ZIBELINE INTERNATIONAL PUBLISHING

Malaysian Journal of Sustainable Agriculture (MJSA)

DOI : http://doi.org/10.26480/mjsa.02.2019.20.26

ISSN: 2521-2931 (Print)
ISSN: 2521-294X (Online)
CODEN : MJSAEJ

CrossMark

RESEARCH ARTICLE

PHENOTYPIC DIVERSITY OF FINGER MILLET (*Eleusine coracana* (L.) Gaertn.) GENOTYPES

Manoj Kandel[1*], Narayan Bhadhur Dhami[1], Jiban Shrestha[2]

[1]Nepal Agricultural Research Council, Hill Crops Research Program (HCRP), Baiteshwor-4, Dolakha, Nepal
[2] Nepal Agricultural Research Council, Agriculture Botany Division (ABD), Khumaltar, Lalitpur, Kathmandu, Nepal
****Corresponding author email: manojkandel24@gmail.com***

ARTICLE DETAILS

Article History:

Received 1 January 2019
Accepted 19 February 2019
Available online 22 February 2019

ABSTRACT

An experiment was conducted at Hill Crops Research Program (HCRP), Kabre, Dolakha under Nepal Agricultural Research Council, Nepal (NARC), during rainy season of 2018 with objective to identify the level of genetic difference present in the finger millet genotypes being cultivated for selecting genotypes in different agro-climatic region in Nepal using descriptive statistics, correlation analysis, cluster analysis and principle component analysis. P value of REML procedure revealed that significant variation was observed in 16 finger millet genotypes for baring head, days to 50% flowering, days to 50 % heading, days to 75 % maturity, finger length, flag leaf length, plant stand, plant height, number of finger, peduncle length, no of productive tiller, thousand grain weight, grain yield and straw yield showed selection and development of suitable varieties for different agro-climatic region of Nepal. Traits baring head, finger length, number of fingers, flag leaf length, peduncle length, productive tiller, thousand kernel weight, plant stand, straw yield were positively correlated with grain yield revealed that selection within this is importance for improvement grain yield. Cluster I consists up six early mature genotypes named as KLE-178,GE-0383, ACC#6022,GE-0382,KLE-0150,ACC#0124 can be used to development of early mature genotypes for mountain regions where chilling stress occurs at maturity period whereas similarly cluster II, III and IV consisted up 10 late mature genotypes named as ACC#2843, ACC#2860, ACC#8827-1,Sailung-Kodo-1,NE-1703-34,KLE-236,ACC#2311,GE-0356, farmer's variety, GE-0480 can be used to develop high yielding late mature varieties for mid hill and terai regions these genotypes may be of interest to researcher for selection of materials for breeding program in different agro-climatic region of Nepal.

KEYWORDS

Genetic variation, Traits, Multivariable analysis, Genotypes, Finger millet

1. INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn*)* (2n=4x=36) is most important small minor grain cereals grain crop which is suitable for traditional low input-based cereals farming system [1]. In world it is ranks 4th among the most grown cereals after pearmillet, sorghum and prossomilet and foxtail millet and in Nepalese context it is also ranked 4th position in the case of production (2,66,799 hectare), total production (3,02,397M tons) and productivity after paddy, maize and wheat [2]. It is grown in marginal land of tropical to subtropical areas of world due to its hardy nature and in our context, it grown up to 3150 m due to rich in finger millet genotypes diversity [3]. It has been found large diversity in various region of Nepal about 790 accessions including two wild species—E. indicaand E. aegyptica [4]. Its variety improvement is most possible area in our context due to rich at both varietal and population levels [5]. In this scenario changing climatic scenario, finger millet taking into consideration scope for increasing the areas due to adaptability to is suited for low and marginal lands and also for harsh weather conditions. Thus, phenotypic variability evaluation is one of importance steps for drawing meaningful conclusions for its crop improvement [6,7]. Nutritional values of finger millet contain, moisture 13.24%, protein 7.6%, carbohydrate 74.36%, fiber 1.52%, minerals 2.35%, fat 1.35%, energy 341.6 cal/100g [8]. It is rich in micronutrient such calcium and iron in other cereals crops so it helps to alleviation of malnutrition and anemia in countries where it is widely consumed as a staple food [9]. Due to its nutritional awareness to public and more focuses research in major cereals it gets less importance in breeding program [10].

But now days because of its nutritional and health benefits awareness, Plant breeders give more attention for its research. The status of finger millet is now changing from neglected and underutilized crop to future smart crops for health food and functional food product with high value. For breeding programs of crop improvement information on genetic variation in the landraces, accession and genotypes is a must essential [11,12]. Grain yield is dependent traits and selection based on yield attributing traits help plant breeder indirectly improve yield [13]. Thus, rich at both varietal and population levels this crop indicates there is much scope for crop improvement [14].

