



Identification of promising finger millet landraces for the mid-hills of Nepal

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ABSTRACT

Finger millet is the fourth important food crop of Nepal. National Agriculture Genetic Resources Center (NAGRC) holds 1055 accessions of finger millet in its ex-situ depository. These accessions are poorly exploited in breeding programs due to a lack of ample characterization data. A total of 19 landraces were evaluated with Kabre kodo-2 (check) in three replications at Khumaltar, Lalitpur during 2020 and 2021 as pre-breeding experiments. Analysis of variances for agro-morphological traits revealed elite landraces having higher grain and straw yield, earlier maturity, optimum plant height, and blast resistance. NGRC04849 from Rukum produced the highest grain yield (3580 kg/ha) followed by NGRC01497 from Jajarkot (3567 kg/ha), NGRC05050 i.e. Kabre kodo-2 (3434 kg/ha) and NGRC06490 from Sindhuli (3368 kg/ha) consisting a separate cluster in a dendrogram. NGRC01483 from Okhaldhunga was the earliest (131 days) in maturity followed by NGRC04849 from Rukum (147 days) whereas Kabre kodo-2 matured in 156 days. NGRC03484 (Dhading) and NGRC04769 (Ilam) were found resistant for all three blast diseases (leaf, neck and finger blast) whereas NGRC01639 (Syangja), NGRC04804 (Dolakha) and NGRC04852 (Sindhupalchok) were found resistant for neck and finger blast. We found strong positive correlations between grain and straw yield ($r=0.71$), heading and maturity days ($r=0.59$), and neck and finger blast ($r=0.59$). Strong negative correlation of days to maturity with neck ($r=-0.44$) and finger blast ($r=-0.42$) suggests blast resistance in early maturing landraces. These elite landraces could be either utilized in finger millet improvement program or deployed to farmers' field analogous to Khumaltar condition.

Keywords: accession, elite lines, finger millet, genebank, landraces, pre-breeding

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INTRODUCTION

Finger millet [*Eleusine coracana* (L.) Gaertn., $2n=4x=36$] was domesticated in eastern Africa around 3000 BC and introduced into Indian subcontinent around 1000 BC (Hilu et al. 1979, Upadhyaya et al. 2006). It is the fourth among millet crops in the world after sorghum, pearl millet and foxtail millet (Upadhyaya et al. 2007). The area and production under finger millet in many countries is not precisely available because the production statistics of this crop is often clubbed with other millets (Upadhyaya et al. 2010). It is cultivated in 3.8 million ha (12% of the total millet area) in the world with coverage in more than 25 countries of Africa and South Asia (Bora 2013, Kumar et al. 2016, Hittalmani et al. 2017, Upadhyaya et al. 2010, Vetriventhan et al. 2016). It is grown in the wide range of environment from the tropical coastal regions of India (Upadhyaya et al. 2006) to high mountains (3,130 masl) of Nepal (Bastola et al. 2015, Gaihre et al. 2021). It is a climate resilient crop grown in marginal land and stress environments with very low or minimum input (Goron et al. 2015).

Finger millet is called as *kodo* in Nepali, where it is ranked 4th most important crop of the country after rice, maize and wheat in terms of area and production. It is cultivated in 214,477 ha and produced 284,352 tons with an average productivity of 1.33 t ha⁻¹ (MoAFE 2026). Finger millet is well recognized as nutrient-rich cereal which contains calcium (0.34%), dietary fiber (18%), protein (6-13%), minerals (2.5-3.5%), phytates (0.48%) and phenolic compounds (0.3-3%) (Chandra et al. 2016). It is enriched with calcium, iron, zinc, proteins and calories (O’Kennedy et al. 2006, Upadhyaya et al. 2011) and valued for its health beneficial effects like anti-diabetic, anti-tumorigenic, antioxidant and antimicrobial properties (Devi et al. 2011, Kumar et al. 2016, Nakarani et al. 2020). Besides food and nutrition, it has been an integral component of agro-tourism in Nepal due to its *dhindo* (thick porridge) and high-quality *raksi* (home-made wine) (Ghimire et al. 2017, Gaihre et al. 2021, Joshi et al. 2020).

Finger millet research got very low priority in Nepal resulting only five varieties released (Okhle-1, Dalle-1, Kabre kodo-1, Kabre kodo-2, Shailung kodo-1) and Rato kodo registered in five decades (SQCC 2022). Difficulty in hybridization due to small grain size hindered the finger millet improvement in the developing countries like Nepal. Pre-breeding is the most important avenue to open the door for the utilization of genebank accessions in breeding program. Globally, a total of 36,873 finger millet accessions has been conserved in ex-situ genebanks (Vetriventhan et al. 2020). International Crop Research Institute for Semi-Arid Tropics (ICRISAT) has the largest collection with 5940 accessions in the world with a core subset of 622 accessions (Upadhyaya et al. 2006). NAGRC holds 1055 finger millet accessions in long-term conservation (Genebank, 2022). A total of 300 finger millet accessions collected from 54 districts has been extensively characterized at NAGRC Khumaltar, HCRP Kabre and ARS Vijayanagar during 2017 and 2018 (Ghimire et al. 2022, Ghimire et al. 2023). This research has been conducted as a pre-breeding activity to evaluate the selected genotypes from previous experiments in larger plot size and identify elite lines suitable to promote in coordinated varietal trials for the mid-hill environments of Nepal.

