



Research article

Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traitsBigul Thapa Magar^{a,*}, Subash Acharya^a, Bibek Gyawali^a, Kiran Timilsena^b, Jharana Upadhyaya^c, Jiban Shrestha^d^a Prithu Technical College, IAAS, TU, Lamahi, Dang, Nepal^b Department of Plant Breeding, IAAS, TU, Kirtipur, Kathmandu, Nepal^c Nepal Agricultural Research Council, National Maize Research Programme, Rampur, Chitwan, Nepal^d Nepal Agricultural Research Council, National Plant Breeding and Genetics Research Centre, Khumaltar, Lalitpur, Nepal

ARTICLE INFO

Keywords:

Maize
PCV
GCV
Heritability
Genetic advance
Correlation

ABSTRACT

The present study was carried out to study the variation, broad-sense heritability, genetic advance, correlation among traits for growth, yield, and its attributing traits in maize genotypes. Ten maize genotypes were evaluated in a randomized complete block design (RCBD) with three replications from June 2019 to September 2019. The results indicated that the genotypes were significantly different for all traits. For all traits, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). The grain yield showed the highest PCV (26.91%) and GCV (25.9%) whereas leaf width at maturity showed the lowest PCV (4.07%) and GCV (6.05%). Genetic Advance over Mean (GAM) for the traits ranged from the lowest value (0.1%) for days to 50% anthesis to the highest value (51.36%) for grain yield. Higher values of heritability and GAM % were obtained for grain yield (0.93, 51.36%) and 1000 grain weight (0.99, 36.95%) whereas the lowest values of heritability and GAM% were found for leaf length (0.5, 7.25%) and leaf width (0.39, 5.25%). Grain yield showed positive and significant phenotypic correlation with test weight ($r = 0.706$), cob length ($r = 0.671$), cob diameter ($r = 0.573$) and number of rows per cob ($r = 0.539$), respectively. Therefore, traits having high variation can be used as selection indices for indirect selection for the improvement of maize productivity.

1. Introduction

Open-pollinated varieties (OPVs) of maize are mostly farm-bred cultivars that produce grain that may be kept as seed for the following season. OPVs are crucial because they aid in the development of cultivars that can endure extreme cold or drought, as well as those that are resistant to pathogenic organisms or insect pests. These characteristics also help to considerably stabilize yield by reducing excessive variations (Kutka, 2011). This demonstrates that there is an urgent need to conserve and properly utilize the genetically varied open-pollinated genotypes of the local area through various breeding programs, as it provides a selection of the most suitable and compatible variations for the area. It also aids in the exchange of germplasm, which is required in the future for the improvement of new varieties. However, OPVs that are as good as hybrids are not thoroughly evaluated and disseminated in the research

realm to discover the most suited OPV. Crop's effectiveness is determined by the magnitude of genetic variability present in the population, but also by how heritable it is (Hussain et al., 2011).

A breeder will be able to determine to what extent the environment impacts yield by determining genotypic and phenotypic in yield and yield components of diverse crop genotypes (Ullah et al., 2012). Heritability assumes that individuals who are closely connected are more likely to resemble one another than those who are distantly related (Falconer and Mackay, 1996). Heritability estimate helps breeders to allocate resources effectively to select desired traits and to achieve maximum genetic gain with little time and resources (Smalley et al., 2004).

One of the most well-known applications of heritability in quantitative character genetic studies is its predictive role, which aids in determining the reliability of phenotypic value as a guide to breeding value

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(Kumar et al., 2014). Characters having a high heritability can be quickly progressed by using simple selection. Heritability, on the other hand, has been explored and shown to be of no practical value without the involvement of genetic advancements. The quantity of heritable genes gained in a character under a certain selection pressure is referred to as genetic progress. High genetic progress, as well as high heritability estimates, provide the best conditions for selection (Bello et al., 2012). The coefficient of variation depicts the degree of variability present in a large number of different traits, but it does not include the heritable component. A correlation study can also provide trustworthy and helpful information about the type, scope, and direction of selection (Zeeshan et al., 2013). The coefficient of correlations aids in determining the level of relationship between two separate traits as well as the level at which these traits are mutually variable (Boćanski et al., 2009; Nagabhushan et al., 2011). Grain yield is a complicated trait that is influenced by a number of morphological and physiological traits (Crosbie and Mock, 1981). Grain yield can be increased by understanding the relationship correlation between yield and its components and determining the type of relationship between them (Kalla et al., 2001). Another study found that plant height, ear height, and the number of grain rows per ear cob all had a positive and significant correlation with grain yield (Sadek et al., 2006).

