traits (Sharma et al. 2020).

Rice landraces are the reservoir of genetic potential and several resistant genes for biotic and abiotic stresses, where the modern varieties are devoid of such quality (Tiwari et al. 2018). Because of high intra-landrace diversity, many landraces can be improved through pure line selection (Sharma et al. 2007); however, limited work has been done in this aspect. Kaski, Tanahun, Lamjung, Sunsari, and Bara districts are the center of landrace diversity (Joshi et al. 2017). Rice landraces, especially in the core collection from the diversity center, are essential reservoirs of useful genes and can be exploited to both broaden the existing narrow genetic base and enrich the current varieties with important favorable agronomic traits (Juneja 2006). It is, however, necessary to know the extent, magnitude, and pattern of rice diversity for a successful rice breeding program (Singh 2016). The variability in the landraces offers a considerable opportunity for the development of new cultivars through the selection.

The objective of the study was to assess the different diversity indices, variability, and heritability among different traits to support effective selection for successful rice breeding program. The findings of the study would be very vital to identify suitable genetic material and assist in designing the following breeding program to foster the varietal improvement programs.

MATERIALS AND METHODS

Selection of Site and Plant Material

The study was conducted at Agronomy Farm of the Institute of Agriculture and Animal Science (IAAS), Lamjung Campus, Lamjung district of Nepal, during June–November, 2018. Thirty landraces (Table 1) cultivated in a similar climate and altitude of research site were selected and collected from Rainas Municipality, Lamjung, and Bhanu Municipality, Tanahun.

Experimental Design and Data Collection

The landraces of the rice were evaluated in the field during June–November, 2018. The field trials were conducted under irrigated transplanting conditions. The landraces were sown in a raised nursery on June 16, 2018. Twenty-two days old seedlings were subsequently transplanted into the field in alpha-lattice with two replications. Each replication had five blocks, and each block contained six landraces of 2 m² each. Each treatment was transplanted in 5 rows with 20 cm of spacing between row to row and 20 cm between seedling to the seedling.

A fertilizer dose of recommended 100:30:30 kg N:P:K was applied. The entire dosage of phosphorus along with potassium and half dose of nitrogen was applied as a basal dose. The remaining dosage of nitrogen was applied in two splits, one at time of tillering and panicle initiation stage. The standard agronomical practices were adopted for healthy crop growth.

For the assessment of the diversity, 18 qualitative characters were recorded as per the descriptor established by Bioversity International, IRRI & WARDA (2007). The detail description and evaluation stage of the characters were presented in Table 2. For the assessment of the heritability in quantitative characters following parameters were recorded as per the descriptor of Bioversity International, IRRI & WARDA (2007). The detail description and evaluation stage of the characters were presented in Table 3.

Statistical Analysis

The analysis of variance (ANOVA) for different traits was performed on mean data separately to partition the

Table 1. List of rice landraces collected from Lamjung and Tanahun districts, Nepal.

S.N	Name of landraces	Site of collection
1	Pahelo Anadi	Marysangdi Chepe Community Seed Bank, Lamjung
2	Rato Anadi	Local farmer (Rainas Municipality, Lamjung)
3	Gokule Mansuli	Marysangdi Chepe Community Seed Bank, Lamjung
4	Rato Masino	Local farmer (Rainas Municipality, Lamjung)
5	Thakali Lahare Marsi	Local farmer (Rainas Municipality, Lamjung)
6	Pudke Dhan	Local farmer (Rainas Municipality, Lamjung)
7	Eakle	Marysangdi Chepe Community Seed Bank, Lamjung
8	Kalo Masino	Marysangdi Chepe Community Seed Bank, Lamjung
9	Biramful	Marysangdi Chepe Community Seed Bank, Lamjung
10	Indrabeli	Local farmer (Rainas Municipality, Lamjung)
11	Kalo Namdunge	Local farmer (Rainas Municipality, Lamjung)
12	Jarneli	Local farmer (Rainas Municipality, Lamjung)
13	Aanga	Local farmer (Rainas Municipality, Lamjung)
14	Jetho Budo	Marysangdi Chepe Community Seed Bank, Lamjung
15	Kalo Jhinuwa	Marysangdi Chepe Community Seed Bank, Lamjung
16	Jhinuwa Local	Marysangdi Chepe Community Seed Bank, Lamjung
17	Anadi tude	Marysangdi Chepe Community Seed Bank, Lamjung
18	Lekali Marsi	Marysangdi Chepe Community Seed Bank, Lamjung
19	Baryang masino	Local farmer (Rainas Municipality, Lamjung)
20	Sobhara	Local farmer (Rainas Municipality, Lamjung)
21	Marsi	Local farmer (Rainas Municipality, Lamjung)
22	Anadi Local	Marysangdi Chepe Community Seed Bank, Lamjung
23	Pakhe Sali	Marysangdi Chepe Community Seed Bank, Lamjung
24	Mansara	Purkot Community Seed Bank, Tanahun
25	Pahele	Purkot Community Seed Bank, Tanahun
26	Chiniya	Purkot Community Seed Bank, Tanahun
27	Juhari	Purkot Community Seed Bank, Tanahun
28	Seto Anadi	Purkot Community Seed Bank, Tanahun
29	Kathe	Purkot Community Seed Bank, Tanahun
30	Bihari	Purkot Community Seed Bank, Tanahun