The aim of this study was to conduct to know the availability of genetic diversity in the available accessions or genotypes. The objective of this study was to determine genetic variations in 16 finger millet genotypes for quantitative traits, which may contribute to formulation of suitable selection indices for crop improvement as well as will identify the level of genetic difference present in the finger millet genotypes being cultivated for selecting genotypes in different agro-climatic region in Nepal.

Table 1: Comparison of nutritional values of finger millet and other cereals.

Crop Product	Amount of Nutrients per 100 gram raw grain				
	Carbohydrate(g)	**Protein (g)**	**Fiber (g)**	**Iron (mg)**	**Calcium (mg)**
Finger millet	**72**	**7.3**	**3.6**	**3.9**	**344**
Buckwheat	72	13.3	1.7	2.3	18
Barley	74	13.6	2.4	1.7	26
Amaranthus	68	9.4	2.2	5.2	37
Foxtailmillet	66	12.3	8	2.8	31
Prosomillet	73	12.5	2.2	3	14
Sorghum	72	8.5	1.6	11.2	22
Potato	23	1.6	0.6	0.5	10
Rice	78	6.8	0.2	0.7	10
Maize	72	9.2	-	1.2	
Wheat	71	11.8	1.2	5.3	41

Source: Nutritive value of Nepali Foods: National Nuritional Program 2061, Nutritive Value of Indian Foods, NIN, 1993. Millets: Future Food and Farming, India

2. MATERIALS AND METHODS

The field experiment was conducted on finger millet research field at Hill Crop Research Program (HCRP), Kabre, Dolakha under Nepal Agricultural Research Council, Nepal (NARC), during rainy season of 2018. Dry nursery beds were established of each genotype on July 2018. Each nursery row was 1 m in length and applied with equal amount of farmyard manure. No chemical fertilizers were applied on nursery beds. The seed rate was 10 kg ha-1. The age of seedlings was 27 days during transplanting. The field experiment was conducted in Random complete block design (RCBD) with three replications. Each replication comprised of sixteen blocks/plots. Randomization of experimental materials was done with the software CROPSTAT. The plot size was 6 m2. Seeding was done continuously by manually and seed rate was 10 kg/ha Fertilizers were applied at the rate of 30:30:0kg/ha N: P2O5: K2O respectively and in addition to this 10-ton farmyard manure per hectare as applied before one month of sowing [16].

Half dose of N and full doses of P and K were applied basal dose and remaining half of N was applied as side dressing at tillering growth stage. Transplanting of 2-3 seedlings per hill was done on 13th July. with a spacing of 10cm between rows and 10 cm between hills. There was a gap of 0.5m between plots and 2 m between replications. Bunds were constructed between the plots and replications. Weeds are the major problem in finger millet, especially during 2-3 weeks after sowing. The plots were kept free of weeds manually. Data 14 quantitative (days to heading, days to flowering, days to maturity, flag leaf length, finger length, Plant stand per square meter, peduncle length, bearing head per square meter, productive tillers number per plant, plant height, finger number per ear, thousand kernel weight, straw yield per plot, grain yield per plot) traits were recorded following finger millet descriptors [17]. Grain yield was recorded for net harvested area.

Each plot was harvested excluding border rows and grain moisture content for each plot was recorded and grain yield was adjusted to 12 % moisture basis. The grain yield per plot was converted into ton/ha by using formula as given below [17]. The data recorded on different parameters from field were first tabulated and processing in Microsoft excel (MS- Excel, 2010), then subjected GenStat to obtain ANOVA and all values were expressed as mean values. Correlation coefficients of different traits using SPSS program were carried out using the formula [18]. Hierarchical clustering using Ward's minimum-variance method with squared Euclidean distance and principal component analysis using correlation matrix for 14 quantitative characters was performed using MINITAB 14 software [19]. P values less than 0.05 and 0.01 were considered statistically significant and statistically highly significant, respectively.

$$\text{Grain yield}\left(\frac{t}{ha}\right) = \frac{\text{Yield of plot(kg)} \times 10 \times (100 - \text{Grain moisture})}{\text{Net harvested area(m2)} \times (100 - 12)}$$

Table 2: Names genotypes of finger millets used for research at HCRP (2018).

S. N	Name of genotypes	S.N.	Name of genotypes	S.N.	Name of genotypes
1	KLE-178	7	GE-0356	13	ACC#8827-1
2	ACC#2843	8	KLE-0150	14	ACC#2860
3	GE-0383	9	KLE-236	15	ACC#2311
4	ACC#6022	10	GE-0480	16	Farmer's variety
5	GE-0382	11	ACC#0124		
6	Sailung-Kodo-1	12	NE-1703-34		

3. RESULTS

3.1 Analysis of Variance

The result of ANOVA of fourteen yield related traits for sixteen genotypes is presented in Table 2. The ANOVA showed highly significant difference ($p<0.01$) among the tested genotypes for all characters except for days to flowering and plant height showed significant difference ($p<0.05$) indicating the presence of variability which can be exploited through selection. Thus, there is ample scope for selection for finger millet improvement. Mean, F-test value, least significant value (LSD 0.05) and coefficient of variation (CV %) for fourteen characters were presented in Table 3. Variation in grain yield was high, genotypes GE-0356 had produces maximum grain yield (0.8533 t/ha) fallowed by Sailing kodo-1 (0.78 t/ha) and GE-0480(0.76 t/ha). Days to flowering and days to maturity were ranges of KLE-178(79) - ACC# 0124 (90) days and Local (130) - KLE-0150 (143) days, respectively. These traits showed high variation and selection of maturity classes that are suitable for cropping system is possible.