The objective of this study was to determine the variability of morpho-physiological and yield traits in maize varieties, as well as their correlation.

2. Materials and methods

2.1. Site selection for research materials

From June 2019 to September 2019, the experiment was carried out in the research field of Prithu Technical College, IAAS, Lamahi Municipality Ward No. 5 of Dang district. Geographically, it is located at 27° 42.09' N latitude and 82° 30.49' E longitude, with a 257 masl altitude.

The physical and chemical examination of soil in this location revealed that silt predominated over sand and clay in the soil, resulting in a silt loam texture with a slightly acidic pH (6.67). The soil had an organic carbon level (0.55%) and available total nitrogen (0.0545%), available phosphorous (35.44 kg ha⁻¹), and available potassium content (200 kg ha⁻¹).

Temperatures ranged from 14.11°C to 31.27 °C, with an average of 22.69 °C, at the experimental site. Rainfall totaled 938.1 mm on average. The highest and lowest temperatures observed during the crop growing season were in June (39 °C) and July (26 °C), respectively. Similarly, the greatest precipitation (22 mm) and relative humidity (87.3%) were recorded in July and August, respectively.

2.2. Selection of the genotypes

The planting genotypes of open pollinated varieties viz Arun-2, Rampur Composite, Poshilo Makai-2, Arun-4, HG-AB, RampurS13F26, SINIBP-UTYF, CelayaGhoga, Posilo Makai-1, and Manakamana-3 were obtained from National Maize Research Program (NMRP), Rampur, Chitwan, Nepal.

2.3. Experimental design and cultural practices

Ten genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Individual plots had 4 rows of 5m length, with a spacing of 75 cm × 25 cm (row to row × plant to plant). One week before sowing, 6 t ha⁻¹ well-decomposed farmyard manure (FYM) was mixed into the soil, and 120:60:40 kg N:P: K [nitrogen (N), phosphorus (P) and potassium (K)] ha⁻¹ was applied through Urea, Diammonium Phosphate (DAP), and Muriate of Potash (MOP). During final land preparation, a half dose of N, a full dose of P, and a full dose of K was administered as a basal dose. The remaining half of the N dose was

applied in two splits for application in 45 and 90 days following seeding. During the maize growing season, two hand weedings and hoeing were completed. The first weeding was carried out after 18 days of sowing, while the second took place after 36 days. At three critical growth stages, the crop was irrigated: knee-high stage, tasseling stage, and milking stage. The National Maize Research Program, Rampur, Chitwan, Nepal, recommended a package of procedures, which were followed during intercultural operation.

2.4. Data collection and observations

For all traits, data was obtained from ten randomly selected plants from each experimental plot. These selected plants were observed for phenological traits (days to silking, days to tasseling, and anthesis silking interval (ASI)), biometrical traits (Plant and ear height, leaf parameters, cob length, width, and diameter), and yield and yield attributing traits (Number of kernel rows per cob, number of kernel per rows, 1000 grain weight). Grain yield (kg ha⁻¹) at 15% moisture content was calculated using fresh ear weight with the help of the below (Eq. 1) formula:

$$\text{Grain yield (kg ha}^{-1}\text{)} = \frac{\text{F.W. (kg plot)} \times (100 - \text{HMP}) \times \text{S} \times 10000}{(100 - \text{DMP}) \times \text{NPA}} \quad (1)$$

Where,

F.W. = Fresh weight of ear in kg per plot at harvest

HMP = Grain moisture percentage at harvest

DMP = Desired moisture percentage, i.e. 15%

NPA = Net harvest plot area, m²

S = Shelling coefficient, i.e. 0.8

This formula was also adopted by Carangal et al. (1971) and Shrestha et al. (2015) to adjust the grain yield (kg ha⁻¹) at 15% moisture content. This adjusted grain yield (kg ha⁻¹) was again converted to grain yield (t ha⁻¹).