MATERIALS AND METHODS

Experiment Materials and Site

This study used 20 finger millet genotypes conserved at NAGRC including 19 landraces collected from 19 districts of Nepal and a released variety Kabre kodo-2 as a check. Detail passport information (local names, collection districts and geo-coordinates) of these genotypes has been presented in Table 1. Field experiments were conducted at the experimental field of NAGRC Khumaltar, Lalitpur (1360 masl, 27.65°N, 85.32°E) that represents mid-hill

environment of Nepal. It received the total annual rainfall of 1000-1525 mm with monthly average minimum and maximum temperature ranges from 4-21°C and 17-29°C, respectively (Genebank 2021, Genebank 2022). The site has fluvial non-calcareous slightly acidic soil with 53.4% sand, 16.5% clay, 2.5% organic matter and pH value of 6.2 (<https://soil.narc.gov.np>).

Table 1. Passport details of 20 finger millet genotypes used in the experiments.

Entry	Accession	Local name	District	Latitude (°N)	Longitude (°E)	Altitude (m)
1	NGRC01429	Nangkatuwa	Sankhuwasabha	27.24	87.34	1237
2	NGRC01483	Asoje kodo	Okhaldhunga	27.02	86.50	825
3	NGRC01497	Asoje kodo	Jajarkot	28.87	82.44	1850
4	NGRC01639	Danja kodo	Syangja	28.10	83.87	840
5	NGRC01645	Rato kodo	Jumla	29.29	82.15	2290
6	NGRC03484	Tauke kodo	Dhading	28.10	85.07	1200
7	NGRC03577	Lapre kodo	Bajura	29.49	81.46	1500
8	NGRC03580	Kalo kodo	Achham	29.06	81.18	1000
9	NGRC03630	Mudke kodo	Baglung	27.93	85.66	1765
10	NGRC03683	Chyalda kodo	Rasuwa	28.17	85.32	1947
11	NGRC04727	Local kodo	Dandeldhura	29.29	80.58	1144
12	NGRC04769	Mansire kodo	Ilam	26.99	87.88	840
13	NGRC04804	Jhuppe kodo	Dolakha	27.74	86.17	960
14	NGRC04817	Lamre kodo	Dailekh	28.54	81.38	1190
15	NGRC04849	Thulo kodo	Rukum	28.79	82.47	867
16	NGRC04852	Arun kodo	Sindhupalchok	27.74	85.81	1000
17	NGRC04871	Local kodo	Udayapur	26.77	86.83	139
18	NGRC06483	Mudke kodo	Tanahun	28.05	84.46	735
19	NGRC06490	Hasure kodo	Sindhuli	27.27	85.99	1250
20	NGRC05050	Kabre kodo-2	HCRP Kabre	27.64	86.15	1400

General Methodology

The experiment was laid out in randomized complete block design (RCBD) with 20 entries and three replications. Seeds were sown in the nursery bed on 24 May 2020 and 7 June 2021. In both the years, 30-day-old seedlings of each genotype were transplanted in each plot of 6 m² area where a total of 300 seedlings were accommodated. Each plot was constituted by 10 rows of 3 m length with 20 cm spacing between rows and 10 cm between plants within rows. Chemical fertilizers were applied at the rate of 20:10:10 kg/ha N:P₂O₅:K₂O as basal doses followed by 40 kg/ha N top dressed in two split doses at 15 and 30 days after transplanting. Manual weeding was done just before urea top dressing at 15 days interval after transplanting. The experimental field was not provided with the irrigation and none of the genotypes were subjected to any kind of pesticides application.

Data Recording and Analysis

Agronomic data on various traits such as days to 50% flowering, days to 80% maturity, number of heads per m², grain yield (kg/ha, adjusted to 14% grain moisture), fresh straw yield (t/ha), stem borer at heading stage, leaf blast at seedling stage, neck and finger blast at grain filling stage were recorded based on whole plot data whereas measurements for other quantitative traits such as plant height (cm), number of fingers per head, etc were taken from

five randomly selected plants. Morphological data were recorded as per the standard descriptors of finger millet (IBPGR 1985). Data on leaf, neck and finger blast was scored in 0-9 scale and reaction levels were estimated as resistant (0-1), moderately resistant (2-3), moderately susceptible (4-5), susceptible (6-7) and highly susceptible (8-9) (Ghimire et al 2022). The frequency of each descriptor state of qualitative measurements such as head type, stem borer, leaf blast, neck blast and finger blast susceptibility were tabulated using Microsoft Excel. All quantitative measurements were tabulated in Excel and Analysis of Variance (ANOVA) was performed using 'variability' package (Popat et al 2020) of R statistical software (R Core Team, 2020) and different variance components (mean, standard error of mean, minimum, maximum, mean sum of squares, probability value, broad sense heritability (h^2 bs), genotypic variance (σ^2 g) and phenotypic variance (σ^2 p) were calculated. Clustering observations and correlation analysis were done using Minitab-17 (Minitab 2010).

