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RESEARCH ARTICLE

CHARACTERIZATION OF QUALITATIVE AND QUANTITATIVE TRAITS FOR DIVERSITY ASSESSMENT AND CORRELATION STUDIES IN FOXTAIL MILLET (*SETARIA ITALICA* (L.) BEAUV.)

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ABSTRACT

A higher level of variability can be found in Nepalese foxtail millet. To assess potential traits for further breeding activities and estimate the genetic diversity, phenotypic and genotypic coefficient of variation, heritability, genetic advance, and correlation coefficient for 15 different genotypes of foxtail millet, an experiment was conducted in alpha lattice design with 3 replications at Agronomy farm of IAAS, Lamjung, Nepal during March- June 2021. The analysis of variance revealed highly significant differences among the accessions for all the traits observed indicating the presence of a sufficient amount of variability. The value of the Shannon index ranged from 0.245 (plant anthocyanin coloration of the basal sheath) to 1.309(grain color) which indicates that the characters were more diverse for grain color while the value of evenness ranged from 0.22 (plant: anthocyanin coloration of the basal sheath) to 0.965(panicle density) indicating that the characters are more evenly distributed for the intensity of green leaf foliage. High PCV, high GCV, high heritability, and high genetic advance per mean were found for flag leaf length, peduncle length, no. of nodes, and yield per hectare. It indicates that these traits are less influenced by the environment and hence can be exploited by pure line and mass selection methods for crop improvement. Yield per hectare was positively and significantly correlated with grain per panicle (r=0.4**) and no. of nodes (r=0.39**). A strong positive correlation was observed between plant height and the number of nodes, flag leaf width, panicle length, and flag leaf length indicating their consideration for further breeding activities. The findings of the study can be crucial in identifying better-performing genotypes that can help develop improved varieties

KEYWORDS

Correlation, Diversity, Foxtail millet, Genetic Advance, Heritability

1. INTRODUCTION

Foxtail millet *belonging* to the subfamily Panicoidea and tribe Paniceae includes grain, wild, and weed species along with their different breeding systems, life cycles, and ploidy levels (Lata et al., 2013). It is one of the oldest cultivated crops in the world and was domesticated around 11000 years ago from the wild species green foxtail (*Setaria viridis)* in northern China (Doust et al., 2009; Yang et al., 2012). Nowadays it is cultivated in 26 countries extensively in India, Nepal, Sri Lanka, Pakistan, Russia, Ukraine, the Middle East, Turkey, and Romania (Ravi, 2004). According to it ranks second in the most widely cultivated species among millets and the most important millet in East Asia (Kumari et al., 2011). In Nepal, it is cultivated in hills and mid-hills districts, especially in the Karnali zone. It is also widely distributed in Mugu, Kalikot, Humla, Jumla, Bajhang, Bajura, Dolpa, Lamjung, Gorkha, Ramechhap, Kavre, etc. where it is grown sole as well as intercropped with finger millet (*Eleusine coracana* Gaertn.), proso millet (*Panicum miliaceum* L.), beans (*Phaseolus vulgaris*), amaranths (*Amaranthus hypochondriacus*), maize (*Zea mays* L.), etc. (Ghimire et al., 2017).

Nutritionally, foxtail millet has a higher nutrient content compared to the major cereals such as wheat and rice (Parameswaran and Sadasivam, 1994). Singh and Raghuvanshi have reported that it has a high content of amino acids, phytochemicals, micronutrients, and antioxidants as compared to non-millet cereals and hence is called 'Nutri cereals (Singh and Raghuvanshi, 2012). Similarly, because of its small diploid genomes (2n=18), short life cycles, self-pollination, small adult height, and prolific seed production, domesticated foxtail millet has been used as the novel model species for the functional genomics of the grass crop, particularly for the study of the C_4 photosynthesis (Muthamilarasan and Prasad, 2015). Moreover, foxtail millet is considered a neglected and underutilized crop (NUS) in Nepal that has tremendous potential to contribute to food security, nutrition, dietary and culinary diversification, health, and income generation along with its better adaptability to marginal and harsh climatic conditions. It is a traditional staple food used as rice, porridge, alcoholic beverage, and even as an offering to the local deities in drier parts of the high mountain landscape (Joshi et al., 2020).

Despite its tremendous value, it is still underutilized. In Nepal, research on NUS had been started in 1991 but systematic conservation of these crops was started in 2010 but the efforts are not still sufficient. Some research has been conducted on NUS but for a short period (5 years) it could not significantly contribute to the development and utilization of these crops (Joshi et al., 2020). Further, a higher level of variability can be found in Nepalese foxtail millet. Therefore, Nepal can be one of the centers of diversity for foxtail millet (Nakayama et al., 1999). So, it is imperatively

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important to evaluate the local genotypes of foxtail millet to incorporate them in the plant breeding and crop improvement programs. Knowledge of variability, genetic diversity, heritability, genetic advance, and genetic advance per mean is a prerequisite for successful plant breeding programs. Similarly, correlation studies help to know the association between yield and yield attributing traits for the indirect selection of traits contributing to yield (Adhikari et al., 2018).

Therefore, the objective of the study was to assess the different diversity indices, phenotypic and genotypic coefficient of variation, heritability, and genetic advance per mean and correlation between different quantitative characters. The findings of the study would be crucial in identifying promising parental lines that would aid in future plant breeding and crop improvement programs in foxtail millet. This study can be a bridge for the existing research gap in foxtail millet and a comprehensive reference for the development of improved foxtail millet varieties.