2.5. Data observation and analysis

Following the collection of data, grain yield (t ha⁻¹) was computed using the formula proposed by Bartaula et al. (2019), Carangal et al. (1971), and Shrestha et al. (2018) by adjusting grain moisture to 15%. The data on all of the characters were subjected to standard analysis of variance methods (Panse and Sukhatme, 1967).

The phenotypic and genotypic coefficients of (Singh and Chaudhary, 1985), Heritability (in the broad sense) (Johnson et al., 1955), genetic advance (Burton, 1952), and genetic advance as a percentage of the mean (Johnson et al., 1955) were all calculated. The GCV (Eq. 2), PCV (Eq. 3), Heritability (Eq. 4), Genetic advance (Eq. 5), Genetic advance percentage of mean (GAM) (Eq. 6) were calculated using below formulas;

$$\text{GCV}(\%) = \frac{\sqrt{\delta^2 g}}{x} \times 100 \quad (2)$$

$$\text{PCV}(\%) = \frac{\sqrt{\delta^2 p}}{x} \times 100 \quad (3)$$

where: $\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance and x = sample mean.

$$\text{Heritability (h}^2\text{)} = \frac{\delta^2 g}{\delta^2 p} \quad (4)$$

$$\text{Genetic advance (GA)} = (K) (\delta^2 p) (h^2), \quad (5)$$

where GA = expected genetic advance, K = selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes, δp = phenotypic standard deviation and h^2 = heritability (in broad sense).

Table 1. Mean sum of squares for different traits of ten maize genotypes.

| Traits | Mean sum of squares | |
|-------------------------------------|---------------------|-----------------|
| | Genotypes (df = 10) | Error (df = 20) |
| Plant height (after flowering) (cm) | 375.3* | 119.6 |
| No. of leaves above cob | 0.6276** | 0.1618 |
| No. of leaves below cob | 0.5628* | 0.1868 |
| Leaf length at maturity (cm) | 61.49** | 15.32 |
| Leaf width at maturity (cm) | 0.5059* | 0.175 |
| Days to 50% anthesis | 27.121** | 26.79 |
| Ear height (cm) | 120.47 | 56.73 |
| Tassel length (cm) | 36.05** | 4.09 |
| Anthesis Silking Interval (ASI) | 1.3212** | 0.2212 |
| Cob length (cm) | 3.165* | 0.978 |
| Cob weight (g) | 774.2** | 229.5 |
| Cob diameter (cm) | 0.13728* | 0.04435 |
| No. of row per cobs | 5.818** | 0.627 |
| No. of grains per row | 15.74 | 10.48 |
| 1000 grain weight (g) | 5886** | 19 |
| Grain yield (t ha ⁻¹) | 3.495** | 0.09 |

* = Significant at 5% level of significance, ** = Significant at 1% level of significance.

Expected genetic advance percentage of mean (GAM) was calculated according to Shukla et al. (2006) as;

$$GAM = \frac{GA}{x} \times 100 \tag{6}$$

where x = Grand mean

The Pearson correlation coefficient of growth, yield and its attributing traits was worked out according to the procedure outlined (Eq. 7). The correlation coefficient was calculated using SPSS 20.

$$r = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2} \sqrt{\sum_i (y_i - \bar{y})^2}} \tag{7}$$

Where,

r = Pearson correlation coefficient

x_i = x variable, y_i = y variable

\bar{x} = Mean of x variable

\bar{y} = Mean of y variable

2.6. Statistical analysis

Excel 2010 was used to process the experimental data, while R-studio 3.5.0 and SPSS 20 were used to analyze it. Randomized complete block design (RCBD) with one-way ANOVA was used to analyze data. The treatment means were compared using the least significant difference (LSD) at 5% level of significance (Gomez and Gomez, 1984).

3. Results and discussion

Field studies were conducted to determine the genetic variability and correlations in agro-morphological traits in maize genotypes. The findings were evaluated and discussed, with evidence from earlier studies to back them up.

3.1. Genetic variability

The presence of significant variation in genotypes for most of traits was given in Table 1.