RESULTS

Qualitative Traits Analysis

Frequency of qualitative data for different traits were presented in **Table 2**. Although the insect and disease resistance are quantitative traits, score data were converted to qualitative classes. Three types of heads namely open, semi-compact and compact were observed in tested genotypes. Nine out of 20 genotypes were with compact heads (mostly higher yielding genotypes) followed by open type heads in seven genotypes. Four genotypes showed resistant and nine genotypes showed moderately resistant reaction with stem borer. Four, 11 and five genotypes showed resistant reaction for leaf, neck and finger blast diseases.

Table 2. Frequency of head types, and reactions of stem borer and different blast diseases in tested genotypes.

Trait	Class	Number	Genotypes
Head type	Open	7	NGRC01639, NGRC01645, NGRC03577, NGRC03630, NGRC04769, NGRC04817, NGRC06483
	Semi-compact	4	NGRC01483, NGRC03580, NGRC03683, NGRC04804
	Compact	9	NGRC01497, NGRC05050, NGRC04849, NGRC06490, NGRC04852, NGRC01429, NGRC04871, NGRC04727, NGRC03484
Stem borer	Resistant	4	NGRC01483, NGRC01645, NGRC03630, NGRC04727
	Moderately resistant	9	NGRC01429, NGRC01639, NGRC03484, NGRC03577, NGRC03580, NGRC04769, NGRC04849, NGRC04852, NGRC05050
	Moderately susceptible	2	NGRC03683, NGRC04871
	Susceptible	2	NGRC01497, NGRC06483
	Highly susceptible	3	NGRC04804, NGRC04817, NGRC06490
Leaf blast	Resistant	4	NGRC03484, NGRC03630, NGRC04769, NGRC05050
	Moderately resistant	6	NGRC01483, NGRC01645, NGRC03580, NGRC04804, NGRC04871, NGRC06483
	Moderately susceptible	5	NGRC01639, NGRC03683, NGRC04727, NGRC04849, NGRC06490
	Susceptible	4	NGRC01429, NGRC03577, NGRC04817, NGRC04852
	Highly susceptible	1	NGRC01497
Neck blast	Resistant	11	NGRC01429, NGRC01639, NGRC01645, NGRC03484, NGRC03577, NGRC03683, NGRC04769, NGRC04804, NGRC04852, NGRC04871, NGRC06483
	Moderately resistant	5	NGRC03580, NGRC03630, NGRC04817, NGRC06490, NGRC05050
	Moderately susceptible	4	NGRC01483, NGRC01497, NGRC04727, NGRC04849

Trait	Class	Number	Genotypes
Finger blast	Resistant	5	NGRC01639, NGRC03484, NGRC04769, NGRC04804, NGRC04852
	Moderately resistant	6	NGRC01483, NGRC01645, NGRC03577, NGRC03683, NGRC06490, NGRC05050
	Moderately susceptible	5	NGRC01429, NGRC01497, NGRC04817, NGRC04849, NGRC04871
	Susceptible	4	NGRC03580, NGRC03630, NGRC04727, NGRC06483

Variance Components

Mean, SE, minimum-maximum, mean square due to genotypes, probability value, broad-sense heritability (h^2bs), genotypic variance (σ^2g), phenotypic variance (σ^2p) and genetic advance as percentage of mean (GAM) have been presented in Table 3. Wider range for grain yield, straw yield, heads/m², heading days and maturity days was observed in 2020 compared to 2021. In the analysis of quantitative traits, total number of heads/m² showed the lowest h^2bs estimates (27.3% and 33.3, respectively in 2020 and 2021) whereas days to heading showed the highest h^2bs estimates (59.7% and 56.6, respectively in 2020 and 2021). Estimation of GAM ranged from the lowest of 8.2% for maturity days and heads/m² in 2021 to the highest of 34.7% and 26% for straw yield and grain yield in 2020.

Table 3. Variance components of finger millet genotypes for different agronomic traits.

Variable	Year	Mean $\pm$ SE	Range	MSG	P-value	h^2bs (%)	σ^2g	σ^2p	GAM (%)
DTH	2020	101 $\pm$ 3.6	78-131	211.2	0.000	59.7	57.5	96.3	11.9
	2021	101 $\pm$ 3.4	81-128	166.9	0.000	56.6	44.3	78.3	10.2
DTM	2020	157 $\pm$ 6.6	126-191	438.6	0.001	44.0	102.7	233.2	8.8
	2021	156 $\pm$ 5.7	131-188	347.7	0.000	46.5	83.8	180.2	8.2
PHT	2020	117 $\pm$ 7.5	85-162	419.1	0.008	33.4	83.9	251.2	9.3
	2021	118 $\pm$ 8.4	80-161	694.0	0.000	42.9	160.2	373.6	14.5
HPM	2020	267 $\pm$ 21.3	165-338	2896.0	0.024	27.3	511	1874	9.1
	2021	279 $\pm$ 15.7	180-332	1840.7	0.008	33.3	368	1105	8.2
FPH	2020	6.5 $\pm$ 0.49	4.4-9.8	2.022	0.003	37.4	0.43	1.16	12.8
	2021	6.5 $\pm$ 0.64	4.0-10.0	3.589	0.002	39.6	0.79	2.00	17.9
GY	2020	2709 $\pm$ 351.6	1108-4607	1195388	0.001	42.6	274868	645652	26.0
	2021	2447 $\pm$ 304.8	1500-4017	937844	0.001	44.1	219693	498457	23.3
SY	2020	13.5 $\pm$ 1.9	5.3-23.8	41.21	0.000	50.2	10.3	20.6	34.7
	2021	15.2 $\pm$ 1.4	8.3-20.5	16.09	0.005	36.0	3.4	9.4	14.9