2. MATERIALS AND METHODS

2.1 Experimental Site and Planting Materials

The study was conducted to access diversity indices (Shannon Weiner Index and Evenness), phenotypic and genotypic coefficient of variation, heritability, genetic advance per mean, and correlation between different quantitative traits. The experimental material comprised fifteen genotypes of foxtail millet (Table 1) collected from Ghanpokhara community seed bank, Ghanpokhara, Lamjung, and National Genetic Resource Centre, Khumaltar, Lalitpur, Nepal. The experiment was conducted from 23rd March to 29th July 2021 at the Agronomy farm of the Institute of Agriculture and Animal Science (IAAS), Lamjung Campus, Lamjung, Nepal, geographically located at the 632 masl with the sub-tropical type of climate.

Table 1: List of genotypes along with the place of collection

S.N.	Name of accessions	Places of collection
1.	NGRCO 7417	National Genetic Resource Centre, Khumaltar,
2	NGRCO 7419	National Genetic Resource Centre, Khumaltar,
3	NGRCO 7420	National Genetic Resource Centre, Khumaltar,
4	NGRCO 7416	National Genetic Resource Centre, Khumaltar,
5	NGRCO 8391	National Genetic Resource Centre, Khumaltar,
6	Pahelo Kaguno Jumla	Ghanpokhara Community Seed Bank, Lamjung
7	Pahelo Kaguno Humla	Ghanpokhara Community Seed Bank, Lamjung
8	NGRCO 7421	National Genetic Resource Centre, Khumaltar,
9	NGRCO 6108	National Genetic Resource Centre, Khumaltar,
10	NGRCO 7949	National Genetic Resource Centre, Khumaltar,
11	NGRCO 6659	National Genetic Resource Centre, Khumaltar,
12	Seto Kaguno Jumla	Ghanpokhara Community Seed Bank, Lamjung
13	Kalo Kaguno Jumla	Ghanpokhara Community Seed Bank, Lamjung
14	Bariyo Kaguno Lamjung	Ghanpokhara Community Seed Bank, Lamjung
15	Seto Kaguno Kaski	Ghanpokhara Community Seed Bank, Lamjung

2.2 Experimental design and field layout

The field trial was conducted under rainfed conditions in an alpha lattice design with 15 foxtail millet genotypes as treatments and three replications with a spacing of 1m between replications. Each replication had three blocks with a block spacing of 50cm. Each block had five plots and each plot was 25cm apart. Each plot measured 1m^2 and was cultivated with five rows of the crop at a distance of 25 cm between the rows.

2.3 Cultural practices

Direct and continuous row sowing of seed with the row-row spacing of 25 cm was done on 23rd March 2021. A complete dose of fertilizer was applied at the rate of 60: 30: 20 NPK at the time of field preparation (Ojha et al., 2018). All the standard agronomic packages of practices were followed for the healthy and proper growth of the crop.

2.4 Data collection

15 different qualitative traits were recorded as per the descriptor established by UPOV(2013) and IBPGR (1985) for the assessment of diversity. The detailed description and evaluation stage of the traits are depicted in Table 2. Similarly, ten different quantitative traits were assessed for the estimate of heritability, genetic advance per mean, and correlation between traits according to the descriptor established by UPOV (2013) and IBPGR (1985) was used. The detailed description and evaluation stage of the traits are presented in Table 3.

Table 2: Qualitative data recording guidelines

S.N.	Qualitative characters	Descriptor	Evaluation phase
1.	Plant: anthocyanin coloration of the basal sheath	(1) absent (2) medium (3) strong	15 DAS
2.	Intensity of green leaf foliage	(1) light (3) medium (5) dark	35 DAS
3.	Plant growth habit	(1) erect (2) semi-erect (3) spreading	35 DAS
4.	Leaf altitude of blade	(1) erect (2) semi-erect (3) slightly drooping (4) strongly drooping	47DAS
5.	Anther color	(1) white (2) orange (3) brown	65 DAS
6.	Panicle length of bristle	(1) short (3) medium (5) long	65 DAS
7.	Flag leaf anthocyanin coloration of blade	(1) absent (3) medium (5) very strong	71 DAS
8.	Glume anthocyanin color	(1) absent (9) present	83 DAS
9.	Sheath pubescence	(1) essentially glabrous (5) medium pubescent (9) strongly pubescent	83 DAS
10.	Panicle altitude in relation to stem	(1) erect (2) semi-erect (3) horizontal (4) drooping	92 DAS

Table 2: Qualitative data recording guidelines

11.	Panicle type	(1) conical (2) spindle (3) cylindrical (4) club (5) duck mouth (6) cat foot (7) branched	92 DAS
12.	Panicle density	(1) lax (3) medium (5) dense	92 DAS
13.	Lobe compactness	(3) loose (5) medium (7) compact (9) spongy	92 DAS
14.	Grain color	(1) whitish (2) grey (3) yellow (4) brown (5) red (6) black	92 DAS
15.	Dehusked grain color (non-polished)	(1) whitish (2) grey (3) yellow	92 DAS

Table 3: Quantitative data recording guidelines

S.N.	Quantitative characters	Evaluation phase	Procedure
1.	Flag leaf length	71 DAS	Measured from ligule to tip of flag leaf
2.	Flag leaf width	71 DAS	Measured at the widest point of the flag leaf
3.	Peduncle length	71 DAS	Measured from the topmost node to the base of inflorescence
4.	Plant height	71 DAS	Measured from ground level to tip of inflorescence
5.	Stem length	71 DAS	Measured from the ground level to the base of
6.	No. of nodes	71 DAS	Counted from the ground level to the top excluding the peduncle
7.	Panicle length	92 DAS	Measured from the lowest branch to the tip of the last branch of the panicle
8.	Thousand seed weight	92 DAS	1000 seeds from each plot were randomly taken from randomly selected sample panicles and weight was determined using an electronic balance.
9.	Grain per panicle	92 DAS	The grain from randomly selected panicles was counted and recorded.
10.	Yield per hectare	92 DAS	Recorded as kg/ha

2.5 Statistical Analysis

The R studio software package and Microsoft Excel 2016 were used for statistical analysis.