Growth characters showed high variation ranging from ranging from KLE-236 (7.67)–Sailung kodo-1 (11.67) cm in flag leaf length, KLE-236(70.90)-ACC#2311 (137.1) cm in plant height, KLE-178 (3)– GE-0382(6) in productive tiller number and ACC#6022(59.33) –ACC#2311(71) in plant stand per meter square. Yield attributing traits showed high variation ranging from GE-0383(69)- Sailung Kodo-1 (114) in bearing head per square meter, KLE-178 (5.0) –ACC#2311 (9.3) in number of finger per head,NE-1703-34 (2.6) – GE-0480(3.4) gram in thousand grain weight and Farmer's (local) variety (7.94)–GE-0480 (10.78) ton per hectare in straw yield. Studying the variation among agronomic and yield attributing traits of finger millet genotypes is very important for every breeding program as the most of them are highly correlated and have direct effect on yield, they can either affects yield positively or negatively depending upon their variation. High variability existing in these genotypes brings forward the much-needed information for genetic improvement program of finger millet. Thus, measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of phenotypic observations [6,7]. A researcher also observed substantial variation among finger millet entries has also been reported in previous studies [10]. Other researchers also reported that significant difference in the results would be due to the inclusion of diverse accessions in Asia in this study especially those from India [20]. Thus, basic objective of study the analysis of variance in any breeding program is the improvement of crop yield and quality for increases productivity of that crop association of character.

Estimates of phenotypic correlation coefficient for most of characters are presented in Table 4. Grain yield per plot had positive and significant phenotypic association with baring head, finger length, number of fingers per head, flag leaf length, peduncle length, productive tiller, thousand kernel weight, plant stand, straw yield. Similarly, the positive and significant association of straw yield with plant height, number of fingers per head, days to 50 % flowering, days to maturity.

Table 3: Mean, F-test, coefficient of variation and least significant difference for yield and yield attributing traits among 16 genotypes of Finger millet (*Eleusine coracana* L. Gaertn)

Entries	BH	DAF	DOH	DTM	FL	FLL	PS	PH	NF/H	PL	PT	TGW	GY	SY
KLE-178	**77**	**85**	**79**	**133**	**7.00**	**8.67**	**62.33**	**114.90**	**5.10**	**17.33**	**3.0**	**3.00**	**0.3767**	**8.33**
ACC#2843	97	81	74	139	7.67	8.67	67.33	110.10	5.17	18.67	4.3	2.90	0.6411	9.22
GE-0383	**69**	**89**	**82**	**137**	**8.33**	**10.00**	**61.00**	**126.00**	**6.40**	**21.33**	**4.3**	**3.27**	**0.6811**	**8.89**
ACC#6022	**82**	**89**	**82**	**136**	**7.00**	**8.00**	**59.33**	**109.80**	**6.77**	**16.00**	**3.3**	**3.07**	**0.4517**	**10.33**
GE-0382	**102**	**86**	**80**	**136**	**9.67**	**11.33**	**69.00**	**117.30**	**7.27**	**21.67**	**6.0**	**3.17**	**0.8533**	**9.11**
Sailung-K.1	114	88	82	137	10.00	11.67	69.67	127.30	7.40	22.33	5.0	3.40	0.7811	9.50
GE-0356	77	79	72	137	8.33	10.00	64.67	113.20	7.43	18.33	3.7	2.63	0.5567	8.56
KLE-0150	**111**	**87**	**80**	**143**	**9.67**	**10.33**	**68.00**	**107.40**	**7.70**	**20.33**	**4.0**	**3.10**	**0.7000**	**6.94**
KLE-236	91	88	81	140	6.67	7.67	68.33	70.90	8.17	21.67	4.0	3.10	0.6256	8.44
GE-0480	87	88	82	139	9.33	10.67	62.00	112.40	8.40	18.33	4.3	3.40	0.7683	10.78
ACC#0124	**98**	**90**	**84**	**137**	**6.33**	**8.00**	**63.33**	**109.40**	**8.43**	**18.33**	**3.3**	**3.30**	**0.5389**	**8.00**
NE-1703-34	95	80	73	132	7.00	8.33	61.67	123.30	8.47	16.67	3.3	2.60	0.4528	8.67
ACC#8827-1	95	82	75	139	7.00	8.67	62.00	115.00	8.83	17.33	4.0	3.20	0.5289	9.44
ACC#2860	112	83	75	139	9.33	10.33	69.00	105.00	9.03	19.00	4.0	3.00	0.7100	8.61
ACC#2311	109	83	76	134	8.00	8.67	71.00	137.10	9.30	18.00	4.7	3.10	0.6917	8.56
Local variety	82	81	75	130	7.33	9.00	69.33	123.20	6.40	18.00	3.7	3.20	0.5289	7.94
G.Mean	94	85	78	137	8.04	9.38	65.50	113.90	7.51	18.96	4.1	3.09	0.6180	8.83
F-test	<.001	0.003	<.001	<.001	<.001	<.001	<.001	0.028	<.001	<.001	<.001	<.001	<.001	<.001
CV(%)	3.1	4.2	3.8	2.71	10.2	8.6	3.1	14.5	0.69	7	14.3	4.8	6.4	5.6
LSD($_{0.05}$)	4.84	5.8	5.02	1.2	1.3	1.33	3.4	27.5	5.5	2.2	0.96	0.24	0.066	0.831