Note: DTH=Days to heading, DTM=Days to maturity, PHT=Plant height (cm), HPM=Number of heads per m², FPH=Number of fingers per head, GY=Grain yield (kg/ha), SY=Straw yield (t/ha), SE=Standard error of mean, MS=Mean sum of squares, h^2bs =Heritability in broad sense, σ^2g =Genotypic variance, σ^2p =Phenotypic variance, GAM=Genetic advance with percentage of mean

Agronomic Performance of the Genotypes

Significant difference was observed between the genotypes for all agronomic traits in individual years (Table 3) and while combined over years (Table 4). Two landraces namely NGRC04849 and NGRC01497 produced grain yield significantly at par with check variety Kabre kodo-2 (NGRC05050). Genotypes producing significantly higher grain yield also yielded significantly higher straw. NGRC01483 from Okhaldhunga was the earliest genotype to flower (88 days) which flowered two weeks earlier than the released variety Kabre kodo-2.

Table 4. Mean performance of the genotypes over years for different agronomic traits.

Genotype	Grain yield (kg/ha)		Straw yield (t/ha)		Days to heading		Plant height (cm)		Number of heads/m ²	
NGRC04849	3580	a	18.0	ab	95.7	fgh	121.6	bcd	291	ab
NGRC01497	3567	a	19.5	a	94.7	gh	125.2	abcd	292	ab
NGRC05050	3434	ab	18.6	a	101.7	def	122.4	bcd	313	a
NGRC06490	3368	abc	19.4	a	99.5	efg	117.7	bcde	287	ab
NGRC04852	3150	abc	12.6	def	111.0	b	111.2	defg	310	a
NGRC04817	3114	abc	16.5	abc	100.0	efg	131.4	ab	286	ab
NGRC01429	3083	abc	18.0	ab	99.7	efg	138.6	a	230	e
NGRC04804	3044	abcd	13.8	cdef	119.3	a	130.8	ab	277	abcd
NGRC04769	2922	bcde	16.1	abcd	92.0	hi	97.4	gh	313	a
NGRC01639	2809	cde	13.3	cdef	112.2	b	109.5	defg	278	abcd
NGRC04727	2784	cde	14.5	bcde	97.3	fgh	125.0	abcd	258	bcde
NGRC04871	2779	cde	12.0	ef	104.5	cde	130.1	ab	287	ab
NGRC03580	2439	def	13.2	cdef	94.5	ghi	128.3	abc	284	abc
NGRC01483	2380	efg	12.3	ef	88.3	i	89.8	h	277	abcd
NGRC03683	2367	efg	10.8	ef	103.8	cde	103.3	efgh	240	e
NGRC03577	2165	fgh	13.1	cdef	91.2	hi	100.5	fgh	250	cde
NGRC03630	2140	fgh	11.9	ef	107.5	bcd	129.9	abc	279	abcd
NGRC06483	1989	fgh	11.5	ef	108.0	bc	113.8	cdef	238	e
NGRC03484	1792	gh	12.1	ef	104.2	cde	103.1	efgh	246	de
NGRC01645	1658	h	10.5	f	94.7	gh	116.5	bcdef	231	e
Grand mean	2728		14.4		101.0		117.3		273	

Note: Genotype means that do not share a letter are significantly different.

Correlations Between the Traits

The Pearson's correlation coefficients (r) have been presented in **Table 5**. Out of the 55 trait associations, 23 associations were found statistically significant. Among them, 17 trait pairs were very strongly correlated ($p < 0.001$) but 32 trait pairs were not associated significantly ($p > 0.05$) (Table 5).

Table 5. Pearson's correlation coefficient (r) between different agronomic traits of finger millet.