2.5.1 *Shannon -Diversity Index*

The Shannon index was calculated according to the formula given by (Spellerberg and Fedor, 2003)

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

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

pi= $\frac{population\ bearing\ given\ character\ of\ a\ trait}{total\ population}$

2.5.2 *Evenness*

It is calculated according to the procedure given by (Magurran, 2004):

Evenness (E)= $\frac{H\prime}{\ln(S)}$

Where S= total number of variation case

2.5.3 *Genotypic and Phenotypic Coefficient of Variation*

The genotypic and phenotypic variance of various traits was calculated according to the procedure introduced by (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)= $\frac{\sigma g}{x} * 100$

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

Where,

σg= genotypic standard deviation

σp= phenotypic standard deviation

x= General mean of the trait

The GCV and PCV values were categorized as low for 0-10%, moderate for 10-20%, and high for = >20% (Sivassubramanian and Madhavamenon, 1973)

2.5.4 *Broad sense heritability (h^2bs)*

According to the formula given by (Burton and DeVane, 1953)

$h^2bs = \frac{Vg}{VP} * 100 = \frac{\sigma 2g}{\sigma 2p} * 100$

where

Vg= genotypic variance

Vp= phenotypic variance

Heritability was categorized as low for a percentage value of 0-30%, medium for 30-60%, and high for above 60% (Johnson et al., 1955)

2.5.5 *Genetic advances (GA) and genetic advance per mean*

According to the formula given by (Johnson et al., 1955)

GA= K. σ_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^2bs = broad sense heritability

The genetic advance as per mean (GAM) was calculated as

GAM = $\frac{GA}{Grand\ mean} * 100$

The range of genetic advance per mean was classified as suggested by (Johnson et al., 1955).

Low: Less than 10%

Moderate: 10-20%

High: More than 20%

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2.5.6 Pearson's correlation coefficient:

It was calculated in the R studio software package. The effects were classified based on the scale given by (Lenka and Misra, 1973):

Value	Scale
More than 1.00	very high
0.30-0.99	High
0.20-0.29	Moderate
0.10-0.19	low
0.00-0.09	negligible

3. RESULT AND DISCUSSION

3.1 Qualitative characters

Qualitative characters illustrate stable and discrete inheritance and are used as plant descriptors to identify genotypes, which are less environment-dependent (Nirubana et al., 2019). The frequency distribution for 15 qualitative traits is calculated and presented in Table 4. Concerning plant: anthocyanin coloration of the basal sheath, 93.33% of the genotypes lack anthocyanin, for flag leaf anthocyanin coloration of the blade, 86.67% lack anthocyanin, and glume anthocyanin color, 66.67% lack anthocyanin pigmentation. The genotypes with anthocyanin pigmentation were more resistant to blast disease, thereby contributing to increasing yield (Rao, 1948). 40% of the genotypes have light green leaf foliage whereas 60 % have a moderately green leaf. Plant growth habit with a semi-erect type (53.33%) was more frequent compared to erect (40%) and spreading (6.67%) types.

The maximum number of genotypes (53.33%) exhibited semi-erect followed by erect (33.33%) and slightly drooping type (13.33%) for leaf altitude of the blade. The anther color showed less variability: 80% were brown followed by 20% orange anther. The panicle length of bristle was found to be short for 46.67% of the genotypes, 33.33% of them were long and 20% of them were medium in length. The bristles with silica play an important role in insect pest resistance and therefore help to increase yield (Liang, 2006). Among the genotypes, essentially glabrous and moderately pubescent leaves each exhibited 46.67% of the total while 6.67 % of leaves were strongly pubescent. The finding of the study for sheath pubescence was similar to the finding by (Banu et al., 2018). The genotypes with drooping panicle altitude were higher in frequency (60%) compared to 20% semi-erect and horizontal type each. The frequency of the conical type of panicle (73.33%) was predominant followed by the cylindrical type (13.33%) and spindle and cat foot each (6.67%).

Considering panicle density, the majority of the genotypes were dense (46.67%), while 26.67% were lax and medium each. The length of branches, grain density, number, and spikelet sterility were high and the average grain weight of the basal spikelet of the panicle of the main shoot was low in compact panicle compared to lax type in rice (Panda et al., 2015). For lobe compactness, 46.67% of the genotypes were compact followed by medium (26.67%), loose (20%), and spongy (6.67%) types. The finding is sympathetic to the finding reported by (Banu et al., 2018). The majority of the genotypes had grain yellowish in color (40%), while 26.67% of them were brown followed by white (20%) and black (2%). A similar result was reported by Vetriventhan for grain color (Vetriventhan, 2011). Regarding dehusked grain color, the frequency of white was 66.67%, yellow (26.67% and grey (6.67%).