BH=Baring Head per square meter, DAF= Days to 50% flowering, DOH=Days to 50 % Heading, DTM= Days to 75 % maturity,FL=finger length(cm),FLL=flag leaf length(cm), PS=plant stand per square meter,PH=Plant height(cm), NF/H=Number of finger per head,PL=Peduncle length(cm),PT=No of productive tiller,TGW=Thousand grain weight (gram),GY=Grain yield (t/ha), SY= Straw yield (t/ha),CV=coefficient of variation (%), LSD=least significant difference at 0.05.<.005 significant at 0.05% level,<.001 significant at 0.01% level.

Table 4: Pearson's Correlation coefficient among thirteen traits of fifty sixteen genotypes of finger millet landraces, at HCRP, Dolakha (2018)

	BH	DAF	DOH	DTM	FL	FLL	GY	NF/H	PL	PT	TGW	PS	PH
DAF	0.005	1											
DOH	-0.023	0.989**	1										
DTM	0.336	0.351	0.273	1									
FL	0.454	0.111	0.106	0.364	1								
FLL	0.304	0.104	0.127	0.237	0.951**	1							
GY	0.512*	0.268	0.258	0.460	0.820**	0.756*	1						
NF/H	0.517*	0.008	-0.041	0.325*	0.105	0.022	0.367*	1					
PL	0.280	0.410	0.405	0.412	0.566*	0.579*	0.747*	-0.023	1				
PT	0.437	0.117	0.133	0.208	0.685*	0.671*	0.884**	0.129	0.683**	1			

TGW	0.140	**0.715***	**0.748****	0.204	**0.256***	0.306	**0.463***	0.083	0.414	0.375	1		
PS	**0.650***	-0.195	-0.187	0.061	0.429	0.324	**0.565***	0.158	**0.513***	**0.562***	0.104	1	
PH	0.035	-0.243	-0.192	**-0.539***	**0.343***	0.316	0.054	-0.047	-0.196	0.214	0.066	-0.002	1
SY	-0.179	**0.217***	0.182	**0.222***	**0.307***	0.148	**0.253***	**0.210***	-0.160	0.218	0.243	-0.403	**0.197***

BH=Baring Head per square meter,DAF= days to 50% flowering,DOH=days to 50 % Heading,DTM= days to 75 % maturity,FL=finger length,FLL=flag leaf length,GY=Grain yield,NF/H=Number of finger per head,PL=Peduncle length,PT=No of productive tiller,TGW=Thousand grain weight, PS=plant stand per square meter,PH=Plant height, SY=Straw yield.** significant at 0.05% level,** significant at 0.01% level.

3.2 Cluster analysis

All the entries were clustered using baring head, days to 50 % flowering, days to 50 % heading, days to 75% maturity, finger length, flag leaf length, number of fingers per head, peduncle length, productive tiller, thousand kernel weight, plant stand per square meter, plant height, grain yield and straw yield as variable. The dendrogram reveled four clusters with minimum 39.13% similarity level in UPGMA clustering. The distance between the cluster centroid was found highest between cluster 3 and 4. and lowest between cluster 1and 2. The cluster was divided in Group A and Group B.Th. Group A consisted of two cluster named as Cluster I and cluster IV whereas Group B consisted of two cluster named as Cluster II and III.

Cluster I consisted of 6 genotypes named as KLE-178, GE-0383ACC#6022, GE-0382, KLE-0150, ACC#0124 which represent 37.5% of total genotypes. The genotypes of in this cluster had high straw yield and lower value for number of fingers per head, peduncle length, productive tiller, plant stand per square meter. This cluster had lower grain yield as compared to other cluster under study condition.