	DTH	DTM	PHT	HPM	FPH	GY	SY	SBS	LBS	NBS
DTH	0.59***									
DTM										
PHT	0.16	0.08								
HPM	-0.02	0.14	0.14							
FPH	-0.29**	-0.27**	0.32***	-0.21*						
GY	-0.01	-0.01	0.32***	0.53***	0.04					
SY	-0.13	-0.18	0.38***	0.40***	0.23*	0.71***				
SBS	0.23*	0.29**	0.02	0.04	-0.05	0.10	-0.19*			
LBS	-0.07	-0.05	0.07	-0.05	0.30**	0.23*	0.18	0.13		
NBS	-0.40***	-0.44***	0.09	0.08	0.07	0.13	0.20*	-0.12	0.17	
FBS	-0.27**	-0.42***	0.24**	-0.13	0.11	-0.15	-0.03	-0.11	0.08	0.59***

Note: DTH=Days to heading, DTM=Days to maturity, PHT=Plant height (cm), HPM=Number of heads per m², FPH=Number of fingers per head, GY=Grain yield (kg/ha), SY=Straw yield (t/ha), SBS=Stem borer score, LBS=Leaf blast scores, NBS=Neck blast scores, FBS=Finger blast scores, *=Significant (p -value: 0.01-0.05), **=Highly significant (p -value: 0.001-0.01), ***=Very highly significant (p -value: <0.001)

Strong positive correlations between grain and straw yield ($r=0.71$), heading and maturity days ($r=0.59$), and neck and finger blast ($r=0.59$), grain yield and number of heads/m² ($r=0.53$), straw yield and number of heads/m² ($r=0.40$), straw yield and plant height ($r=0.38$) were observed. We observed strong negative correlation between days to maturity and neck

blast ($r=-0.44$) as well as days to maturity and finger blast ($r=-0.42$) suggesting the blast resistance in early maturing genotypes (Table 5).

Clustering Genotypes

Based on the observations of agronomic traits, 20 genotypes were grouped into three distinct clusters (**Figure 1A**). Cluster-3 is the smallest cluster formed with four genotypes namely NGRC04849, NGRC01497, Kabre kodo-2 and NGRC06490. These are the members with highest grain yield (3368-3580 kg/ha) and straw yield (18-19.5 t/ha). Members of Cluster-2 produced the lowest grain yield (1658-2439 kg/ha). A two-dimensional PCA plot, explaining 56% of the total variation among the genotypes, showed the clear grouping of lowest yielding genotypes in lower-half and higher yielding genotypes in upper-right portion of the scatter plot (**Figure 1B**).

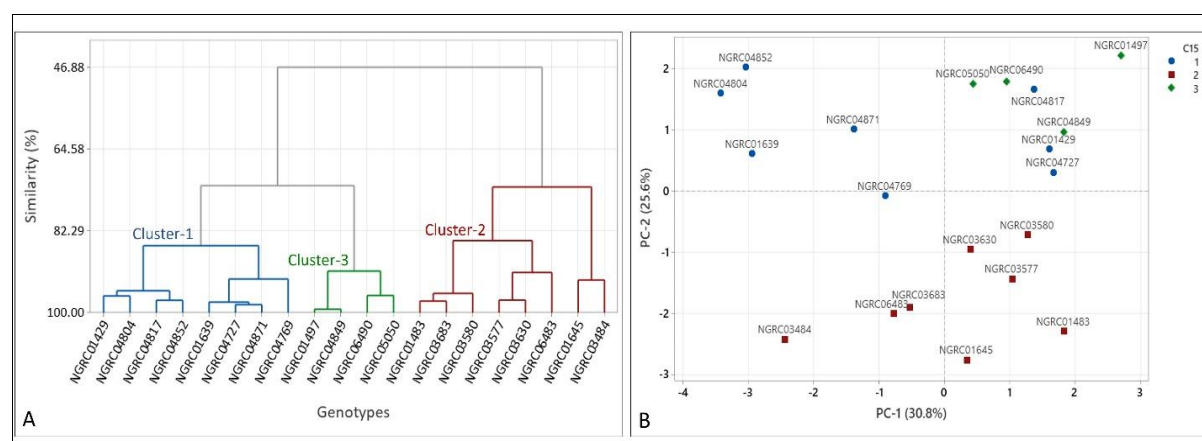


Figure 1A. Dendrogram based on average linkage and Euclidean distance, **1B.** Score plot with PC-1 and PC-2.

DISCUSSION

Genebanks conserve genetically diverse genetic resources, which can be exploited for developing high-yielding and stable crop varieties that contribute to global food security. Finger millet landraces exhibit significant agronomical variation, but their potential for breeding programs not efficiently underutilized in several countries, including Nepal, due to limited attention paid to their characterization, evaluation, and pre-breeding activities. Despite the vast reservoir of genetic resources stored in genebanks, only a meager 10% has been utilized in crop improvement programs, primarily due to poor characterization and evaluation data as well as insufficient pre-breeding researches (Hodgkin et al 2003, Nguyen and Norton 2020). Nepal Genebank has conserved 1055 finger millet accessions but we only evaluated 19 landraces selected from 300 previously characterized landraces in comparatively larger plots, which is not sufficient to identify the high yielding elite genotypes from the country's total genetic diversity.