variability due to various sources. The following genetic parameters were calculated.

Genotypic and Phenotypic Coefficient of Variation

The genotypic and phenotypic variance of various traits were calculated as per the formulae of Burton (1951).

Genotypic variance $(\sigma^2 g) = \dfrac{TMSS - EMSS}{R}$

Error variance $(\sigma^2 e) = EMSS$

Phenotypic variance $(\sigma^2 p)$ = genotypic variance + error variance = $\sigma^2 g + \sigma^2 e$

Genotypic coefficient of variation (GCV) = $\dfrac{\sigma g}{x}$ X 100

Phenotypic coefficient of variation (PCV) = $\dfrac{\sigma p}{x}$ X 100

Where, σg = genotypic standard deviation

Σg = phenotypic standard deviation

x = general means of trait

Sivasubramanian and Madhavamenon (1973) categorized the value of GCV and PCV as: low = 0–10%; moderate = 10–20%; and high = >20%.

Broad Sense Heritability (h$^2_{bs}$)

The ratio of genotypic variance to phenotypic variance is called as broad-sense heritability (Hanson et al. 1956). Heritability of a trait can be computed using the formula given by Burton and DeVane (1953).

$h^2_{bs} = \dfrac{V_g}{V_p}$ X 100 $= \dfrac{\sigma^2 g}{\sigma^2 p} \times 100$

Table 2. Qualitative characters along with their descriptor and evaluation phase of rice landraces from Lamjung and Tanahun districts, Nepal.

Qualitative traits	Descriptors	Evaluation phase
Basal leaf sheath color	Green, green with a purple line, light purple, purple	Late vegetative
Ligule color	Absent (ligule less), whitish, yellowish green, purple, light purple, purple lines	Late vegetative
Ligule shape	Absent, truncate, acute to acuminate, two cleft	Late vegetative
Collar color	Absent (collarless), green, light green, purple, purple lines	Late vegetative
Auricle color	Absent (no auricles), whitish, yellowish green, purple, light purple, purple lines	Late vegetative
Culm habit	Erect (<15°), semi-erect (intermediate) (~20°), open (~40°), spreading (>60–80°), procumbent (culm rests on the ground surface)	After flowering
Culm: anthocyanin coloration on nodes	Absent, purple, light purple, purple lines	After flowering
Awn distribution	None (awnless), tip only, upper quarter only, upper half only, upper three-quarters only, the whole length	At maturity
Culm: lodging resistance	Very weak, weak, intermediate, strong, very strong	At maturity
Flag leaf: attitude	Erect, Semi-erect (intermediate), horizontal, descending	Early reproductive stage
Lemma: color of apiculus	White, straw, brown, green, red, red apex, purple, purple apex, black	Near maturity
Panicle: exsertion	Enclosed, partly exserted, just exserted, moderately well exserted, well exserted	Near maturity
Panicle: secondary branching	Absent, sparse, dense, clustered	Near maturity
Panicle: shattering	Very low, low, moderate, high, very high	At maturity
Panicle: thresh ability	Difficult, intermediate, easy	After harvest
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

Table 3. Quantitative characters along with procedure and evaluation phase of rice landraces from Lamjung and Tanahun districts, Nepal.