Cluster II consisted of 7 genotypes named as ACC#2843, ACC#2860, ACC#8827-1, Sailung-K.1, NE-1703-34, KLE-236, ACC#2311which represented 43.75 % of total genotypes. The genotypes grouped in this cluster had shorter days to 50% flowering and other intermediate traits values. These genotypes due to shorter days to 50 % flowering and maturity classes that is suitable for different cropping system is possible.

Cluster III consisted of 2 genotypes named as GE-0356, Local variety which represented 12.5 % of total genotypes. This cluster III genotypes had high value for bearing head, finger length, flag leaf length, number of finger per head, productive tiller, thousand kernel weight, plant stand, plant height and grain yield. Since this cluster of lines had superior traits value for study condition, these lines may be of interest to researchers.

Cluster IV consisted up 1 genotype named as GE-0480 which represented 6.25% of total genotypes had high value for days to 50 % flowering, Days to 50 % heading, days to 75 % maturity and peduncle length whereas lower value for finger length, flag leaf length, plant height and straw yield. Grouping accessions with related morphological traits is very critical in every breeding program so as to understand and to have basic information on which and how many accessions possess traits of importance. Group information on which a superior accession with economic traits belong will in future help to check more accessions from the same group with similar or closely related economic traits and further be used in finger millet breeding program [21].

Evaluation of genetic variation based on morphological characters has proved to be very informative enough and can also be manipulated into either selecting superior accessions or to be utilized to select parents for a breeding program [22,23].

Table 5: Distance among the different cluster centroid of 16 genotypes of Finger millet (*Eleusine coracana* L. Gaertn).

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	0	23.4758	36.9069	48.0874
Cluster II		0	22.7882	43.5687
Cluster III			0	65.0195
Cluster IV				0

Table 6: Cluster mean of yield and yield attributing traits among 16 genotypes of Finger millet (*Eleusine coracana* L. Gaertn).

Variable	Cluster I	Cluster II	ClusterIII	Cluster IV	Centroid
No of genotypes	6	7	2	1	20
Bearing head	79	101.7	111.5	91	93.7
Days to flowering	85.1	84.1	85.5	88	84.9
Days to heading	78.6	77.2	79	81	78.2
Days to maturity	135.3	137.8	135.5	140	136.7
Finger length	7.88	8.09	9	6.67	8.04
Flag leaf length	9.39	9.38	10.17	7.67	9.37
Grain yield	0.56	0.63	0.73	0.63	0.61
Number of finger per head	6.75	7.843	8.35	8.17	7.517
Peduncle length	18.22	18.85	20.16	21.67	18.95
Productive tiller	3.7	4.1	4.8	4	4.0
Thousand grain weight	3.09	3.03	3.25	3.1	3.09
Plant stand	63.11	65.76	70.33	68.33	65.49
Plant height	116.5	112.5	132.2	70.9	113.8
Straw yield	9.13	8.57	9.03	8.44	8.83

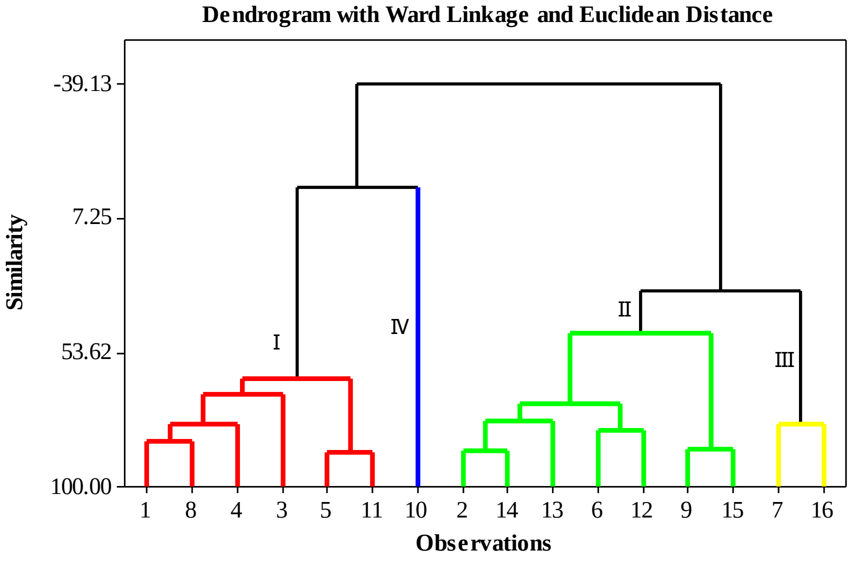

Figure 1: Cluster analysis of yield and yield attributing traits among 16 genotypes of Finger millet (*Eleusine coracana* L. Gaertn).