All agronomic traits showed significant differences between genotypes. Two landraces, NGRC04849 and NGRC01497, produced grain yield that was statistically comparable to the check variety Kabre kodo-2. The genotypes that produced significantly higher grain yield also produced significantly higher straw. NGRC01483 from Okhaldhunga was the earliest genotype to flower two weeks earlier than the released variety Kabre kodo-2. Heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40-59% are medium and values less than 40% are low (Singh 2001). We observed low to medium level of h^2 bs indicating that the inheritance of these traits mostly controlled by environmental variation. Previous researcher reported higher heritability in finger millet as compared to our estimates. Lower estimates of h^2 bs in our study may be due to smaller

number of genotypes, smaller plot size and single location (Teklu et al 2014). This suggest the need of evaluation in multiple locations with larger plot size for effective selection of genotypes. Genetic advance as percentage of mean (GAM) values less than 10% are considered as low, 10-20% are moderate and more than 20% are high (Johnson et al 1955). Based on this demarcation, the high genetic advance was estimated for straw yield in 2020 and for grain yield in both the years. (Sharma et al 2022) reported higher h^2 bs and GAM in finger millet as compared to our estimates. Our observations revealed strong positive correlations between grain and straw yield, heading and maturity days, and neck and finger blast. Additionally, we noted a strong positive correlation between grain yield and the number of heads/m², straw yield and the number of heads/m² as well as straw yield and plant height. We also found a strong negative correlation between days to maturity and neck blast ($r=-0.44$) and finger blast ($r=-0.42$), suggesting that early maturing genotypes have greater blast resistance. Previous research has also indicated a positive correlation between grain yield with straw yield, plant height and number of heads/m² as well as between flowering and maturity days (Bastola et al 2015, Bharati 2011, Kandel et al 2019, Lule et al 2012, Patel et al 2017).

Despite being Nepal's fourth most important cereal, the cultivation area of finger millet has declined over the past decade due to a lack of high-yielding varieties available to farmers. Research by (Anuradha et al 2022) on Indian genotypes and (Wolie and Belete 2012) on Ethiopian genotypes also identified some promising genotypes with a grain yield exceeding 3000 kg ha⁻¹. Since Nepal is a member of the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA), high-yielding genetic resources from outside the country could be introduced through the multilateral system, and crossing between Asian and African genotypes could help to develop high-yielding lines and exploit the extensive genetic variability to improve finger millet productivity in the country.

CONCLUSION

We identified some promising landraces of finger millet from pre-breeding experiments. As compared to the released variety Kabre kodo-2, genotypes NGRC04849 from Rukum and NGRC01497 from Jajarkot were statistically at par for both grain and straw yield. NGRC01483 from Okhaldhunga was the earliest flowering genotype which flowered two weeks earlier than Kabre kodo-2. NGRC03484, NGRC04769, NGRC04804 and NGRC04852 from Dhading, Ilam, Dolakha and Sindhupalchok, respectively were found as resistant genotypes for the both neck and finger blast. These promising landraces need to be included under national coordinated varietal trials by HCRP throughout the mid-hills of Nepal.

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Authors' Contributions

KHG was involved in conceptualizing, designing and implementing this research. RPM, PT, MB, KG, and BKJ were responsible for the literature review and provided critical feedback on the manuscript. All authors read and approved the final manuscript.

Conflicts of Interest

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

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REFERENCES

- Anuradha N, TSSK Patro, A Singamsetti, Y Sandhyarani, U Triveni, A Nirmalakumari, N Govanakoppa, T Lakshmipathy and VA Tonapi. 2022. Comparative study of AMMI- and BLUP-based simultaneous selection for grain yield and stability of finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes. *Front. Plant Sci.* **12**:786839. DOI: <https://doi.org/10.3389/fpls.2021.786839>
- Bastola BR, MP Pandey, BR Ojha, SK Ghimire and K Baral. 2015. Phenotypic diversity of Nepalese finger millet (*Eleusine coracana* (L.) Gaertn) accessions at IAAS, Rampur, Nepal. *Int. J. Appl. Sci. Biotechnol.* **3**(2):285-290. DOI: <https://doi.org/10.3126/ijasbt.v3i2.12413>
- Bharathi A. 2011. Phenotypic and genotypic diversity of global finger millet (*Eleusine coracana* (L.) Gaertn) composite collection. PhD Dissertation, Tamil Nadu Agricultural University, Coimbatore, India.
- Bora P. 2013. Nutritional properties of different millet types and their selected products. MS Thesis, University of Guelph, Ontario, Canada.
- Chandra D, S Chandra, Pallavi and AK Sharma. 2016. Review of Finger millet (*Eleusine coracana* (L.) Gaertn): A power house of health benefiting nutrients. *Food Science and Human Wellness* **5**:149-155. DOI: <http://dx.doi.org/10.1016/j.fshw.2016.05.004>
- Devi PB, VR Bharathi, S Sathyabama, NG Malleshi and VB Priyadarisini. 2011. Health benefits of finger millet (*Eleusine coracana* L.) polyphenols and dietary fiber: a review. *J. Food Sci. Technol.* **51**:1021-1040. DOI: <https://doi.org/10.1007/s13197-011-0584-9>
- Gaihre S, D Gauchan and KP Timsina. 2021. Prospect and potentiality of finger millet in Nepal: Nutritional security and trade perspective. *J Agric. Nat. Res.* **4**(2):63-74. DOI: <https://doi.org/10.3126/janr.v4i2.33657>
- Genebank. 2021. Annual Report 2077/78 (2020/21) (BK Joshi, KH Ghimire, A Karkee, RP Mainali, P Thapa and SK Shrestha, eds). National Agriculture Genetic Resources Center (Genebank), NARC, Khumaltar, Lalitpur, Nepal.
- Genebank. 2022. Annual Report 2078/79 (2021/22) (KH Ghimire, A Karkee, M Bhattarai, RP Mainali, P Thapa and SK Shrestha, eds). National Agriculture Genetic Resources Center (Genebank), NARC, Khumaltar, Lalitpur, Nepal.
- Ghimire KH, B Bhandari, SB Gurung, NB Dhami and BK Baniya. 2017. Diversity and utilization status of millets genetic resources in Nepal. **In:** Proceedings of 2nd National Workshop on Conservation and Utilization of Agricultural Plant Genetic Resources in Nepal (BK Joshi, HB KC and AK Acharya, eds), 22-23 May 2017 Dhulikhel; NAGRC, FDD, DoA and MoAD; Nepal.
- Ghimire KH, HK Manandhar, MP Pandey, BK Joshi, SK Ghimire, A Karkee, SB Gurung, NH Ghimire and D Gauchan. 2022. Multi-environment screening of Nepalese finger millet landraces against blast disease [*Pyricularia grisea* (Cooke) Sacc.]. *Journal of Nepal Agricultural Research Council* **8**:35-52. DOI: <https://doi.org/10.3126/jnarc.v8i.44874>
- Ghimire KH, MP Pandey, BK Joshi, SK Ghimire, HK Manandhar and D Gauchan. 2023. Phenotypic diversity among finger millet (*Eleusine coracana* (L.) Gaertn.) landraces of Nepal. *Genetic Resources* **4**(8):1-14. DOI: <https://doi.org/10.46265/genresj.MYZA2446>

