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

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Submitted 21 December 2019; Revised 25 April 2020; Accepted 13 May 2020

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 genetic 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]

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
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 ($\sigma^2_g$) = \(\frac{TMSS - EMSS}{R}\)

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) = \(\frac{\sigma_g}{\Sigma_x}\) X 100

Phenotypic coefficient of variation (PCV) = \(\frac{\sigma_p}{\Sigma_x}\) X 100

Where, $\sigma_g$ = genotypic standard deviation

$\Sigma_g$ = phenotypic standard deviation

$\Sigma_x$ = 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).

\[ h^2_{bs} = \frac{V_g}{V_p} \times 100 = \frac{\sigma^2_g}{\sigma^2_p} \times 100 \]
### 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 lines                 | 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: exertion                   |Enclosed, partly exerted, just exerted, moderately well exerted, well exerted | 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) | $\text{FGP} = \frac{FG}{TG} \times 100\%$                                                  |                      |
| 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)

\[
GA = K \cdot \sigma_p \cdot h^2_{bs}
\]

where \( GA \) = genetic advance
\( K \) = selection differential (value of \( K = 2.056 \) at 5% selection intensity)
\( \sigma_p \) = 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.

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

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,

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

Where \( P_i \) 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 \( (E) = \frac{R}{\ln(S)} \); 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.
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%).

The results were in accordance with the observation made by Perera et al. (2014). The GCV to PVC of total grain were estimated to be high (71.38%) and a high genetic advance percentage per mean (30.73%). This was similar to findings made by Ameenal et al. (2016). The PCV and GCV of filled grain percentages were estimated to be high (90.55) and 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 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).
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 length 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 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 estimated 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)

| 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
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**

The authors extend their profound gratitude and appreciation to Assistant Professor Roshan Subedi, Assistant Professor Mahesh Jaishi, and Assistant Professor Amit Khanal for their valuable guidance and suggestion throughout the research. The authors also
like to acknowledge Marsyandi Chepe Community Seed Bank, Purkot Community Seed Bank, and local farmers of Rainas for providing valuable landraces for this research.

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