The PCA showed close resemblance with clustering and partition of total variation into 4 PCs having eigen value > 1 explaining about first four principle components and first two principle components revealed that 79 % and 57% of variability among 16 finger millet accessions respectively (Figure 1 and Table 5). However, the remaining component contributed only 21 % towards total diversity for this finger millet accession. Most of variation was contributed from phonological character plant height, productive tiller, and days to flowering, days to heading, flag leaf length, peduncle length, plant stand, bearing head, number of fingers per head, straw yield, finger length and grain yield. This yield attributing traits of finger millet was correlated and can be used in selection for breeding programs. The first principle components were positively contributed by grain yield (0.418), productive tiller (0.368), peduncle length (0.366) and flag leaf length (0.341).Similarly traits Day to flowering (0.517) and days to heading (0.515) were positive contributed to second principle component. The third principle component were negative contributed by plant height (-0.554) and straw yield (-0.398) and positive contributed by days to maturity (0.389).Similarly four principle component were positive contributed by traits peduncle length(0.381) and plant stand (0.226) and negative contributed by number of finger per head(-0.677) and straw yield (-0.467) and bearing head(-0.292).Thus positive relation with grain yield with Productive tiller, Peduncle length, flag leaf length, finger length, number of finger per head, thousand kernel weight, plant stand, straw yield lead to first principle component had variability and selection within this is importance for improvement grain yield under study condition as compared to 4 principle component. The present research revealed that genotypes formed in cluster one in study condition were found most superior than cluster 4 genotypes. This finding PCA supported the result obtained by cluster analysis.

Table 7: The first four principal components of traits used for cluster analysis and PCA and the eigen analysis of the correlation matrix at HCRP, Dolakha (2018).

	Principle component			
Variable	PC1	PC2	PC3	PC4
Eigenvalue	**5.215**	2.7677	1.8258	1.2529
Proportion	0.372	0.198	0.13	0.089
Cumulative (%)	0.372	0.57	0.701	0.79
Bearing head	0.25	-0.232	0.292	-0.292
Days to flowering	0.183	0.517	0.041	0.016
Days to heading	0.181	0.515	-0.011	0.052
Days to maturity	0.216	0.152	0.389	-0.133
Finger length	0.366	-0.158	-0.173	0.01
Flag leaf length	0.345	-0.128	-0.285	0.06
Grain yield	0.418	-0.069	-0.027	-0.05
Number of finger per head	0.102	-0.097	0.281	-0.677
Peduncle length	0.355	0.053	0.113	0.381
Productive tiller	0.368	-0.135	-0.16	0.01
Thousand kernel weight	0.253	0.341	-0.124	-0.059
Plant stand	0.244	-0.335	0.226	0.226
Plant height	0.014	-0.22	-0.554	-0.104
Straw yield	0.04	0.193	-0.398	-0.467

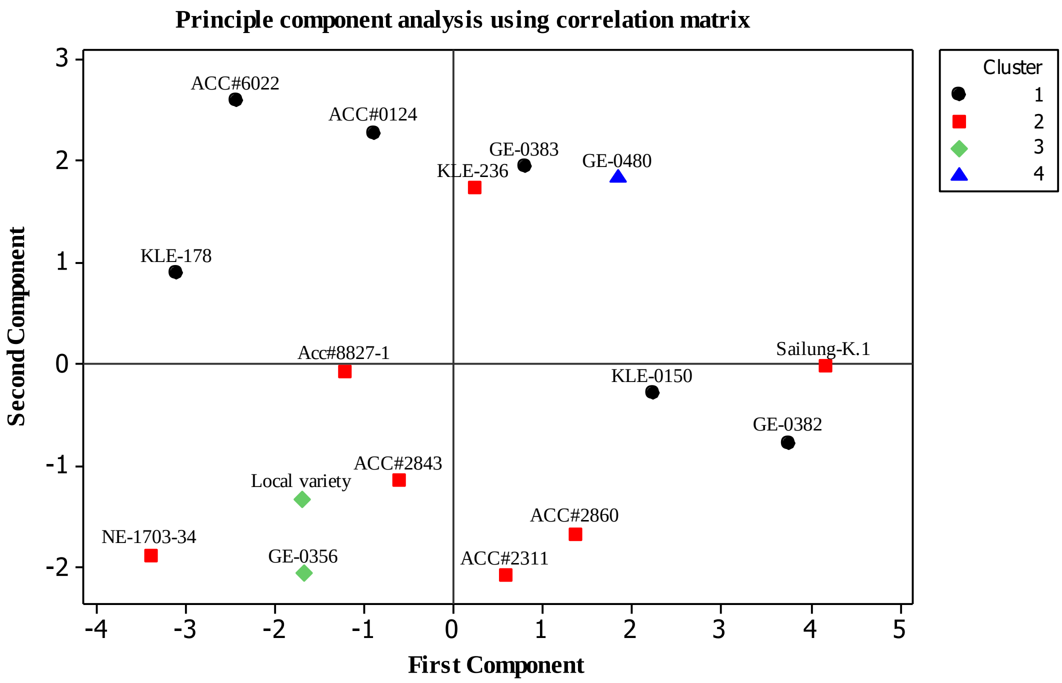

Figure 2: The score plot of first two components among 16 genotypes of Finger millet (*Eleusine coracana* L. Gaertn).

