

REGULAR ARTICLE

ON-FARM DIVERSITY ASSESSMENT AND EVALUATION OF FINGER MILLET GENOTYPES IN THE MID HILLS OF NEPAL

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ABSTRACT

The objective of the study is to assess the phenotypic diversity among the finger millet genotypes and evaluate overall performance for the recommendation of genotypes to the farming community of mid hills of Nepal. The overall performance of 8 candidate genotypes selected from diversity block of 46 varieties in 2015, were assessed in randomized complete block design (RCBD) with three replicates under on-farm conditions in Lamjung district during 2016. Highly significant ($p \leq 0.01$) variability among the selected 8 genotypes for agro-morphological traits viz., plant height, number of fingers per head, grain yield, 1000 grain weight, straw yield, days to heading and maturity was revealed. Strong inter-correlation among grain yield, plant height, time to flowering and straw yield was detected. The traits viz., plant height, grain yield, straw yield, days to heading and days to maturity were the most important traits contributing to the overall variability and thus, provide options for selection.

Keywords: Finger millet, *On-farm*, Agro-morphological traits, Diversity, Nepal

INTRODUCTION

Finger millet (*Eleusine coracana* Gaertn.), is an important food crop in the hills of Nepal. It can tolerate many of the abiotic stress conditions and provides nutritious staple food to millions of small holder farmers of the world [1, 2]. Finger millet belongs to the C4 photosynthetic category of plants [3]. In Nepal, major area of production of finger millet was reported to lie in the mid hills between 600 to 2000 m above from the sea level (masl) representing more than 50% the population of Nepal but the crop is grown in diverse agro-ecological conditions from Terai and Inner Terai (100 masl) to valley, hills and mountain areas up to the elevation of 2500 masl [1]. Finger millet is highly valued due to its nutritional content, being especially rich in calcium, iron, manganese and methionine and tryptophan amino acids [4, 5]. Its slow digestion indicates low blood sugar levels after intake, thereby, it is a safer food for diabetics [6]. Being rich in many nutrients, this millet is highly useful to hardworking farmers metabolically disordered people.

The plant parts have been used in alternative medicine and recent reports validated that [7]. Devi *et al.* [8] reported health benefits of the crop both nutritive and medicinal properties. Finger millet is used in preparation of traditional food products of Nepal. Similarly, finger millet is strongly linked to the cultural value of ethnic communities such as

Gurung, Magar and Tamang and is an important crop in Lamjung where Gurung community predominates.

Finger millet can be used for extended storage as it is less susceptible to pests [9, 10]. It can be utilized for animal feed as well. The green straw contains digestible nutrients is worthy for animal consumption [11]. In the wake of climate change, malnutrition and public health challenges, finger millet has tremendous potential to meet these challenges, provided its drought tolerance and ability to grow as monocrop, relay crop and inter-crop under low inputs conditions in diverse agro-ecology, along with other health-promoting traits valued by humans. In this context, characterization and evaluation of landraces from *ex-situ* collection and *on-farm*, need attention as these valuable genetic resources have been poorly used [12].

The present study was undertaken with the objective of assessing the phenotypic diversity among the available germplasm and evaluating promising genotypes for their agronomic performance under *on-farm* conditions. The information thus generated would be of tremendous value for recommending the superior genotypes to the farming community and facilitating the choice of genitors for effective finger millet breeding programme.

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MATERIALS AND METHODS

Diversity block

In order to assess and evaluate the phenotypic diversity among the 46 landraces, an un-replicated diversity block trial using rod row design was set up in Ghanpokhara VDC (Village Development Committee)-1 of Lamjung district in 2015 under *on-farm* conditions at elevation of 1515 masl. Diversity block is an experimental block of farmers' varieties managed by local institution for research and development purposes [13]. The genotypes included in the study were collected from ex-situ genebank and their sources of collection are depicted in table 1. The findings generated from the study were deployed to enable the selection of the candidate genotypes exhibiting superior agronomic performance for further evaluation in *on-farm* yield trial. Each landrace was planted in two rows of 3m length with the plot size of 1.2 m² with distance of 20 cm between row to row and 10 cm between plant to plant. The experiment plots were managed as per farmers' practice. The UPGMA cluster analysis based on Euclidean distance using JMP 13 was performed to group the landraces into distinct clusters. The observations on seven traits *viz.*, time to heading and maturity, plant height, ear exertion (cm), flag leaf length (cm), finger width (mm) and grain yield (g plot⁻¹) were recorded as per the descriptors of finger millet [14]. The data on grain yield was extrapolated in t ha⁻¹. These traits were considered in UPGMA clustering and the genotypes to be included in the yield trial were identified from the clusters showing high trait values.