Quantitative characters	Procedure	Evaluation phase
Effective tillers (ET)	Counted tillers having a panicle filled with grains.	At maturity
Plant height (cm) (PH)	Length measured from soil surface to the top of the tip of the panicle.	At maturity
Total grains per panicle (TG)	A counted number of grains per panicles of the sampled plant.	After harvest
Filled grains per panicle (FG)	Numbers of fertile grains per panicles of the sampled plant.	After harvest
Filled grain percentage per panicle (FGP)	$\text{FGP} = \dfrac{FG}{TG} \times 100\%$	
Panicle length (cm) (PL)	The length of the main axis of the panicle measured from base to the tip.	After harvest
Grain length (mm)	The distance from the base of the lowermost glume to the tip (apiculus) of the fertile lemma or palea, whichever is longer, was measured. On awned cultivars, length measured to a point comparable to the tip of the apiculus (exclude the awn).	After harvest
Grain width (GW)	The distance across the fertile lemma and palea at the widest point was measured.	After harvest
Flag leaf length (cm) (FLL)	The length of the flag leaf, from the ligule to the tip of the blade was measured.	7 days after anthesis
Flag leaf breadth (cm) (FLB)	The breadth of the flag leaf, measured.	7 days after anthesis
Thousand-grain weight (g) (TGW)	Counting of 1000-grains and their weight was measured.	After harvest
Kernel length (mm) (KL)	Ten milled grains were taken randomly, and the average length was recorded in millimeters.	After harvest
Kernel width (mm) (KW)	Ten milled grains were taken randomly, and the average width was recorded in millimeters	After harvest

Where, V_g = genotypic variance

V_p = phenotypic variance

As suggested by Johnson et al. (1955), h^2_{bs} estimates were categorized as: low = 0–30%; medium = 30–60%; and high = above 60%.

Genetic Advance and Genetic Advance as Percent of Means

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under a certain amount of selection pressure. The expected genetic advance was calculated by the method suggested by Johnson et al. (1955)

$GA = K. \sigma_p. h^2_{bs}$

where GA= genetic advance

K = selection differential (value of K =2.056 at 5% selection intensity)

σ_p = phenotypic standard deviation

h^2_{bs} = broad-sense heritability

The relative utility of genetic advance among the traits was computed as the percentage of genetic advance as followed.

$$\text{Genetic advance as percent of mean} = \frac{GA}{Grand\ mean} \times 100$$

The range of percentage of the genetic progress was classified as suggested by Johnson et al. (1955): low = less than 10%; moderate = 10–20%; high = more than 20%.

Shannon-Diversity Index

The Shannon index was calculated as given by Shannon (1948). Mathematically,

$$\text{Shannon-Weiner index } (H') = -\sum_{i=1}^{R} P_i \ln P_i$$

Where pi is the proportion of the trait, i.e.,

$$P_i = \frac{\text{Population bearing given character of trait}}{\text{Total population}}$$

Simpson Index

Simpson index was calculated as followed by Simpson (1949):

$$\text{Simpson index} = \sum \frac{n(n-1)}{N(N-1)}$$

Where n is the number of landraces bearing a character, and N is the total number of landraces.

Evenness

Species evenness refers to how close in numbers each species in an environment is. Mathematically it is defined as a diversity index, a measure of biodiversity which quantifies how equal the community is numerical. The evenness was calculated as given by Magurran (2004). Evenness $(E) = \frac{H'}{\ln(S)}$; where, S is a total number of variation cases

RESULTS

Assessment of Diversity Indices

Diversity indices of qualitative traits of rice land races studied are presented in Table 4. The Shannon-Weiner index was used to study the richness of character for a trait. The high value of this index represents a more diverse community regarding that trait. Shannon-Weiner index was found to be maximum for panicle shattering (1.41), followed by the culm lodging resistance (1.4) and lemma and palea color (1.38). All these three traits showed five characters each. While the minimum value was found to be 0.15 in culm anthocyanin coloration on nodes followed by collar color and culm habit (0.24). These three traits showed only two types of characters. The characters were evenly distributed in trait Panicle: secondary branching (0.99), where two characters clustered and dense were present in almost equal proportion followed by spikelet fertility (0.89) and panicle shattering (0.88). The minimum evenness was observed in culm anthocyanin coloration (0.21) where only one landrace showed purple coloration while 29 landraces showed no anthocyanin coloration. This trait was followed by culm color and culm habit (0.35).