For all the traits, the GCV values were lower than PCV value, showing that the characters were more influenced by their surrounding environments. According to Sivasubramanian and Menon (1973), the traits evaluated in this study had low (less than 10% phenotypic and genotypic coefficients of variation), moderate (10–20% phenotypic and genotypic coefficients of variation), and high (more than 20% phenotypic and genotypic coefficients of variation). Grain yield was estimated to have high PCV and GCV values (26.91, 25.9). Similarly, low PCV and low GCV (7.96, 5.16), were estimated for traits like plant height (after flowering) (7.96, 5.16), no. of leaves below the ear (7.47, 4.73), leaf length (7.02, 4.97), and width (6.55, 4.07) at maturity, ear height (9.9, 5.17), cob length (7.92, 5.18), cob diameter (6.77, 4.34) and tassel length (6.37, 4.2). The remaining features had either low PCV and high GCV or moderate PCV and low GCV (Table 2). The coefficient of variations (CV), particularly GCV, determines its reliability for use in a breeding program. In breeding works, a high proportion of GCV to PCV is preferred. Grain yield had high PCV and GCV values (26.91, 25.9), whereas 1000 grain weight had intermediate PCV and GCV values (18.11, 18.03).

Table 2. Estimation of PCV, GCV, Heritability, Genetic Gain and GAM for growth, yield and its attributing traits of ten maize genotypes.

| Traits | σ^2_g | σ^2_p | Mean | GCV | PCV | Hbs | GA | GAM (%) |
|-------------------------------------|--------------|--------------|--------|-------|-------|------|-------|---------|
| Plant height (after flowering) (cm) | 85.23 | 204.83 | 179.84 | 5.13 | 7.96 | 0.42 | 12.27 | 6.82 |
| No. of leaves above cob | 0.16 | 0.32 | 5.42 | 7.27 | 10.39 | 0.49 | 0.57 | 10.48 |
| No. of leaves below cob | 0.13 | 0.31 | 7.48 | 4.73 | 7.47 | 0.4 | 0.46 | 6.18 |
| Leaf length at maturity (cm) | 15.39 | 30.71 | 78.89 | 4.97 | 7.02 | 0.5 | 5.72 | 7.25 |
| Leaf width at maturity (cm) | 0.11 | 0.29 | 8.16 | 4.07 | 6.05 | 0.39 | 0.43 | 5.21 |
| Days to 50% anthesis | 0.11 | 26.9 | 46.06 | 0.72 | 11.26 | 0 | 0.04 | 0.1 |
| Ear height (cm) | 21.25 | 77.98 | 89.16 | 5.17 | 9.9 | 0.27 | 4.96 | 5.56 |
| Tassel length (cm) | 3.15 | 7.24 | 42.24 | 4.20 | 6.37 | 0.44 | 2.41 | 5.71 |
| ASI | 0.37 | 0.59 | 3.06 | 19.78 | 25.05 | 0.62 | 0.99 | 32.19 |
| Cob length (cm) | 0.73 | 1.71 | 16.49 | 5.18 | 7.92 | 0.43 | 1.15 | 6.97 |
| Cob weight (g) | 181.57 | 411.07 | 131.61 | 10.24 | 15.4 | 0.44 | 18.45 | 14.02 |
| Cob diameter (cm) | 0.03 | 0.08 | 4.05 | 4.34 | 6.77 | 0.41 | 0.23 | 5.73 |
| No. of row per cobs | 1.73 | 2.36 | 12.88 | 10.21 | 11.92 | 0.73 | 2.32 | 18.03 |
| No. of grains per row | 1.75 | 12.23 | 31.91 | 4.15 | 10.96 | 0.14 | 1.03 | 3.24 |
| 1000 grain weight (g) | 1955.67 | 1974.67 | 245.33 | 18.03 | 18.11 | 0.99 | 90.66 | 36.95 |
| Grain yield (t ha ⁻¹) | 1.14 | 1.23 | 4.11 | 25.9 | 26.91 | 0.93 | 2.11 | 51.36 |

σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance and σ^2_e = Environmental variance, Hbs = Heritability broad sense, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance, GAM = Genetic advance as percent of mean.