4. DISUSSION

Genotypes under study showed significant difference at P= 0.05 level of significant which indicates there is ample of variability which indicates presence of substantial variation which can be exploited through selection (Table 3) and Similar finding was also reported in previous studies [8,24]. The study showed that grain yield per plot had positive and significant phenotypic association with baring head, finger length, number of fingers per head, flag leaf length, peduncle length, productive tiller, thousand kernel weights, plant stand, straw yield. This indicates that increases in these characters may result in increases in grain yield. Found that grain yield correlated positively with straw yield [25]. Similar finding similar result between grain yield and no of finger and flag leaf length [26]. A group researcher found similar association with productive tiller number and 1000 kernel weight on finger millet [27]. The positive and significant association of straw yield with plant height, number of fingers per head, days to 50 % flowering, days to maturity indicates that these traits can be improved simultaneously through selection. Straw yield showed positive and significant phonotypic correlation with number of fingers per head and grain yield, which indicate impressing straw yield increases grain yield too. Days to flowering had high negative genotypic and phenotypic correlations with the key yield related traits of finger width, peduncle length, panicle exertion grains per spikelet, and threshing percent, corroborating results reported [28]. The positive association between plant height and finger length and number of fingers per plant in this study was also reported [29]. Among the four cluster, cluster I consists up early matured type genotypes with low productive tiller and grain yield. The genotypes of this cluster can be used to development of early mature line for mountain regions where chilling stress occurs at maturity period [30]. Similarly, cluster II, III and IV can be used to develop high yielding late mature lines for mid hill and terai regions. The clustering of genotypes based on traits value was confirmed by the principal component analysis [31]. Thus, this study of principal component uses to reduces of original variables into four principal component and information about each variable which support cluster analysis result.

5. CONCLUSION

Thus, natural variation present within genotypes is important for selection and development of suitable varieties for different agro-climatic region of Nepal. Thus, significant variation was observed in 16 finger millet genotypes for baring head, days to 50% flowering, days to 50 % heading, days to 75 % maturity, finger length, flag leaf length, plant stand, plant height, number of finger, peduncle length, no of productive tiller, thousand grain weight, grain yield and straw yield. Grain yield had positive and significant phenotypic association with baring head, finger length, number of fingers, flag leaf length, peduncle length, productive tiller, thousand kernel weight, plant stand, straw yield and selection within this is traits importance for grain yield improvement. Cluster I consist up early matured low grain yield type genotypes and these genotypes can be used to development of early mature varieties for mountain regions where chilling stress occurs at maturity period. Similarly, cluster II, III and IV can be used to develop high yielding late mature varieties for mid hill and terai regions these genotypes may be of interest to researcher for selection of materials for breeding program in different agro-climatic region of Nepal.

REFERENCES

[1] Wolie, A., Dessalegn, T. 2011. Correlation and path coefficient analysis of some yield related traits in finger millet (*Eleusine coracana* L. Gaertn) germplasms in Northwest Ethiopia. African Journal of Agricultural Research, 6, 5099-5105.

[2] MoAD. 2016/17. Statistical Information on Nepalese Agriculture. Agri business promotion and statistical division, Agristatistic section, Singhdurbar, Kathmandu.

[3] Upreti, R.P. 1999. Status of millet genetic resources in Nepal: Wild relatives of cultivated plants in Nepal. Pp. 78-82 in Wild relatives of cultivated plants in Nepal (R. Shrestha and B. Shrestha, eds.). Proceedings of National conference on wild relatives of cultivated plants in Nepal, 2–4 June 1999, Kathmandu. Green Energy Mission (GEM), Kathmandu, Nepal.

[4] Upadhyay, M.P., Joshi, B.K. 2003. Plant genetic resources in SAARC countries: Their conservation and management. pp. 297-422, Nepal chapter. SAARC Agriculture Information Center.

[5] Baniya, B.K., Riley, K.W., Dongol, D.M.S., Sherchand, K.K. 1992. Characterization of Nepalese hill crops landraces (Barley, Buckwheat, Finger millet, Grain Amaranth, Foxtail, Proso and Barnyard millets). NARC-IBPGR, Kabre, Dolakha, Nepal.

[6] Joshi, A.K., Kumari, M., Singh, V.P., Reddy, C.M., Kumar, S., Rane, J., Chand, R. 2007. Stay Green Trait: Variation, inheritance and its association with spot blotch resistance in spring wheat (TriticumaestivumL.). Euphytica, 153, 59-71.

[7] Reddy, C.V.C.M., Reddy, Y.R. 2011. Genetic parameters for yield and quality traits in desi cotton (GossypiumarboreumL). Journal of Cotton Research and Development, 25, 168-170.

[8] Chetan, S., Malleshi, N.G. 2007. Finger mille polyphenols: Characterization and their nutraceuticalpotential. American Journal of Food Technology, 2, 582–592.