Simpson index was used to calculate the probability of any two landraces drawn from noticeably large communities bears different characters for a trait. The value of the Simpson index was found to be maximum for panicle shattering and culm lodging resistance, each equal to 0.75, followed by lemma and palea color (0.74). Higher the value of Simpson index higher the probability of obtaining two different characters for a trait under random selection. The minimum value was found to be 0.07 for culm anthocyanin coloration indicating dominance of a single character of a trait.

Table 4. Diversity indices of qualitative traits of rice landraces from Lamjung and Tanahun districts, Nepal.

Character	Shannon index	Simpson index	Evenness
Auricle colour	0.49	0.25	0.44
Awn	0.59	0.34	0.54
Awn distribution	0.81	0.4	0.5
Basal leaf sheath (colour)	0.63	0.35	0.57
Collar colour	0.24	0.13	0.35
Culm habit	0.24	0.13	0.35
Culm: anthocyanin colouration on nodes	0.15	0.07	0.21
Culm: lodging resistance	1.4	0.75	0.87
Flag leaf: attitude	1	0.62	0.91
Leaf blade pubescence	0.93	0.59	0.85
Lemma and palea colour (late)	1.38	0.74	0.86
Lemma:colour of apiculus	0.84	0.51	0.76
Ligule colour	0.5	0.33	0.72
Ligule shape	0.33	0.19	0.47
Panicle: exsertion	1.12	0.65	0.81
Panicle: shattering	1.41	0.75	0.88
Panicle: threshability	0.8	0.5	0.73
Panicle: secondary branching	0.68	0.51	0.99
Spikelet: fertility	0.98	0.62	0.89

Table 5. Analysis of variance for quantitative characteristics in rice landraces from Lamjung and Tanahun districts, Nepal.

Charac-teristics	Mean sum of squares of source of variation			
	Replication (df = 1)	Treatment (df = 29)	Block/ Rep (df = 8)	Error (df =21)
PH	415.75*	464.58***	49.52	94.79
FG	707.3	3535.9***	135.3	175.4
TG	653.40	1849.46***	195.42	308.87
FGP	1.80	575.97***	25.95	31.11
PL	30.1467	27.69***	4.17	4.87
GL	0.11881	2.72828***	0.11464	0.08535
GW	0.00007	0.291***	0.0057	0.0182
KL	0.41500	1.32159 ***	0.04893	0.07922
KW	0.000375	0.212018***	0.004890	0.010441
FLL	9.616	79.807***	24.724*	9.554
FLB	0.043740	0.063489***	0.034606*	0.011943
ET	1.6667	6.9218 ***	1.8608	1.73
TGW	6.667**	41.304***	0.805	0.825

*=significant at 5%, **= significant at <1%, ***=significant at <0.1%
PH = plant height, FG = filled grain, TG = total grain, FGP = filled grain percentage, PL = panicle length, GL = grain length, GW = grain width, KL = kernel length, ET = effective tiller, KW = kernel width, FLL = flag leaf length, FLB = flag leaf breadth, TGW = thousand grain weight

Analysis of Variance

Analysis of variance depicting mean squares for different traits studied is presented in Table 5. The results revealed that mean squares due to landraces were highly significant (p<0.001) for all the characteristics, indicating considerable genetic variation for different traits among the landraces under study, and this could be utilized for the screening in future breeding programs.

The Estimate of Genetic Parameters

The estimate of genetic parameters of quantitative traits in rice landraces studied is presented in Table 6. The study showed that plant height varied from 124.63 cm (Gokul Mansuli) to 193.83 cm (Jhinuwa Local) with a mean average plant height of 156.91 cm. The plant height was found to have low GCV (8.67), but moderate PCV (10.66), and high heritability (66.11%) with moderate genetic advance percentage per mean of 14.49%. The results for plant height were similar to Kole et al. (2010) for GCV and heritability, Yadav et al. (2017) for PCV, and Perera et al. (2014) for moderate genetic advance percentage per mean.