Table 4: Frequency distribution of 15 qualitative traits of 15 foxtail millet genotypes

S.N.	Qualitative characters	Descriptor	Frequency	Frequency (%)
1.	Plant: anthocyanin coloration of the basal sheath	(1) absent	14	93.33
		(2) medium	0	0.00
		(3) strong	1	6.67
2.	Intensity of green leaf foliage	(1) light	6	40
		(3) medium	9	60
		(5) dark	0	0.00
3.	Plant growth habit	(1) erect	6	40
		(2) semi-erect	8	53.33
		(3) spreading	1	6.67
4.	Leaf altitude of blade	(1) erect	5	33.33
		(2) semi-erect	8	53.33
		(3) slightly drooping	2	13.33
		(4) strongly drooping	0	0.00
5.	Anther color	(1) white	0	0.00
		(2) orange	3	20
		(3) brown	12	80
6.	Panicle length of bristle	(1) short	7	46.67
		(3) medium	3	20
		(5) long	5	33.33
7.	Flag leaf anthocyanin coloration of blade	(1) absent	13	86.67
		(3) medium	1	6.67
		(5) very strong	1	6.67
8.	Glume anthocyanin color	(1) absent	10	66.67
		(9) present	5	33.33
9.	Sheath pubescence	(1) essentially glabrous	7	46.67
		(5) medium pubescent	7	46.67
		(9) strongly pubescent	1	6.67
10.	Panicle altitude in relation to stem	(1) erect	0	0.00
		(2) semi-erect	3	20
		(3) horizontal	3	20
		(4) drooping	9	60

Table 4: Frequency distribution of 15 qualitative traits of 15 foxtail millet genotypes

11.	Panicle type	(1) conical	11	73.33
		(2) spindle	1	6.67
		(3) cylindrical	2	13.33
		(4) club	0	0.00
		(5) duck mouth	0	0.00
		(6) cat foot	1	6.67
		(7) branched	0	0.00
12.	Panicle density	(1) lax	4	26.67
		(3) medium	4	26.67
		(5) dense	7	46.67
13.	Lobe compactness	(3) loose	3	20
		(5) medium	4	26.67
		(7) compact	7	46.67
		(9) spongy	1	6.67
14.	Grain color	(1) whitish	3	20
		(2) grey	0	0.00
		(3) yellow	6	40
		(4) brown	4	26.67
		(5) red	0	0.00
		(6) black	2	13.33
15.	Dehusked grain color (non-polished)	(1) whitish	10	66.67
		(2) grey	1	6.67
		(3) yellow	4	26.67

3.2 Diversity indices

Diversity indices of qualitative traits studied in foxtail millet genotypes are presented in Table 5. The Shannon- Weiner index was used to study both the abundance and evenness of characters of the trait. The higher the value of the index, the higher the diversity in the given trait and species in a particular community. The lower the value of the index, the lower the diversity in the trait and species in the given community. A value of H =0 indicates a community that has only one species. Shannon Weiner index was found to be maximum for grain color (H' = 1.309), followed by lobe compactness (H'= 1.21), and panicle density (H'= 1.06). This means that the genotypes had shown the most diversity in these traits. Similarly, the Shannon- Weiner index was found to be minimum for plant: anthocyanin coloration of the basal sheath (H'=0.245), followed by flag leaf anthocyanin color of the blade (H'=0.49), and anther color (H'=0.5). It indicates that the genotypes were the least diverse for seedling anthocyanin. The evenness of genotypes indicated that the intensity of panicle density (E= 0.97) was more even followed by glume anthocyanin coloration (E= 0.91), and leaf attitude of the blade (E=0.88). Similarly, the minimum value of evenness was observed in plant anthocyanin coloration of the basal sheath (E =0.22) where only one accession showed anthocyanin coloration but the remaining 14 accessions showed no anthocyanin coloration. It was followed by flag leaf anthocyanin coloration of the blade (E= 0.44) and panicle type (E= 0.44).

Table 5: Diversity indices of qualitative traits

S.N.	Characters	Shannon Index	Evenness
1	Plant: anthocyanin coloration of the basal sheath	0.24493	0.22
2	Intensity of green leaf foliage	0.673012	0.61
3	Plant growth habit	0.882311	0.8
4	Leaf attitude of blade	0.970116	0.88
5	Panicle length of bristle	1.043757	0.69
6	Anther color	0.500402	0.46
7	Flag leaf anthocyanin color of the blade	0.485094	0.44
8	Glume anthocyanin coloration	0.636514	0.91
9	Sheath pubescence	0.891867	0.81
10	Panicle attitude in relation to stem	0.950271	0.69
11	Panicle type	0.857174	0.44
12	Panicle density	1.060602	0.965
13	Lobe compactness	1.210558	0.87
14	Grain color	1.309526	0.73
15	Dehusked grain color	0.803315	0.73

3.3 Analysis of variance (ANOVA)

Analysis of variance for different characters studied is presented in Table 6. The results revealed highly significant differences among the accessions for all the traits observed indicating the presence of a sufficient amount of variability. The considerable genetic variation for different traits among the accessions can be valuable in the selection and screening for future breeding programs.