[9] Babu, B.K., Senthil, N., Gomez, S.M., Biji, K.R., Rajendraprasad, N.S., Kumar, S.S., Babu, R.C. 2006. Assessment of genetic diversity among finger millet (*Eleusine coracana* L. Gaertn) accession using molecular markers.

Genetic Research and Crop Evolution, 54, 339-404.

[10] Daba, C. 2000. Variability and Association among Yield and Related Traits in Finger Millet [E*leusine coracana* (L) Gaertn]. M.Sc. thesis, Alemaya University.

[11] Adeniji, O.T., Peter, J.M., Bake, I. 2008. Variation and interrelationship for pod and seed yield characters in Bambara groundnut (Vignasubterrenea) in Adamawa state, Nigeria. Africaan Journal of Agricultural Research, 3, 617-621.

[12] Basafa, M., Taherian, M. 2009. A study of agronomic and morphological variations in certain Alfalfa (Medicago sativa L.) Ecotypes of the cold region of Iran. Asian Journal of Plant Science, 8, 293-300.

[13] Wilson, J.P., Sanogo, M.D., Nutsugah, S.K., Angarawai, I., Fofana, A., Traore, H., Ahmadou, I., Muuka, F.P. 2008. Evaluation of pearl millet for yield and downy mildew resistance across seven countries in sub – Saharan Africa. African Journal of Agricultural Research, 3, 371-378.

[14] Poehlman, J.M. 1987. Breeding Field Crops. 3rd ed. AVI Publishing Company, Inc. West Port, CT. Pp. 187-213

[15] Singh, K.B., Bejiga, G., Malhotra, R.S. 1990. Association of some characters with seed yield in chickpea collections. Euphytica, 49, 83-88.

[16] MoAC. 2011. Agriculture Diary. 2010-2011.Agriculture information and communication centre. Harihar Vawan, Nepal.

[17] IBPGR. 1985. Descriptors for finger millet (*Elusine coracana* (L.) Gaertn). Rome, Italy: International Board for Plant Genetic Resources. Pp 20. [Online] available: http://www2.bioversityinternational.org/publications/Web_version/417/(Retrieved in 20 Feb, 2018).

[18] Steel, R.G.D., Torrie, J.H. 1980. Principles and procedures of statistics, a biochemical approach. McGraw Hill, Inc. New York.

[19] MINITAB. 2004. Minitab user guide, Releases 14.3 Minitab Inc., UK.

[20] Upadhyaya, H.D., Gowda, C.L.L., Reddy, V.G. 2007. Morphological diversity in finger millet germplasms introduced from Southern and Eastern Africa. Journal of SAT Agricultural Research, 3, 1-3.

[21] Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S., Reddy,V.G., Singh, S. 2004. Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. Genetic Resource and Crop Evolution, 53, 679-685.

[22] Khan, S., Latif, A., Ahmad, Q., Ahmad, F., Fida, M. 2011. Genetic variability analysis in some advanced lines of soybean (Glycine max L.). Asian Journal of Agricultural Science, 3, 138-141.

[23] Lang, M.T., Tu, P.T.B., Thanh, N.C., Buu, B.C., Ismail, A. 2009. Genetic diversity of salt tolerance rice landraces in Vietnamese. Journal of Plant Breed and Crop Science, 1, 230-243.

[24] Naik, B.J., ShankareGowda, B.T., Seetharam, A. 1994. Pattern of variability in relation to domestication of finger millet in Africa and India, pp. In [K.E. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga (eds.)]. Advances in Small Millets. International Science, New York, 347-363.

[25] Tazeen, M., Nadia, K., Farzana, N.N. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. Journal of Food, Agriculture and Environment, 7 (3&4), 278-282.

[26] Sharathbabu, K.S., Shantakumar, G., Salimath, P.M. 2008. Genetic variability and character association in white ragi (*Eleusine coracana* Gaertn). Karnataka Journal of Agricultural Sciences, 21 (4), 572-575

[27] Nandini, B., Ravishankar, C.R., Mahesha, B., Shailaja, H., Kalyana, M.K.N. 2010. Study of correlation and path analysis in F2 population of finger millet. International Journal of Plant Sciences, 5 (2), 602-605.

[28] Bezawelataw, K., Sripichitt, P., Wongyaiw, Hongtrakul, V. 2006. Genetic variation,heritability and path-analysis in Ethiopian finger millet (*Eleusine coracana* (L.) Gaertn) landraces. KasetsartJournal (National Science), 40, 322-334.

[29] Suyambulingam, C., Jebarani, W. 1977. Genetic divergence in short duration ragi *(Eleusine coracana* Gaertn). Madras Agricultural Journal, 64, 816-818.

[30] Dida, M.M., Wanyera, N., Ramakrishnan, S., Harrison-Dunn, M.L., Bennetzen, J.L., Devos, K.M. 2008. Population structure and diversity in finger millet (*Eleusine coracana*) germplasm. Tropical Plant Biology, 1, 131-141.