The value of filled grain per panicle ranged from 9 (Mansara) to 218 (Jarneli), while the total grain ranged from 60 (Mansara) to 230 (Jarneli). The filled grain percentage ranged from 15% (Mansara) to 95.91% (Anadi Seto). The average filled grain per panicle was found to be 122.73, while the total grain and filled grain percentage was found to be 156.9 and 76%, respectively. The GCV and PCV of filled grain were found to be high (33.4 and 35.1, respectively), and high heritability (90.55) was coupled with a high genetic advance percentage per mean (65.34%). This result was in accordance with the observation made by Perera et al. (2014). The GCV to PVC of total grain were estimated to be 17.69 and 20.94, respectively, which showed moderate genotype variability and high phenotypic variability along with high heritability (71.38%) and a high genetic advance percentage per mean (30.73%). This findings were similar to findings made by Ameenal et al. (2016). The PCV and GCV of filled grain percentages were estimated to be high (21.72 and 22.93, respectively), and high heritability (89.75%) was coupled with a high genetic advance percentage per mean (42.3%). A similar result reported by Pratap et al. (2018).

The value of the panicle length varied from 15 cm (Mansara) to 38.5 cm (Pudke Dhan) with a mean value of 27.08 cm. The GCV and PCV were found to be

Table 6. Estimate of genetic parameters of quantitative traits in rice landraces from Lamjung and Tanahun districts, Nepal.

Characteristics	Range		Mean	GCV (%)	PCV (%)	HBS (%)	GAM (%)
	Minimum	Maximum					
PH (cm)	124.63	193.83	156.91	8.67	10.66	66.11	14.49
FG	9.00	218.00	122.73	33.40	35.10	90.55	65.34
TG	60.00	230.00	156.90	17.69	20.94	71.38	30.73
FGP	15.00	95.91	76.00	21.72	22.93	89.75	42.30
PL (cm)	15.00	38.50	27.08	12.47	14.90	70.07	21.47
GL (mm)	6.35	10.50	8.33	13.80	14.24	93.93	27.50
GW (mm)	2.15	4.00	3.01	12.27	13.07	88.18	23.69
KL (mm)	4.50	7.93	6.11	12.91	13.70	88.69	24.99
KW (mm)	1.95	3.27	2.67	11.91	12.51	90.61	23.31
FLL (cm)	25.48	50.96	36.80	16.11	18.17	78.62	29.36
FLB (cm)	1.02	2.10	1.51	10.64	12.87	68.33	18.08
ET	3.00	11.00	6.27	25.70	33.20	59.90	40.89
TGW (g)	17.10	36.40	25.78	17.45	17.81	96.08	35.17

GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, HBS = broad sense heritability, GAM = genetic advance as a percentage of the mean, PH = plant height, FG = filled grain, TG = total grain, FGP = filled grain percentage, PL = panicle length, GL = grain length, GW = grain width, KL = kernel length, KW = kernel width, FLL = flag leaf length, FLB = flag leaf breadth, ET = effective tiller, TGW = thousand grain weight

moderate, with values of 12.47 and 14.9, respectively. The heritability and genetic advance percentage per mean were found to be high, 70.07% and 21.47%, respectively. Ajmera et al. (2017) observed similar results for PCV, GCV, heritability, and genetic advance percentage per mean.

The grain length varied from 6.35 mm (Indrabeli) to 10.5 mm (Jarneli) with a mean value of 8.33 mm, while the grain width varied from 2.15 mm (Kalo Jhinuwa) to 4 mm (Rato Anadi) with the mean value of 3.01 mm. The GCV and PCV of grain lenght were estimated to be moderate value of 13.8 and 14.24, respectively, and heritability was estimated to be high (93.93) coupling with a high genetic advance percentage per mean (27.5%). Similar results were obtained by Ismaeel et al. (2018) for heritability and genetic advance, but the contrary to GCV and PCV, were found low.

Kernel length varied from 4.5 mm (Kalo Namdunge) to 7.93 mm (Jetho Budo) with mean kernel length of 6.11 mm. GCV and PCV of kernel length were estimated to be moderate value being 12.91 and 13.7 with high heritability (88.69) coupled with a high genetic advance percentage per mean (24.99%). Regarding kernel width, it ranged from 1.95 mm (Kalo Jhinuwa) to 3.27 mm (Rato Anadi) with a mean value of 2.67 mm. Concerning kernel width, GCV and PCV were found to be moderate, the value being 11.91 and 12.51, respectively. The kernel width also expressed high heritability (90.61) unison with a high genetic advance percentage per mean (23.31%). The similar results in all parameters were obtained by Bharath et al. (2018).