Table 6: Analysis of variance for 10 traits in foxtail millet

Treatment	Flag leaf length	Flag leaf width	Peduncle length	Plant height	Stem length	No. of nodes	Panicle length	1000 grain weight	Grains per panicle	Yield per hectare(kg/ha)
NGRCO 7417	18.08de	2.04abc	11.64ef	145.93cd	132.5bcd	9.94ab	13.39bcd	1.53def	1484.33a	384.8def
NGRCO 7419	22.99b	1.99abcd	13.67de	129.07de	117.4def	8.83bcde	11.71cd	1.51ef	1028.67abcd	741ab
NGRCO 7420	20.27bcd	2.09abc	16.14cd	155.25bc	142.48abc	9.97ab	11.88cd	1.71cde	1284ab	887.6a
NGRCO 7416	18.88cd	1.82bcde	11.23ef	126.13def	113.9defg	8.03efg	12.18cd	1.89bcde	1366ab	555.5bcde
NGRCO8391	29.49 a	2.13 ab	21.19 ab	179.89a	160.97a	10.23a	18.91a	1.98bc	1294ab	635.33bc
PAHELO KAGUNO JUMLA	20.54bcd	1.79bcde	17.82bc	116.01efgh	104.36efgh	6.2h	11.65cd	1.79bcde	415.33de	91.83h
PAHELO KAGUNO HUMLA	23.07b	1.77cde	23.21 a	104.04fgh	92.2gh	4.4i	11.84cd	2.01bc	471.67de	231.4fgh
NGRCO 7421	29.37 a	1.75cde	9.05 f	169.52ab	152.7ab	9.54abcd	17.364a	1.48ef	93.67e	455cde
NGRCO 6108	10.51f	2.32 a	13.83de	136.5cde	121.3cde	9.16abcde	7.87e	1.73bcde	473de	136.67gh
NGRCO 7949	28.15 a	2.13 ab	13.67de	144.2cd	128.2cde	9.8abc	16.04ab	1.73bcde	786bcd	208.27gh
NGRCO 6659	18.09 de	1.65 de	5.27 g	95.6h	84.88h	7.52fg	10.57de	1.94bcd	891abcd	538.87cde
SETO KAGUNO JUMLA	18.79cd	1.99abcd	20.55ab	129.09de	117.3def	8.53cdef	12.11cd	2.15b	978.33abcd	343.73efg
KALO KAGUNO KASKI	21.71bc	1.82bcde	24.48 a	100.58gh	87.76h	4.53i	10.75de	2.63a	433.67de	213.8gh
BARIYO KAGUNO	14.96 e	1.49e	11.64ef	122.57defg	108.8defgh	8.47def	14.23bc	1.27f	637.67cde	610.63bcd
SETO KAGUNO KASKI	19.94bcd	1.99abcd	12.41 def	105.03fgh	94.1fgh	6.93gh	10.93d	2.15b	1135.67abc	499.1cde
LSD (0.05)	3.18	0.29	3.75	21.22	21.82	1.18	2.75	0.37	568.63	203.87
F test	***	**	***	***	**	***	***	***	***	***
CV, %	8.96	9.18	14.71	9.59	10.99	8.62	12.74	11.93	39.43	27.64
Grand mean	20.99	1.92	15.05	130.63	117.26	8.14	12.76	1.84	851.53	435.6

*Significant at 5 percent level, **significant at 1 percent level ***significant at 0.1 percent level

3.4 Variance, coefficient of variance, heritability, and genetic advance per mean

The estimate of the coefficient of variance, heritability, and genetic advance per mean is represented in Figure 1 and Figure 2. Flag leaf length was found to have high GCV (23.76%), high PCV (26.31%), and high heritability (81.54%) with high genetic advance per mean (44.20%). Similar results were obtained by for GCV, PCV, heritability, and genetic advance per mean (Pallavi et al., 2020; Anuradha and Patro, 2020). The PCV and GCV of flag leaf width were estimated to be moderate (13.5%) and 9.79% with moderate heritability of 52.54% and moderate genetic advance per mean of 14.62%. These results were accompanied by the findings of for moderate PCV and for moderate genetic advance per mean (Mohan et al., 2019; Kavya et al., 2017). Similar findings were reported by for moderate PCV, low GCV, moderate heritability, and moderate genetic advance per mean (Anuradha and Patro, 2020).