Yield trial

The yield trial was conducted during 2016 under *on-farm* conditions in Ghanpokhara VDC-1 of Lamjung district located at 28° 17.397' latitude North and 084° 19.344' longitude and altitude of 1525 masl. Total of eight genotypes (six selected from diversity block and two recently released varieties *viz.*, Kabre-2 and Sailung-1) were included in the study for evaluating the agronomic performance. The genotypes included in the study along with their respective distinguishing traits and sources are presented in table 2. The field experiment was laid out in RCBD with three replications. In each replication, each cultivar was grown in a plot of 10 rows with a distance of 20 cm between row to row and 10 cm between plant to plant and the area of each experimental unit was 6 m²(2m x 3m). The sowing of each genotype was done in first week of May, 2016. The local farmer's practices were followed to raise the crop. Well decomposed FYM @ 5-6 t/ha was applied in the field during land preparation. No chemical fertilizers and pesticides were used. Two hand weeding cum hoeing were performed 30 and 60 d after sowing (DAS), respectively. The data were recorded for seven agromorphological traits such as plant height (cm), number of fingers/head, grain yield (g plot⁻¹), 1000 grain weight (g), straw yield (kg plot⁻¹), days to 50% heading and 80% maturity as per the descriptors. The data on grain and straw yield were later extrapolated to t ha⁻¹ for data analysis.

The data collected for evaluation of agronomic traits of the genotypes were subjected to analysis of variance under RCBD using statistical software R and the significance of differences between the means were compared using Least Significant Difference (LSD) at 5 percent level of significance. The Pearson's correlation coefficients between each pairs of traits and principal component analysis (PCA) was conducted using statistical software R

and Minitab 15.0 in order to study the extent of association among the traits and to identify the patterns of agromorphological variation, respectively.

RESULTS AND DISCUSSION

Diversity block

The UPGMA cluster analysis based on Euclidean distance of 46 genotypes revealed five different clusters (fig. 1 and table 3). Cluster II was found to be the largest cluster containing 30 landraces with higher mean values of yield, finger width, flag leaf length and ear exertion while lower mean values for phenological traits. The cluster V which contained only landrace genotype *viz.*, Lamsare Kodo also showed higher values for the desirable agronomic traits. Despite being desirable for most of the traits, cluster I, III and IV were found to be unworthy in terms of yield and phenological traits. The six landraces *viz.*, Chhatre, Chhangre Kodo, Nangre Kodo (Lamjung), Dalle Kodo, Lamsare Kodo and Syakhkhad Kodo for displaying superior performance in terms of agronomic and phenological traits were selected for further evaluation and validation.

Yield trial

Highly significant variation was noted among the selected genotypes for all the agronomical traits *viz.*, days to heading and maturity, plant height, number of fingers, grain yield, 1000 grain weight and straw yield. Substantial variations in finger millet have also been reported in previous studies by [15-18]. The mean performance of the genotypes for these traits are shown in table 4. NGRCo1431 (Chhatre) recorded the highest plant height (109.33±1.45 cm) which was at par with Chhangre kodo and Lamsare kodo. Similarly, NGRCo1431 (Chhatre) recorded the highest grain yield (1.80±0.06 t ha⁻¹) and highest number of finger (10.67±0.33). NGRCo5049 (Sailung-1) recorded the highest 1000 grain weight (3.33±0.07 g) being statistically at par with Dalle kodo and Lamsare kodo. Syakhkhad kodo recorded the highest straw yield (7.61±1.03 t ha⁻¹) and highest number of days to 50% heading (145±1.00). Similarly, Lamsare kodo was found to be the earliest to 50% heading (136.67±0.88 d) and 80% maturity (175.33±0.33 d).

The association among the agronomical traits was estimated by correlation analysis (table 5). Plant height exhibited highly significant positive correlation with grain yield ($r=0.577$) while significant positive correlation with straw yield ($r=0.441$) was detected. Highly significant positive correlation ($r=0.568$) was found between grain yield and straw yield. Days to 50% heading exhibited highly significant positive correlation with straw yield ($r=0.597$). Highly significant positive correlation between plant height and grain yield was also reported by Ulaganathan and Nirmalakumari [19], Assefa and Fetene [20] and Duke [9]. Similarly, Bastola *et al.* [2] found highly significant positive inter-correlation between plant heights, grain yield per plant, days to 50% flowering and straw yield per plant. The present findings are in concordance with Ulaganathan and Nirmalakumari [19], Bastola *et al.* [2], Duke [9] and Assefa and Fetene [20].