The flag leaf length in the study varied from 25.48 cm (Kalo Namdunge) to 50.96 cm (Aaga) with a mean value of 36.8 cm, while the flag leaf breadth varied from 1.02 cm (Aaga) cm to 2.1 cm (Pahelo Anadi) cm with mean value of 1.51 cm. The GCV and PCV were estimated to be moderate, 16.11 and 18.17 for flag leaf length and 10.64 and 12.87 for flag leaf breadth, respectively. The heritability for flag leaf length was high (78.62) coupled with a high genetic advance percentage per mean (29.36%), whereas flag leaf breadth had a high heritability (68.33) coupled with moderate genetic advance percentage per mean (18.08%). Similar results were found for GCV and PCV of both traits by Chakraborty and Chakraborty (2010), but the findings of Bharath et al. (2018) for heritability and genetic advance per mean for both characteristics.

The effective tiller number ranged from 3 (Anadi Tude) to 11 (Bihari) with mean average effective tiller 6.27. The GCV and PCV of effective tiller were found to be high with values of 25.7 and 33.2, high heritability (59.9) with 40.89% genetic advance percentage per mean. The result was following the other findings (Bharath et al. 2018; Chakraborty and Chakraborty 2010).

Thousand grain weight varied from 17.1 g (Kalo Masino) to 36.4 g (Rato Masino) with a mean 1000 grain weight of 25.78 g. The GCV and PCV were found to be moderate with values of 17.45 and 17.81, respectively, while heritability and genetic advance per mean were found to be high with values of 96.08 and 35.17. Ismaeel et al. (2018) and Bhadru et al. (2012)

also reported moderate PCV and GCV, along with high heritability and high genetic advance.

DISCUSSION

For all traits considered, PCV was found to be greater than GCV, indicating that the apparent variation is not only genetic, but also influenced by the growing environment in the expression of the traits. However, the differences were as low as 0.36 (1000-grain weight) to as high as 7.5 (effective tiller). The low difference may be either due to lower sensitivity of landrace to the environment or greater role of genetic control governing the character. It also implies that the traits are less affected by environment, and selection based on phenotype independent of landraces could be effective for the improvement of such traits.

Lower GCV and PCV indicate a narrow genetic base for these traits. Improvement in these traits can be brought about by hybridization or induced mutagenesis to widen the genetic base, followed by pedigree selection in advanced generations (Nirmaldevi et al. 2015). The GCV provides a measure of comparison of variability and sometimes gives some indication regarding the validity of traits for selection. However, it does not provide a clear picture of the extent of genetic gain to be expected from the selection of phenotypic traits unless heritable fraction of variation (heritability) is known (Burton and DeVane 1953).

Heritability is the proportion of phenotypic variation in a population that is due to genetic variation between individuals. Phenotypic variation among individuals may be due to genetic, environmental factors, or random chance. Heritability analyzes the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population (Kumar et al. 2012). A character exhibiting high heritability may not necessarily give high genetic advance. Johnson et al. (1955) have shown that high heritability should be accompanied by high genetic advance to arrive at a more reliable conclusion. Therefore, it should be combined with information on genetic advances. Thus, a character possessing high heritability along with high genetic advance will be valuable in the selection program.

The filled grain showed a high coefficient of genotypic variation (33.4) followed by effective tiller (25.7) and filled grain percentage (21.72). Thousand grain weight (0.36), kernel length (0.79) and width (0.6), grain length (0.44) and width (0.8) all exhibited small difference between the PCV and GCV indicating the presence of high genetic variability among the landraces and less influence of environment for the characteristics studied. Under such situations, the selection based on phenotype alone can be effective for these traits. Similar findings

were made by Perera et al. (2014). All traits under study showed a high amount of heritability ranging from 96.08 (1000-grain weight) to 59.9 (effective tiller). The low value of heritability of effective tiller compared with the other traits also indicates the presence of environmental effect, which is also verified by the huge difference of GCV and PCV for that trait (7.5). High heritability in unison with high genetic advance percentage per mean was obtained in total, filled and filled grain percentage, grain length and width, kernel length and width, flag leaf length, and 1000-grain weight. It indicated that the traits were mostly governed by additive gene effects and direct selection of these traits based on phenotypic expression by simple selection method will be effective due to accumulation of more additive genes leading to further improvement.