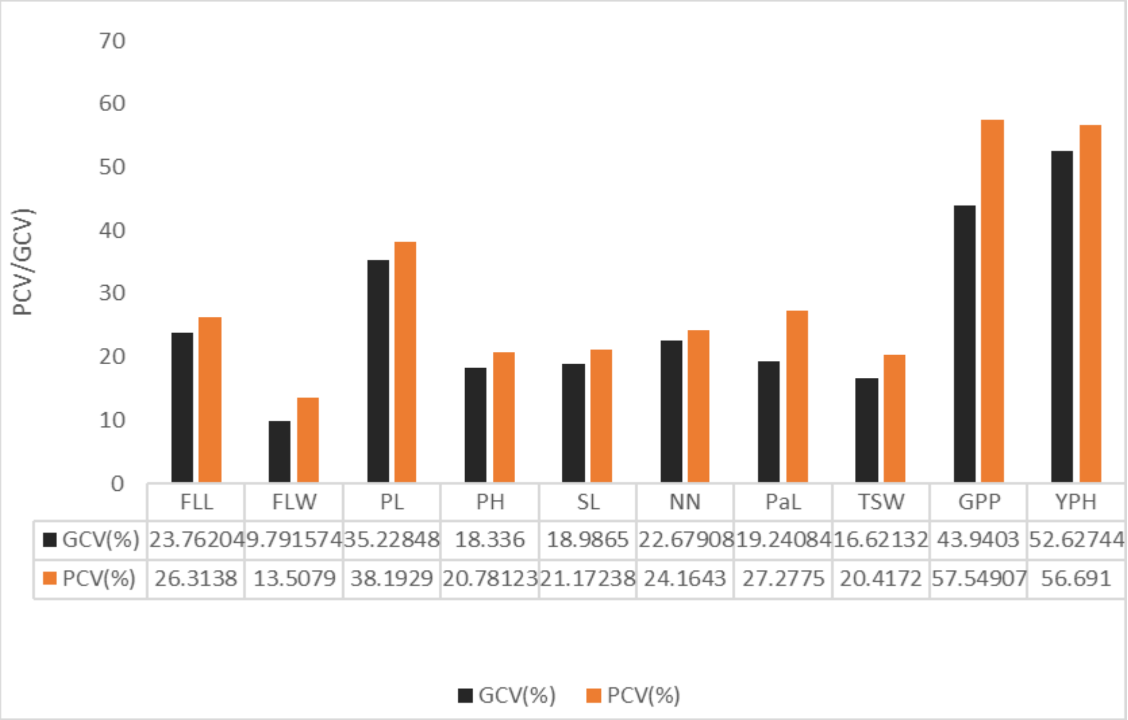
The peduncle length was found to have high GCV (35.22%), high PCV (38.19%), and high heritability of 85.07% with a high value of genetic advance per mean (64.98%). These findings were similar to for high PCV and GCV and for high heritability and genetic advance per mean (Pallavi et al., 2020; Bhakuni et al., 2021). Plant height was estimated to have moderate GCV (18.33%), high PCV (20.78%), and high heritability of 77.85% with high genetic advance per mean of 33.32%. These results are in accordance with the results reported by for high heritability and high genetic advance for plant height (Bhakuni et al., 2021). Similarly, Anuradha and Patro found the same result for the high heritability of plant height in foxtail millet (Anuradha and Patro, 2020). The PCV and GCV for stem length were estimated to be 21.17 % and 18.98% and heritability of 80.41% with high genetic advance per mean of 35.07%.

The number of nodes was found to have high PCV (24.16%) high GCV (22.67%) and high heritability of 88.08% with high genetic advance per mean of 43.84. Panicle length was found to have moderate GCV (19.24%), high PCV (27.27%), and moderate heritability of 49.75% with high genetic advance per mean (27.95%). Similar results were reported for high GCV, PCV, moderate heritability, and high genetic advance per mean (Pallavi et al., 2020). TSW was found to have moderate GCV (16.62 %), high PCV (20.41%), and high heritability (66.27%) with high genetic advance per mean of 27.87%. Similar results were reported by for high PCV, high heritability, and high genetic advance per mean (Karvar et al., 2020; Pallavi et al., 2020). Grain per panicle was found to have high GCV (43.94%), high PCV (57.54%), and moderate heritability of 58.29% with high genetic advance per mean of 69.11%. Yield per hectare was found to have high GCV (52.63%), high PCV (56.69%), and high heritability of 86.17% with high genetic advance per mean of 99.35%. Similar results were reported for high PCV, high GCV, high heritability, and high genetic advance per mean (Ashok et al., 2016; Mohan et al., 2019; Bhakuni et al., 2021).

Most of the traits under study exhibited slightly higher PCV than GCV which indicates that the variation is not only due to genetic factors but also due to the influence of environmental factors. The lower the difference between PCV and GCV indicates the lower effect of the environment and greater influence of the genetic factors for the expression of the characters thus providing a higher scope for crop improvement. So, the selection can be done based on the phenotype independent of genotype for crop improvement (Dhakal et al., 2020) Higher difference between the PCV and GCV indicates that the expression of traits is more susceptible to environmental factors. Moderate PCV and GCV values indicate the existence of moderate variability that can be exploited for crop improvement through selection in advanced generations (Amarnath et al., 2018; Brunda et al., 2014).

The genetic coefficient of variation alone would not indicate the proportion of total heritable variation. Heritability together with genetic advance is essential for the study of total heritable variation. The broad sense of heritability includes the contribution of additive gene effects, allelic interactions due to dominance, and non-allelic interactions due to epistasis. Genetic advance provides knowledge about expected genetic gain for a particular trait after selection. High heritability and high genetic advance per mean were found for flag leaf length, peduncle length, plant height, stem length, number of nodes, thousand seed weight, and yield per hectare. It indicates that these traits are controlled by additive gene action and have less influence of the environment. Hence, the traits with high heritability and high genetic advance per mean can be exploited by pure line selection and mass selection methods for crop improvement (Brunda et al., 2014; Mohan et al., 2019).