Table 3. Pearson's correlation coefficient among growth, yield and its attributing traits of ten maize genotypes.

| | PH | NLAC | NLBC | LLM | LWM | EH | TL | ASI | CL | CW | CD | NRPC | NGPR | TGW | GY |
|------|---------|---------|---------|---------|---------|---------|--------|---------|--------|---------|--------|---------|---------|--------|---------|
| PH | 1 | | | | | | | | | | | | | | |
| NLAC | 0.429* | 1 | | | | | | | | | | | | | |
| NLBC | 0.467** | 0.08 | 1 | | | | | | | | | | | | |
| LLM | 0.654** | 0.360* | 0.326 | 1 | | | | | | | | | | | |
| LWM | 0.543** | 0.341 | 0.335 | 0.462** | 1 | | | | | | | | | | |
| DTA | 0.178 | 0.523** | 0.302 | 0.466** | 0.27 | 1 | | | | | | | | | |
| EH | 0.850** | 0.318 | 0.542** | 0.624** | 0.432* | 0.125 | 1 | | | | | | | | |
| TL | 0.401* | 0.491** | 0.154 | 0.384* | 0.128 | 0.285 | 0.258 | 1 | | | | | | | |
| ASI | 0.089 | -0.22 | 0.11 | 0.14 | 0.038 | -0.193 | 0.078 | 0.117 | 1 | | | | | | |
| CL | 0.446** | 0.375* | 0.327 | 0.391* | 0.469** | 0.214 | .417* | -0.011 | 0.014 | 1 | | | | | |
| CW | 0.382* | 0.125 | 0.237 | 0.178 | 0.015 | -0.071 | 0.296 | -0.042 | 0.12 | 0.619** | 1 | | | | |
| CD | 0.252 | 0.317 | 0.522** | 0.322 | 0.244 | 0.319 | 0.354* | 0.079 | 0.038 | 0.628** | 0.264 | 1 | | | |
| NRPC | -0.02 | 0.234 | 0.34 | 0.265 | 0.218 | 0.521** | 0.08 | -0.001 | -0.021 | 0.427* | 0.079 | 0.587** | 1 | | |
| NGPR | 0.143 | -0.019 | -0.12 | -0.107 | 0.15 | -0.181 | 0.119 | -0.363* | -0.269 | 0.469** | 0.434* | -0.108 | -0.208 | 1 | |
| TGW | 0.364* | 0.198 | 0.259 | 0.348* | 0.234 | 0.301 | 0.292 | 0.217 | -0.208 | -0.037 | -0.201 | 0.075 | 0.075 | -0.145 | 1 |
| GY | 0.336 | 0.477** | 0.398* | 0.528** | 0.447** | 0.26 | 0.329 | 0.239 | -0.108 | 0.671** | 0.121 | 0.573** | 0.539** | -0.151 | 0.706** |

PH = Plant height after flowering, NLAC = No. of leaves above cob, NLBC = No. of leaves below cob, LLM = Leaf length at maturity, LWM = Leaf width at maturity, DTA = Days to 50% anthesis, EH = Ear height, TL = Tassel length, ASI = Anthesis Silking Interval, CL = Cob length(cm), CW = Cob weight(g), CD = Cob diameter (cm), NRPC = No. of rows per cob, NGPR = No. of grains per row, TGW = 1000 grain weight (g and GY = Grain yield (t ha⁻¹).

** Correlation is significant at the 0.01 level.

* Correlation is significant at the 0.05 level.

Kandel et al. (2017) and Sharma et al. (2018) reported similar findings. Earlier researchers (Nzuve et al., 2014) provided the results of moderate PCV and GCV estimates for trait plant height before maturity, cob weight (Alake et al., 2008), and 1000 grain weight similarly seen in our experiment (Hefny, 2011). Plant height after flowering showed a greater difference between phenotypic and genotypic variance, indicating that these traits were heavily influenced by the environment. The plant height result was identical to those of Ojo et al. (2006) and Kashiani et al. (2010). The presence of a significant degree of genetic diversity is indicated by GCV, but the amount of heritable variation can only be assessed using heritability estimates and genetic gain (Rao and Rao, 2015).