CONCLUSION

There exists vast diversity among the rice landraces of Lamjung and Tanahun districts, as indicated by the Shannon-Weiner and Simpson diversity index. Analysis of variance revealed the highly significant differences among the landraces for all the traits under study. The landraces exhibited a wide range of variability for most of the characteristics which indicated ample scope for selection of promising genotypes from a present set of landraces for yield improvement. Ten traits showed high heritability coupled with a varietal genetic advance. Thus we can conclude that the crop improvement can be made based on selection for those trait as it indicates the presence of additive gene action. The selection cannot be made alone based on phenotype for effective tiller due to high environmental effect and low heritability. Flag leaf breadth and plant height exhibited a low genetic advance, although it expressed high heritability because of the presence of the non-additive gene action, and this cannot be used for crop improvement solely based on selection. Future rice breeding programs can exploit the rice landraces based on the study, which identified the presence of diversity and variability in the landraces.

ACKNOWLEDGEMENT

REFERENCES

Ajmera, S., Kumar, S. & Ravindrababu, V. (2017) Evaluation of genetic variability, heritability and genetic advance for yield and yield components in rice genotypes. *International Journal of Current Microbiology and Applied Sciences*. 6 (10), 1657–1664.

Ameenal, M., Shalini, T., Govintharaj, P., Manonmani, S., & Robin, S. (2016) Assessment of parental genetic variability in rice. *International Journal of Agriculture Sciences*. 8, 2917–2919.

Bhadru, D., Lavuri, K., Pasha, M. & Naik, R. (2012) Effect of environment on genetic parameters of hybrid rice. *International Journal of Applied Biology and Pharmaceutical Technology*. 3 (2), 182–187.

Bharath, M., Mohan, M., Vanniarajan, C., Gridhari, V. & Senthil, N. (2018) Genetic variability studies in ADT 43/Seeraga samba cross derivatives of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 9 (4), 1450.

Bioversity International, IRRI and WARDA. (2007) *Descriptors for Wild and Cultivated Rice* (Oryza *spp*.). Rome, Los Baños & Cotonou, Benin. Bioversity International, International Rice Research Institute & WARDA, Africa Rice Center.

Burton, G. (1951) Quantitative inheritance in pearl millet (*Pennisetum glaucum*). *Agronomy Journal*. 43, 409–417.

Burton, G. & DeVane, E. (1953) Estimating heritability in tall fescue (*Festuca Arundinacea*) from replicated clonal material. *Agronomy Journal*. 45, 478–481.

CDD (2017) *Rice varietal mapping in Nepal: Implication for development and adoption*. Hariharbhawan, Kathmandu, Crop Development Directorate.

Chakraborty, R., & Chakraborty, S. (2010) Genetic variability and correlation of some morphometric traits with grain yield in bold grained rice (*Oryza sativa* L.) gene pool of Barak valley. *American-Eurasian Journal of Sustainable Agriculture*. 4(1), 26–29.

Chauhan, B., Jabran, K., & Mahajan, G. (2017) *Rice Production Worldwide*. Switzerland. Springer Publication.

Gauchan, D. (1999) *Economic Valuation of Rice Landraces Diversity: A Case Of Bara District, Tarai, Nepal*. A scientific basis of in situ conservation of agrobiodiversity on-farm: Nepal's contribution to the global project. Working paper NP 1/99.

Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956) Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal*. 48, 268–272.

Ismaeel, M., Shah, S. M. A., Rahman, A. U., & Raza, M. A. (2018) Heritability and heterosis for yield and yield related traits in rice. *Sarhad Journal of Agriculture*. 34(3),543–549.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 47, 314–318.

Joshi, B. K. (2017) Plant breeding in Nepal past present and future. *Journal of Agriculture and Forestry University*. 1, 1–33.

Joshi, B. K., Hay, F., Sapkota, S., & Ebana, K. (2017) Nepalese rice around the world. In: *Rice science and Technology*. Paudel et al. (Eds.) Hariharbhawan and Khumaltat, Nepal. Crop Development Directorate and Agronomy Society of Nepal.

Juneja, S., Das, A., Joshi, S., Sharma, S., Vikal, Y., Patra, B., Bharaj, T., Sindhu, J. & Singh, K. (2006) *Oryza nivara* the progenitor of *O. sativa* L. subspecies indica harbours rich genetic diversity as measured by SSR markers. *Current Science*. 91(8), 1079–1085.

