Received: 25 May 2022 | Revised: 07 Jun 2022 | Accepted: 28 Jun 2022

Electronic Journal of Plant Breeding

Research Article

Revealing genetic diversity in finger millet [*Eleusine Coracana* (L.) Gaertn] germplasm collected from Uttarakhand hills

Wanna Soe, A. S. Jeena, Usha Pant, Anil Kumar, Rohit* and Divya Chaudhary

Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand, India.
***E-Mail:** rohit8zed@gmail.com

Abstract
Twenty-nine genotypes of finger millet including six checks namely VL324, VL347, VL348, VL352, VL315 and VL149 were used in the present study for estimating the genetic diversity. The study revealed highly significant variance in genotypes for all fourteen traits. The coefficient of variance varied between 4.62 and 14.41 per cent. Grain yield per plot showed the highest GCV (37.33%) and PCV (40.02 %) followed by biological yield per plot GCV (26.21%) and PCV (29.75%). High heritability coupled with high genetic advance was observed in 1000 grains weight, grain yield per plot, days to 50% flowering and biological yield per plot. All 29 genotypes of finger millet genotypes were sorted into eight non-overlapping clusters using Mahalanobis D^2 statistics. Cluster I and cluster VIII had the greatest inter-cluster D-value (19.80), followed by cluster I and cluster VII (18.72). 1000 grains weight contributed maximum towards the total divergence.

Keywords: Diversity, Finger millet, GCV, Mahalanobis D^2, PCV

INTRODUCTION

Eleusine coracana, commonly known as finger millet, is a crop grown for food, fodder, and nutraceutical purposes. It is a hardy crop that may thrive in a variety of environments and be stored for long periods of time (Sood, *et al.,* 2018). In high-temperature, arid climates with limited soil fertility, it can generate reasonable grain and fodder yields. These features are attributed in part to its C4 pathway's efficient carbon concentrating mechanism (Goron and Raizada, 2015). Among millets, finger millet ranks fourth in importance after sorghum, pearl millet and foxtail millet (Sharma *et al.,* 2018). India, Central African countries and Nepal are the major growers of this crop. India is the world's leading producer of finger millet, with 1.74 million tons produced on 0.99 million hectares and an average yield of 1761 kg per hectare in 2019-20. (Directorate of Economics and Statistics, 2021). With its nutraceutical composition and climate resilient features finger millet is an ideal choice to address issues like global hidden hunger, urban health disorders and climate change hence considered as a "future crop" (Gupta *et al.,* 2017). Finger millet is a rich source of micronutrients, especially calcium, iron and zinc and contains 8-10 times more calcium than the other cereal crops such as rice or wheat (Rao and Deosthale, 1988; Gull, *et al.,* 2014). Finger millet is considered as a food for long subsistence owing to its slower digestibility (Devi *et al.,* 2014; Singh and Raghuvanshi, 2012). It is also rich in antioxidants and anti-aging compounds, it has pleiotropic health benefits like reduced risk of

cancer, cardiovascular and neuro-degenerative diseases, infections, aging and diabetes (Nakarani *et al.,* 2021).

Finger millet is considered to have originated in the Ethiopian and Ugandan highlands, and it was domesticated in western Uganda and the Ethiopian highlands at least 5000 years ago. (de Wet *et al.,* 1984). The Indian subcontinent is the secondary center of diversity for finger millet; and was introduced around 3000 years ago from Africa (Dida and Devos, 2006). There are nine species reported under the genus *Eleucine*, these include eight African species (*(E. africana, E. coracana, E. kigeziensis, E. indica, E. floccifolia, E. intermedia, E. multiflora and E. jaegeri*) and one New World species (*E. tristachya* Lam.) native to Argentina and Uruguay (Lovisolo and Galati 2007, Mirza and Marla, 2019). Cultivated finger millet (*Eleusine coracana subsp. coracana*) (2n = 4x = 36, AABB) is presumably derived by selection from the wild population of the *E. coracana subsp. africana* (Phillips, 1972, Hilu and de Wet, 1976, Bisht and Mukai, 2002). There are four cultivated races of finger millet based on inflorescence morphology, namely elongata, plana, compacta and vulgaris (de Wet *et al.,* 1984; Bharathi, 2011). India is bestowed with rich genetic diversity of finger millet; this crop has been an integral part of Indian history, culture and medicine from antiquity. India holds the largest collections of finger millet germplasm worldwide (Ramakrishnan *et al.,* 2016). The Himalayan region harbors a rich diversity of flora and fauna. Finger millet is an essential part of subsistence agriculture in this region. It is a popular staple crop in hilly Himalayan states of India and is traditionally cultivated and consumed in the hilly state of Uttarakhand. (Bhat *et al.,* 2019). The diversity of finger millet in this region offers opportunities for new research, conservation, and development. Genetic diversity analysis is critical for increasing finger millet output by selecting elite germplasm with a variety of positive features for direct use in breeding operations (Joshi *et al.,* 2021). Genetic parameters aid in distinguishing gene activity and identifying the components of genetic variation, as well as assisting in the selection of a suitable breeding strategy. Mahalanobis' D^2 statistic (Mahalanobis, 1936) is a multivariate analysis tool that uses a quantitative way to measure biological population divergence. It has been effectively used to plant species. The present study was carried out to study the magnitude of genetic differences and identification of superior germplasm accessions contributing as potential donors for future exploitation through hybridization followed by selection in Finger millet improvement.