- Goron TL, VK Bhosekar, CR Shearer, S Watts and MN Raizada. 2015. Whole plant acclimation responses by finger millet to low nitrogen stress. *Front. Plant Sci.* **6**:652. DOI: <https://doi.org/10.3389/fpls.2015.00652>
- Hilu KW, JMJ deWet and R Harlan. 1979. Archaeobotanical studies of *Eleusine coracana* ssp. *coracana* (Finger millet). *Amer. J. Bot.* **66**(3):330-333. DOI: <https://doi.org/10.2307/2442610>
- Hittalmani S, HB Mahesh, MD Shirke, H Biradar, G Uday, YR Aruna, HC Lohithaswa and A Mohanrao. 2017. Genome and transcriptome sequence of finger millet (*Eleusine coracana* (L.) Gaertn) provides insights into drought tolerance and nutraceutical properties. *BMC Genomics* **18**:1-16. <https://doi.org/10.1186/s12864-017-3850-z>
- Hodgkin T, VR Rao, A Cibrian-Jaramillo and S Gaiji. 2003. The use of ex-situ conserved plant genetic resources. *Plant Genet Res* **1**(1):19-29. DOI: <https://doi.org/10.1079/PGR200313>
- IBPGR. 1985. Descriptors for finger millet. International Board for Plant Genetic Resources **23p**. IBPGR Secretariat, Rome, Italy. <https://hdl.handle.net/10568/72880>
- Johnson HW, HF Robinson and RE Comstock. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* **47**: 314-318. DOI: <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Joshi BK, D Joshi and SK Ghimire. 2020. Genetic diversity in finger millet landraces revealed by RAPD and SSR markers. *Nepal J Biotechnol.* **8**(1):1-11. DOI: <https://doi.org/10.3126/njb.v8i1.30204>
- Kandel M, NB Dhami and J Shrestha. 2019. Phenotypic diversity of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. *Malaysian Journal of Sustainable Agriculture* **3**(2):20-26. DOI: <http://doi.org/10.26480/mjsa.02.2019.20.26>
- Kumar A, M Metwal, S Kaur, AK Gupta, S Puranik, S Singh, M Singh, S Gupta, BK Babu, S Sood and R Yadav. 2016. Nutraceutical value of finger millet [*Eleusine coracana* (L.) Gaertn] and their improvement using omics approaches. *Front. Plant Sci.* **7**:934. DOI: <https://doi.org/10.3389/fpls.2016.00934>
- Lule D, K Tesfaye, M Fetene and S deVilliers. 2012. Multivariate analysis for quantitative traits in finger millet (*Eleusine coracana* subsp. *coracana*) population collected from eastern and southern Africa: detection for patterns of genetic diversity. *Int. J. Agric. Res.* **7**(6):303-314. DOI: <https://doi.org/10.3923/ijar.2012.303.314>
- MINITAB. 2010. Minitab 17 Statistical Software. State College, Pennsylvania: Minitab, Inc. <https://www.minitab.com>
- MOAFE. 2026. Statistical Information on Nepalese Agriculture 2081/82 (2024/2025). Government of Nepal. Ministry of Agriculture, Forests and Environment. Singhadurbar, Kathmandu, Nepal. <https://www.moafe.gov.np/category/statistics-related-to-agriculture/>
- Nakarani UM, D Singh, KP Suthar, N Karmakar, P Faldu and HE Patil. 2020. Nutritional and phytochemical profiling of nutraceutical finger millet (*Eleusine coracana* L.) genotypes, *Food Chemistry*. DOI: <https://doi.org/10.1016/j.foodchem.2020.128271>
- Nguyen GN and SL Norton. 2020. Genebank Phenomics: A Strategic Approach to Enhance Value and Utilization of Crop Germplasm. *Plants* **9**:817. DOI: <https://doi.org/10.3390/plants9070817>
- O’Kennedy MM, A Grootboom and PR Shewry. 2006. Harnessing sorghum and millet biotechnology for food and health. *J. Cereal Sci.* **44**(3):224–235. DOI: <https://doi.org/10.1016/j.jcs.2006.08.001>
- Patel SN, HE Patil and RC Popat. 2017. Genetic diversity study in finger millet (*Eleusine coracana* L.) genotypes: A multivariate analysis approach. *Int. J. Pure App. Biosci.* **5**(5):183-189. DOI: <http://dx.doi.org/10.18782/2320-7051.5430>