Kole, P., Chakraborty, N., & Bhat, J. (2010) Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. *Tropical Agricultural Research and Extension*. 11, 60–64.

Kumar, S., Singh, D., Satyendra, Sirohi, A., Kant, S., Kumar, A., Pal, K., & Kumar, M. (2012) Variability, heritability and genetic advance in rice (*Oryza sativa* L.) under aerobic condition. *Environment & Ecology*. 30 (4), 1374–1377.

Magurran, A. E. (2004) *Measuring Biological Diversity*. Hoboken, NJ, United States. Wiley.

Mann, C. (1997) Reseeding the green revolution. *Science*. 277, 2038–2042.

MOAD. (2018) *Statistical Information on Nepalese Agriculture 2016/2017*. Singha Durbar, Kathmandu, Nepal. Ministry of Agricultural Development. Monitoring, Evaluation and Statistics Division, Agri Statistics Section.

Nirmaldevi, G., Padmavathi, G., Kota, S., & Babu, V.s R. (2015) Genetic variability, heritability and correlation coefficient of grain quality characters in rice. *SABRAO Journal of Breeding and Genetics*. 47(4), 424–433.

Perera, I., Senanayake, S. G. J. N., Sumith, D., & Abeysiriwardena, Z. (2014) Genetic parameters and correlations of yield attributing characteristics of weedy rice in Sri Lanka. *Journal of the National Science Foundation of Sri Lanka*. 42, 299–306.

Pratap, A., Bisen, P., Loitongbam, B., Sandhya, & Singh, P. K. (2018) Assessment of genetic variability for yield and yield components in rice (*Oryza sativa* L.) germplasms. *International Journal of Bio-resource and Stress Management*. 9(1), 087–092.

Shannon, C.E. (1948) A mathematical theory of communication. *The Bell System Technical Journal*. 27. 379–423.

Sharma, R. C., Chaudhary, N. K., Ojha, B., Yadav, L., Pandey, M. P., & Shrestha, S. M. (2007). Variation in rice landraces adapted to the lowlands and hills in Nepal. *Plant Genetic Resources: Characterization and Utilization*. 5(03), 120–127.

Sharma, S., Pokhrel, A., Dhakal, A. & Poudel A. (2020). Agro-morphological characterization of rice landraces (*Oryza sativa* L.) of Lamjung and Tanahun District, Nepal. *Annals of Plant Sciences*. 9(2), 3731–3741.

Shivapriya, M., & Hittalmani, S. (2006) Genotype specific fingerprints and molecular diversity of Indian local and landraces detected in rice (*Oryza sativa* L.) using DNA markers. *Indian Journal of Genetics*. 66(1), 1–5.

Simpson, E. H. (1949) Measurement of diversity. *Nature*. 163. 688.

Singh, N., Choudhury, D. R., Tiwari, G., Singh, A. K., Kumar, S., Srinivasan, K., Tyagi, R. K., Sharma, A. D., Singh, N. K., & Singh, R. (2016) Genetic diversity trend in Indian rice varieties: an analysis using SSR markers. *BMC Genetics*. 17, 1–13.

Sivasubramanian, S., & Madhavamenon, P. (1973) Genotypic and phenotypic variability in rice. *Madras Agriculture Journal*. 60(9-13), 1093–1096.

Tilman, D. (1998) The greening of green revolution. *Nature*. 396, 211–212.

Tiwari, D. N., Bastola, B. R., & Ghimire, B. (2018) Agro-morphological variability of upland rice hill landraces evaluated at Central Terai Region of Nepal. *International Journal of Advances in Scientific Research and Engineering*. 4(4), 45–51.

Tiwari, D. N., Tripathi, S. R., Tripathi, M. P., Khatri, N., & Bastola, B. R. (2019) Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*. 2019, pp:9.

Upreti, H. (2017) Distribution patterns of rice landraces in different agro-ecological zones of Nepal. In: *Rice Science and Technology*. Paudel et al. (Eds.) Hariharbhawan and Khumaltar, Nepal. Crop Development Directorate and Agronomy Society of Nepal.

Yadav, R., Rajpoot, P., Verma, O., Singh, P., Singh, P., & Pathak, V. (2017) Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for grain yield and it's contributing attributes under sodic soil. *Journal of Pharmacognosy and Phytochemistry.* 6(5), 1294–1296.