Table 6 presents the principal component and % of contribution of each component to the total in the finger millet genotypes. The first accounted for 43.07% of the total variation in the population. Plant height, grain yield, straw yield and days to 50% heading contributed more to the first component. Second principal component

accounted for 24.76% of total variation. Number of fingers per head and grain yield contributed heavily to the second component in positive direction while 1000 grain weight and days to 80% maturity contributed more to the second component in negative direction. The third principal component accounted for 15.07% of the total variation. 1000 grain weight and grain yield contributed more to the third component in positive direction while days to 80% maturity contributed more to the third component in negative direction. The first three principal components with Eigen value ≥ 1 accounted for 82.89% of the total variation. Similar findings with regard to grain yield per plant, plant height and days to flowering were reported by Salini *et al.* [21] and Ulaganathan and Nirmalakumari [19] in proso millet and finger millet, respectively. Previous studies support the findings [22-25]. The present finding indicated that indirect selection based on plant height, days to 50% heading and straw yield would be instrumental in identifying superior genotypes for finger millet crop improvement programme.

Despite the promise of the finger millet in regard to climate change adaptation, medicinal and nutritional benefits, cultivation trend of finger millet is decreasing in Nepal [26, 27] because of various socioeconomic constraints such as labour-intensive farming practice and post-harvest processing difficulties, identification of location specific varieties and unsupportive agricultural policies. In order to address these challenges, GEF/UNEP funded project on Local Crops [28] prioritized research on i) Participatory variety selection and grass root breeding to improve productivity and tolerance to stress [29]; ii) Diversity sourcing of seeds to match farmers' needs through rapid detection, *on-farm* evaluation and dissemination of choice varieties, iii) Technology diversification for processing and value chain enhancement of local crops, and iv) Community seed banks establishment for strengthening local seed security and agro-biodiversity conservation [30].

Table 1: List of landraces of finger millet *al. ong* with their collection site included in the diversity block trial in Lamjung in 2015

Entry	Local name	Collection site	Entry	Local Name	Collection Site
1	Setokodo	Bhojpur	24	Chayalte/Seto	Dolakha
2	Dhankodo	Bhojpur	25	Seto Mudke	Dolakha
3	Nangrekodo	Bhojpur	26	Syakkhad	Dolakha
4	Nangkatuwakodo	Dhankuta	27	Bikase Lamo	Dolakha
5	Kattikekodo	Sankhuwasabha	28	Bikase	Dolakha
6	Chhatrekodo	Tehrathum	29	Paheli	Dolakha
7	Andhikholekodo	Lamjung	30	Nangre	Dolakha
8	Baidikodo	Tanahun	31	Seto	Dolakha
9	Kalomaurelo	Kaski	32	Mathillo Paheli	Dolakha
10	Jhupekodo	Baglung	33	Laribari	Dolakha
11	Jhyapekodo	Kaski	34	Dalo Dalle	Dolakha
12	Lurkekodo	Parbat	35	Chalyte	Dolakha
13	Kattikekodo	Syangja	36	Botange	Dolakha
14	Jhaprekodo	Gulmi	37	Seto	Lamjung
15	Dallekodo	Ramechhap	38	Sangle	Lamjung
16	Nuwakotekodo	Solukhumbu	39	Larfare	Lamjung
17	Local kodo	Gorkha	40	Khro	Lamjung
18	Kodo	Baitadi	41	Lafre	Lamjung
19	Kalokodo	Darchula	42	Kekro	Lamjung
20	Kabrekodo	Mustang	43	Dalle	Lamjung
21	Kyarkodo	Sindhupalchok	44	Nangre	Lamjung
22	Local kodo	Baitadi	45	Lamsare	Lamjung
23	Dalle	Dolakha	46	Chhangre	Lamjung

Table 2: List of finger millet genotypes included in the yield trial during 2016 along with their distinguishing traits and sources