- Popat R, R Patel and D Parmar. 2020. Package 'variability': Genetic Variability Analysis for Plant Breeding Research. R package version 0.1.0. <https://cran.r-project.org>
- R Core Team. 2020. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. <https://www.r-project.org>
- Sharma N, BB Bandyopadhyay, S Chand, PK Pandey, DC Baskheti and BK Alam. 2022. Genetic diversity, trait association and cause effect analysis in selected genotypes of finger millet [*Eleusine coracana* (L.) Gaertn.]. J. Environ. Biol. **43**:551-561. DOI: <http://doi.org/10.22438/jeb/43/4/MRN-2052>
- Singh BD. 2001. Plant Breeding: Principles and Methods. 6th ed, Kalyani Publishers, New Delhi, India.
- SQCC. 2022. Notified and de-notified varieties till 2079/05/30. Seed Quality Control Center, Ministry of Agriculture and Livestock Development. Hariharbhawan, Lalitpur, Nepal. <https://www.sqcc.gov.np>
- Teklu DH, SA Kebede and DE Gebremichael. 2014. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Asian Journal of Agricultural Research **8**:181-194. DOI: <https://doi.org/10.3923/ajar.2014.181.194>
- Upadhyaya HD, CLL Gowda and GV Reddy. 2007. Morphological diversity in finger millet germplasm introduced from southern and eastern Africa. J. SAT Agric. Res. **3**(1):1-3. http://oar.icrisat.org/2656/1/Morphological_diversity_in_finger.pdf
- Upadhyaya HD, CLL Gowda, RPS Pundir, GV Reddy and S Singh. 2006. Development of core sub set of finger millet germplasm using geographical origin and data on 14 quantitative traits. Genet. Resour. Crop Evol. **53**:679-685. DOI: <https://doi.org/10.1007/s10722-004-3228-3>
- Upadhyaya HD, NDRK Sarma, CR Ravishankar, T Albrecht, Y Narasimhudu, SK Singh, SK Varshney, VG Reddy, S Singh, SL Dwivedi, N Wanyera, COA Oduori, MA Mgonja, DB Kisandu, HK Parzies and CLL Gowda. 2010. Developing a mini-core collection in finger millet using multilocation data. Crop Sci. **50**:1924-1931. DOI: <https://doi.org/10.2135/cropsci2009.11.0689>
- Upadhyaya HD, S Ramesh, S Sharma, SK Singh, SK Varshney, NDRK Sarma, CR Ravishankar, Y Narasimhudu, VG Reddy, KL Sahrawat, TN Dhanalakshmi, MA Mgonja, HK Parzies, CLL Gowda and S Singh. 2011. Genetic diversity for grain nutrients contents in a core collection of finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm. Field Crops Research **121**:42-52. DOI: <https://doi.org/10.1016/j.fcr.2010.11.017>
- Vetriventhan M, HD Upadhyaya, SL Dwivedi, SK Pattanashetti and SK Singh. 2016. Finger and foxtail millets. In: Genetic and genomic resources for grain cereals improvement (M Singh and HD Upadhyaya, eds). San Diego: Academic Press; 2016. p.291-319. DOI: <https://doi.org/10.1016/B978-0-12-802000-5.00007-1>
- Vetriventhan M, VCR Azevedo, HD Upadhyaya, A Nirmalakumari, J Kane-Potaka, S Anitha, SA Ceasar, M Muthamilarasan, BV Bhat, K Hariprasanna, A Bellundagi, D Cheruku, C Backiyalakshmi, D Santra, C Vanniarajan and VA Tonapi. 2020. Genetic and genomic resources, and breeding for accelerating improvement of small millets: current status and future interventions. Nucleus **63**:217-239. DOI: <https://doi.org/10.1007/s13237-020-00322-3>
- Wolie A and K Belete. 2012. Genetic divergence and variability studies in some Ethiopian finger millet germplasm collections. Scholarly J. Agric. Sci. **3**(4):110-116. DOI: <https://www.researchgate.net/publication/315892606>