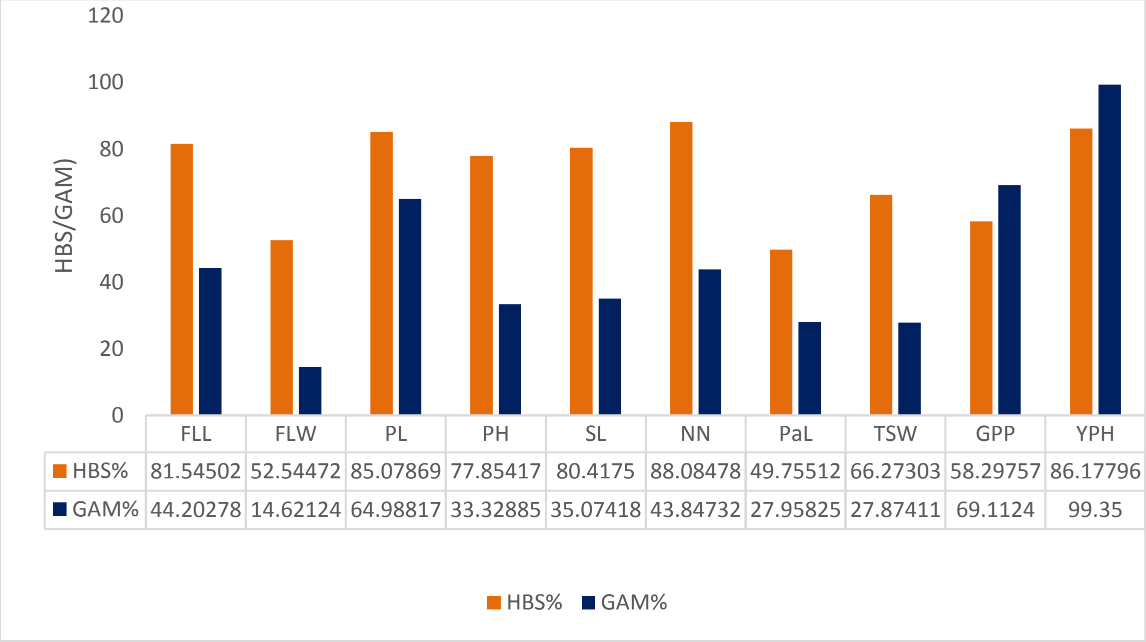
Similarly, moderate heritability with moderate genetic gain per mean was found for flag leaf width. This can be exploited by mass selection, progeny selection, hybridization, and simple selection. Moderate heritability with high genetic advance per mean was found for panicle length and grain per panicle which indicates the presence of both additive and nonadditive gene action. Hence the simple selection is not rewardable in this case (Ashok et al., 2016). Heterosis breeding has to be followed for breeding programs. Hence, the traits having high heritability coupled with high genetic advance per mean like flag leaf length, peduncle length, plant height, stem length, number of nodes, thousand seed weight, yield per hectare. Thus, these can be exploited in breeding programmes based on simple selection.



	FLL	FLW	PL	PH	SL	NN	PaL	TSW	GPP	YPH
■ GCV(%)	23.76204	9.791574	35.22848	18.336	18.9865	22.67908	19.24084	16.62132	43.9403	52.62744
■ PCV(%)	26.3138	13.5079	38.1929	20.78123	21.17238	24.1643	27.2775	20.4172	57.54907	56.691

Figure 1: PCV and GCV values for quantitative characters

(GCV=genotypic coefficient of variation, PCV= phenotypic coefficient of variation, FLL= flag leaf length, FLW= flag leaf width, PL=peduncle length, PH= plant height, SL= stem length, NN= number of nodes, PaL = panicle length, TSW= thousand seed weight, GPP= grain per panicle, YPH=yield per hectare)



	FLL	FLW	PL	PH	SL	NN	PaL	TSW	GPP	YPH
■ HBS%	81.54502	52.54472	85.07869	77.85417	80.4175	88.08478	49.75512	66.27303	58.29757	86.17796
■ GAM%	44.20278	14.62124	64.98817	33.32885	35.07418	43.84732	27.95825	27.87411	69.1124	99.35

Figure 2: Heritability and Genetic advance per mean for quantitative characters

(HBS=broad sense heritability, GAM=genetic advance as a percent of mean, FLL= flag leaf length, FLW= flag leaf width, PL=peduncle length, PH= plant height, SL= stem length, NN= number of nodes, PaL= panicle length, TSW= thousand seed weight, GPP= grain per panicle, YPH=yield per hectare)

3.5 Pearson's Correlation Analysis

The correlation coefficient is used to measure the statistical relationship between two variables that assist in the indirect selection of traits for crop improvement programs (Adhikari et al., 2018). Yield per hectare was found to have a highly significant and positive correlation with grain per panicle (r = 0.4**) and no. of nodes (r = 0.39**). A similar result was found by for no. of nodes (Kandel et al., 2020). Nodes act as the central hub for the allocation of mineral nutrients regulated by node-based transporters contributing to an increase in yield (Yamaji and Ma, 2017). Therefore, these traits can be considered to increase yield per hectare. Thousand seed weight was found to have a highly significant and positive correlation with peduncle length (r = 0.48***). Similarly, it was found to have a negative but highly significant correlation with no. of nodes (r = -0.51***), and plant height (r = -0.35*). It suggests that the increase in height leads to the higher accumulation of photosynthates in vegetative parts rather than reproduction and augments susceptibility to lodging (Roy et al., 2015).

This result was in accord with the finding of for plant height and for peduncle length (Amgai et al., 2011; Pallavi et al., 2020). In general negative correlation indicates the retrogressive association between the traits and simultaneous selection can be considered for a variety of improvement activities (Osundare et al., 2017). Panicle length was found to have a highly significant and positive correlation with flag leaf length (r = 0.74***), plant height (r = 0.69***), and no. of nodes (r = 0.41**). Similar results were found by for flag leaf length and plant height (Sapkota et al., 2016). Number of nodes was found to have highly significant and positive relationship with plant height (r = 0.76***), significant and positive correlation with flag leaf width (r = 0.39**), panicle length (r = 0.41**), yield per hectare (r = 0.39**), grain per panicle (r = 0.41**). Similarly, it was found to have a negative and highly significant correlation with thousand seed weight (r = -0.51***) and peduncle length (r = -0.37*). The result was sympathetic to the finding reported by for plant height, panicle length, yield per hectare, and thousand seed weight (Kandel et al., 2020).