S. No.	Genotypes	Distinguishing traits	Source
1	NGRC01431 (Chhatre)	Spike looks like umbrella	Lamjung
2	Chhangre kodo	Light red, medium sized grain, erect finger/spike	Lamjung
3	Nangre kodo	Spike looks like claw	Lamjung
4	Dalle kodo	Compact head and closed fingers	Lamjung
5	Lamsare kodo	Tiny black grains	Lamjung
6	Syakkhad kodo	Green compact ear with slightly incurved finger	Dolakha
7	NGRC05050 (Kabre-2)	Green compact ear with green nodal pigmentation	NAGRC*
8	NGRC05049 (Sailung-1)	Compact ear with incurved finger with purple node	NAGRC*

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Table 3: Number of genotypes in each cluster along with mean value±SD and range of agro-morphological traits

Cluster	Member	Days to heading	Days to maturity	Plant height (cm)	Ear exertion (cm)	Flag leaf length (cm)	Finger width (mm)	Grain yield (t ha ⁻¹)
I	9	107.55±6.21 (98-117)	156.77±7.05 (150-166)	113.67±17.65 (102-125)	14.67±1.58 (12-17)	29±2.50 (25-32)	8.44±0.53 (8-9)	0.74±0.37 (0.37-1.56)
II	30	126.33±6.29 (114-136)	174.17±9.53 (152-194)	123.07±13.29 (94-143)	15.67±2.77 (11-23)	31.20±3.74 (23-39)	9.13±1.07 (7-12)	1.90±0.70 (0.71-3.17)
III	3	134.67±2.31 (132-136)	180±13.45 (165-191)	103±6.08 (99-110)	16±1.00 (15-17)	32.67±3.51 (29-36)	7.67±0.57 (7-8)	1.17±0.36 (0.82-1.55)
IV	3	138.33±8.02 (130-146)	193.67±12.70 (179-201)	112.33±9.29 (102-120)	10.67±3.79 (8-15)	31.33±3.05 (28-34)	9±0.00	1.83±0.89 (0.80-2.35)
V	1	130	184	121	14	37	12	3.81

fig. in the parentheses indicate the range of agro-morphological traits within each cluster

Table 4: Mean values±Standard Error (S.E.) of agro-morphological traits of eight selected finger millet genotypes tested at Ghanpokhara VDC-1, Lamjung in 2016

Genotypes	Plant height (cm)	No. of fingers head ⁻¹	Grain yield (t ha ⁻¹)	1000 grain weight (g)	Straw yield (t ha ⁻¹)	Days to 50% heading	Days to 80% maturity
Chhangre Kodo	108.67±3.28a	10.00±1.00a	1.44±0.10b	2.77±0.03d	5.50±0.10cd	140.33±0.67cd	193.33±0.33b
Dalle Kodo	86.67±3.67c	9.33±0.88ab	1.51±0.05b	3.23±0.03a	5.06±0.06d	138.00±0.58d	189.67±0.67c
Lamsare Kodo	108.33±2.40a	7.00±0.00de	1.71±0.18ab	3.23±0.06a	6.67±0.25ab	141.67±0.33bc	194.67±0.88b
Nangre Kodo	99.67±2.85b	8.33±0.67bc	1.55±0.05a	3.17±0.07bc	5.61±0.06bc	136.67±0.88e	175.33±0.33d
NGRC01431 (Chhatre)	109.33±1.45a	10.67±0.33a	1.80±0.06a	2.47±0.07e	6.39±0.06bc	142.33±1.33ab	188.33±0.33c
NGRC05049 (Sailung-1)	101.67±3.76a	7.67±0.33cde	1.10±0.09c	3.33±0.07a	5.61±0.11bcd	143.67±1.67ab	198.00±0.00a
NGRC05050 (Kabre-2)	84.67±3.06c	6.00±0.00e	0.89±0.04c	2.60±0.06e	5.17±0.10d	138.33±1.20de	188.67±0.33c
Syakhkhad Kodo	104.00±1.73a	7.33±0.33de	1.83±0.10a	3.07±0.03c	7.61±1.03a	145.00±1.00a	194.00±0.58b
p-value	0.0001	0.0007	<0.00001	<0.00001	0.0032	0.0001	<0.00001
SE. m±	3.93	0.82	79.66	0.08	0.31	1.30	0.65
LSD(p ≤ 0.05)	8.44	1.75	170.85	0.16	0.67	2.78	1.40
CV (%)	4.80	12.06	11.00	3.11	10.75	1.13	0.42

Mean values in columns with different letters are significantly different ($p \leq 0.05$) according to Fisher's LSD test