3.2. Heritability and genetic advance

In our findings, we found low (less than 30%), moderate (30–60%), and high (more than 60%) estimates of heritability for the various traits studied, as defined by Johnson et al. (1955). Grain yield (93% heredity) and 1000 grain weight (93% heritability) were shown to have higher heritability estimations (99%). Similarly, heritability estimates for the number of grains per row (14%) and plant height (20%) had lower values. The rest of the qualities studied were moderately heritable. Table 2 shows the heritability estimates for all traits. Similarly, GAM for the traits under consideration in our study ranged from 0.1% for days to 50% anthesis to 51.36% for grain yield. According to Johnson et al. (1955), the observed GAM values were classified as low (less than 10%), moderate (10–20%), and high (greater than 20%). Table 2 shows the GAM estimates for all traits. Grain yield (0.93, 51.36), 1000 grain weight (0.99, 36.95) had greater estimates of heredity and GAM percent but leaves length (0.5, 7.25) and breadth (0.39, 5.25) at maturity, as well as cob length (0.5, 5.25), had higher estimates of heritability but low GAM (0.43, 6.97).

When additive gene effects controlled a characteristic, it usually resulted in both higher heritability and genetic advance, whereas when non-additive gene actions controlled a trait, it might result in high heritability but poor genetic advance (Mohana Krishna et al., 2009). High estimates of heritability for most of the variables suggested that variations were passed down to progeny, implying that a high-yielding variety may be developed by selecting desirable genotypes. High heritability provided more options for selecting plant material with the desired features. Our findings on the heritability of traits namely grain yield, number of rows per ear, and anthesis-silking interval (ASI) were consistent with those of Shengu (2017). Heritability estimations for the trait number of grains per row, on the other hand, contradicted the report. According to Najeeb et al. (2009), high heritability and high genetic progress are not always linked. As a result, high heritability does not imply a large genetic gain. A heritability estimate in conjunction with genetic advance is proposed to anticipate the effectiveness of picking superior genotypes. As demonstrated in Table 2, low estimates of heritability as well as GAM were found for the traits namely days to 50% anthesis, number of grains per row, and plant height before maturity. Because most of the variants are impacted by environments, the direct selection isn't suggested because these features are driven by non-additive gene activity. Tilahun et al. (2014) came to the conclusion that these types of traits require better management methods rather than selection to increase trait performance.

3.3. Phenotypic correlation coefficient

Estimates of the phenotypic correlation for traits are shown in Table 3. Grain yield showed positive and significant phenotypic correlation with test weight (r = 0.706), cob length (r = 0.671), cob diameter (r = 0.573) and number of rows per cob (r = 0.539), respectively. Test weight was the most yield attributing traits, followed by cob length, cob diameter, and a number of kernels per row; thus, simultaneous selection for these traits could boost grain production. Alvi et al. (2003), Prakash

et al. (2006), and Bartaula et al. (2019) all found similar results. The selection of those traits would suggest an indirect selection of genotypes for grain yield if there is a positive and high correlation between them. Malik et al. (2005) reported similar findings in line with Kumar et al. (2014), the trait-like ASI revealed a negative correlation with grain yield. If ASI is a long crop, it will have more vegetative growth and less time for reproductive growth, resulting in lower productivity.

4. Conclusion

All traits were significantly different, showing the availability of genetic variability among the maize genotypes that can be used in yield improvement. In all traits tested, PCV is larger than GCV, indicating that there was an environmental influence. Higher GCV, PCV, heritability, and high GAM for traits, thousand-grain weights, days to anthesis, and grain yield indicated efficient indirect selection for higher grain yield. The high correlation of grain yield was found with the traits test weight, cob length, cob diameter and a number of grain rows per cob for these traits might bring an improvement in grain yield.

Declarations

Author contribution statement

Bigul Thapa Magar; Subash Acharya; Bibek Gyawali; Kiran Timilsena: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Wrote the paper.

Jharana Upadhyay; Jiban Shrestha: Contributed reagents, materials, analysis tools or data; Wrote the paper.

Funding statement

This work was supported by research fund of Institute of Agriculture and Animal Science, Prithu Technical College, Tribhuvan University, Nepal.

Data availability statement

Data will be made available on request.

Declaration of interests statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

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