Peduncle length was found to have a positive and highly significant correlation with thousand seed weight (r = 0.48***) and a negative and significant correlation with no. of nodes (r = -0.37*). A similar result was reported by for thousand seed weight (Pallavi et al., 2020). Plant height was found to have a highly significant and positive relation with no. of nodes (r= 0.76***), flag leaf width (r =0.54***), panicle length (r = 0.69***), and flag leaf length (r = 0.49***). Similarly, plant height was found to have a negative and a highly significant correlation with thousand seed weight (r= -0.35*). The finding was supported by for thousand seed weight and by for panicle length (Amgai et al., 2011; Anuradha and Patro (2020). The result was in accord with the finding obtained by for panicle length, flag leaf length, and flag leaf width (Pallavi et al., 2020). Flag leaf length was found to have a highly significant and positive relationship with panicle length (r =0.74***), plant height, and stem length (r =0.49***). Similar result was reported by (Pallavi et al., 2020). Flag leaf width was found to have a highly significant and positive correlation with stem length and plant height (r = 0.54***) and no. of nodes (r = 0.39**). Similarly, FLW was found to have a positive and significant relationship with grain per panicle (r = 0.32*). A similar result was reported by for plant height (Sapkota et al., 2016).

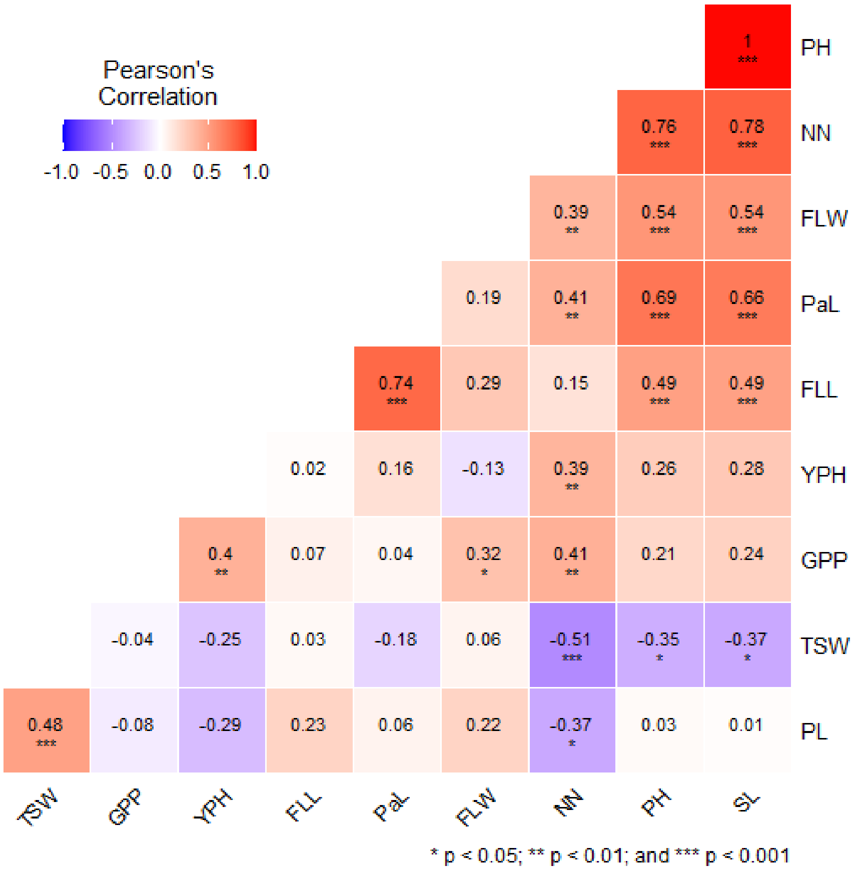


Figure 3: Pearson's correlation matrix

Flag leaf length (FLL), Flag leaf width (FLW), Peduncle length (PL), Plant height (PH), Stem length (SL), Panicle length (PaL), No of nodes (NN), Grain per panicle (GPP), Thousand Seed weight (TSW) and Yield per hectare (YPH).

4. CONCLUSION

Nepal is one of the centers of diversity for foxtail millet with high genetic diversity of this crop. However, Nepalese farmers do not have sufficient improved variety officially released due to the lack of substantial research on this crop. So, this research emphasizing the assessment of diversity indices, evaluation of inheritance of yield and its related traits, expected genetic advance, and association between different traits provides a huge opportunity for the development of new cultivars through selection. The results from the study revealed highly significant differences among the accessions for all the traits observed indicating the presence of a sufficient amount of variability.

The highest Shannon Weiner Index value for grain color indicated the presence of maximum diversity for these traits. Similarly, high GCV, high PCV, high heritability, and high genetic advance per mean were found for flag leaf length, peduncle length, number of nodes, and yield per hectare revealing that these traits can be exploited with pureline selection and mass selection methods for crop improvement. Yield per hectare was positively correlated with no. of nodes and grain per panicle which indicates the importance of these traits for crop improvement programmes. Therefore, the considerable genetic variation for different traits among the accessions can be valuable in selection and screening for future breeding programs.

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