Table 5: Correlation matrix between different agro-morphological traits of finger millet

Agro-morphological traits	Plant height	No. of fingers head ⁻¹	Grain yield	1000 grain weight	Straw yield	Days to 50% heading
No. of fingers head ⁻¹	.392					
Grain yield	.577**	.359				
1000 grain weight	-.077	-.288	.065			
Straw yield	.441*	-.105	.568**	.065		
Days to 50% heading	.383	-.105	.262	.068	.597**	
Days to 80% maturity	.208	-.124	-.080	.131	.215	.635**

** Correlation coefficient is significant at $p \leq 0.01$ (2-tailed), * Correlation coefficient is significant at $p \leq 0.05$ (2-tailed)

Table 6: Eigen values, factor scores and contribution of first four principal component axes to the variation in eight selected finger millet genotypes

Agro-morphological traits	PC1	PC2	PC3	PC4
Eigen values	3.0149	1.7329	1.0547	0.7576
Variance (%)	43.07	24.76	15.07	10.82
Cumulative variance (%)	43.07	67.83	82.89	93.72
Plant height	-0.4796	0.2087	-0.0517	-0.1283
No. of fingers head ⁻¹	-0.121	0.6052	-0.2493	-0.5478
Grain yield	-0.4193	0.3762	0.3751	0.0383
1000 grain weight	-0.028	-0.3399	0.7128	-0.5832
Straw yield	-0.5067	-0.0724	0.22	0.4558
Days to 50% heading	-0.4935	-0.3003	-0.229	-0.0005
Days to 80% maturity	-0.2802	-0.4876	-0.4308	-0.3662

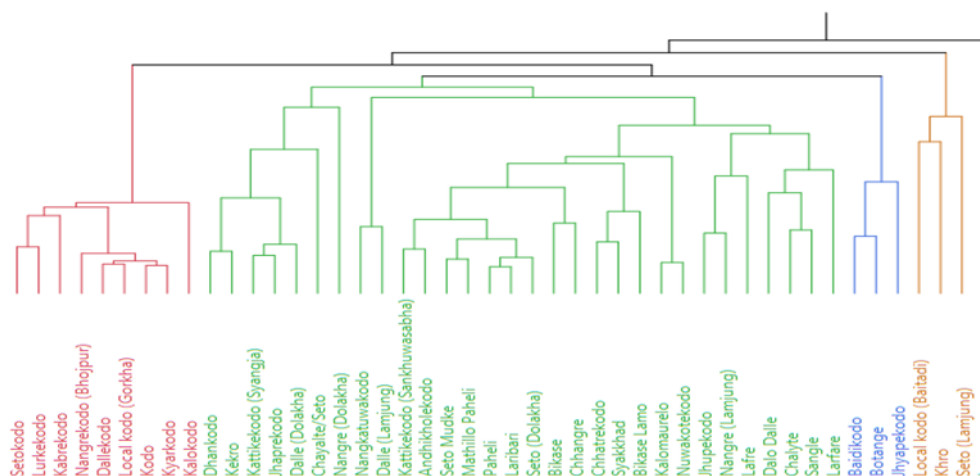


Fig. 1: UPGMA clustering of 46 finger millet genotypes included in diversity block based on average linkage and Euclidean distance

The present investigation, which is part of sourcing local crop diversity that matches farmer’s needs, suggests existence of high level of phenotypic diversity among the finger millet genotypes which would be useful for choosing the genitors for crop improvement programme [31]. The evaluation studies facilitated the identification of robust finger millet varieties *viz.*, Syakkhad kodo, Lamsare kodo and Nangre kodo, diversifying the varietal choices for the farmers in state of very few promising cultivars available in national agricultural system. The findings bolsters the large scale testing of IRD kits for popularizing the variety [31] and registration in national agricultural system. In addition to this, community seed banks (CSBs) and district agriculture development offices (DADOs) can play a pivotal role in popularizing these robust varieties at community level via establishment of demonstration plots and distribution of IRD kits and, ensuring the accessibility of quality seeds by incorporating them in their routine conservation and seed multiplication activity. The wider dissemination and adoption of these robust finger millet varieties will assure augmented production and area coverage of finger millet in the mid-hills warranting food security in the region.

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AUTHOR’S CONTRIBUTIONS

Authors contributed equally to the overall study and manuscript preparation and approved the final version of the manuscript for publication.

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