MATERIALS AND METHODS

The experimental material consisted of twenty-three germplasm accessions of finger millet along with six released varieties namely VL324, VL347, VL348, VL352, VL315 and VL149 as checks. Germplasm accessions were collected from four districts of Uttarakhand *viz.* Bageshwar, Chamoli, Pauri Garhwal and Pithoragarh and the list are presented in **Table 1**. The trial was conducted at the Pantnagar Center for Plant Genetic Resources (PCPGR), Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, during *kharif,* 2020. Pantnagar is located at the latitude of 29.50^{0}N, a longitude of 79.30^{0}E, and an elevation of 243.84 meters above mean sea level. The university is located in the *Tarai* region, in the foothills of the Shivalik Himalayan range, in the subtropical zone.

The experiment was laid in Randomized Complete Block Design with three replications. Each entry was sown in a single row plot measuring 2 meters long and plot to plot spacing was kept to 30 centimeters. Recommended package of practice was followed to raise a good crop. Data was recorded for fourteen quantitative traits. Days to 50% flowering (DF), days to maturity (DM), biological yield per plot (BY) and grain yield per plot (GY) were taken on a plot basis, while for flag leaf blade length (FLBL), flag leaf blade width (FLBW), peduncle length (PL), ear head length (EHL), the number of productive tillers per plant (TLN), finger number on main ear (FNE), finger length (FL), finger width (FW), plant height (PH), 1000 grain weight (1000GW) were recorded on a random sample of five plants from each plot.

The data were subjected to analysis of variance followed by estimation of genetic parameters using the "variability" package (Popat *et al.,* 2020) in the R-studio. The mean of each replication and overall mean values of each trait was used to obtain the D^2 distance and group the genotypes according to D^2 statistics, using the "biotools" package (da Silva, 2021) of the R-studio. Based on the squared generalized Mahalanobis distance the importance

Table 1. Germplasm collected from four districts of Uttarakhand, India

Genotypes	Total Number	District	State
GP-2017-687, GP-2017-689, GP-2017-733 and GP-2017-602	4	Bageshwar	Uttarakhand
GP-2016-131, GP-2017-579, GP-2016-126, GP-2016-129, GP-2017-275, GP-2016-198, GP-2016-188, GP-2017-479, GP-2016-191, GP-2016-193 and GP-2017-461	11	Pithoragarh	Uttarakhand
GP-2018-1253, GP-2017-888, GP-2018-1249, GP-2018-1240, GP-2017-889 and GP-2018-1237	6	Chamoli	Uttarakhand
GP-2017-529 and GP-2017-502	2	Pauri Garhwal	Uttarakhand

proportion and the cumulative proportion of each variable were obtained using "singh" statistic from the same package (Singh, 1981). R-statistical software packages "ggplot2" (Wickham, 2016), "dendextend" (Galili, 2015) and "circlize" (Gu *et al.,* 2014) were used to draw figures and graphs.

RESULTS AND DISCUSSION

The weekly meteorological data during the crop season is presented in **Fig. 1**. The maximum and minimum temperatures recorded were 39.7 ^{0}C and 18 ^{0}C during the second week of July and the third week of October, respectively. Maximum rainfall of 213.20 mm was received during the last week of July. Overall, the average weekly rainfall during the cropping season was 57.14 mm. The average weekly sunshine hours was 7.26 hrs for the cropping season. Rainfall throughout the vegetative and flowering stages of the plants produced lodging in some lines, resulting in yield losses in select genotypes.

Analysis of variance revealed significant and substantial phenotypic variability for yield and yield related traits in the experimental material. The coefficient of variation was registered lowest for 1000 grains weight (4.62%), followed by days to 50% flowering (5.82%) and plant height (5.90%), all of which had lower coefficients of variation, indicating that these traits represented best genetic potentials. Meanwhile, the highest coefficient of variation was found in grain yield per plot (14.41 %), followed by biological yield per plot (14.07 %), and flag leaf blade width (13.99 %), showing that environmental fluctuations had a greater impact on these variables. Based on the mean performance, GP2016/131 recorded the highest grain yield per plot of 207.67 g, while GP2017/529 had the lowest grain yield per plot of 60.55 g. The general mean for grain yield per plot was 113.17 g, and three genotypes *viz*. GP 2016/131(207.67 g), GP 2017/733 (198.20 g) and GP2 017/689 (188.33 g) surpassed the best check VL 149 (187.57 g). Similarly, biological yield per plot averaged 646.29 g, with the highest value of 1006.67 g in VL 324 and the lowest in GP2016/191 (387.33 g). The general mean for days to flowering and days to maturity was 77.17 days and 108.02 days, respectively. VL 347 was the earliest to flower and mature, requiring just 60 days to reach 50% flowering and 88 days to reach full maturity. Meanwhile, genotype GP2016/126 took the highest number of days for 50% flowering and maturity, with 98 and 138 days, respectively. GP2016/131 possessed the maximum values for flag leaf blade length (39.33 cm) and flag leaf blade width (1.13 cm). Thousand grains weight showed a wide from 1.45 g in GP2018/1240 to 2.85 g in VL 352, the general mean of 2.12 g was registered for this trait. None of the accessions was found superior to best check VL 352 for 1000 grains weight. Further, descriptive statistics of fourteen quantitative traits are furnished in **Table 2**.

Among, accessions highest mean performance in desired direction was exhibited by GP 2017/889 (61 days) for days to 50% flowering, GP 2016/131 (39.33 cm) for flag leaf blade length, GP 2016/131 (1.13 cm) for flag leaf blade width, GP 2017/687 (23.47 cm) for peduncle length, GP 2016/193 (19.93 cm) for ear head length, GP 2017/733 (3.20) for the number of productive tiller per plant, GP 2016/198 (9.0 fingers) for finger number on main ear, GP 2017/479 (10.30 cm) for finger length,

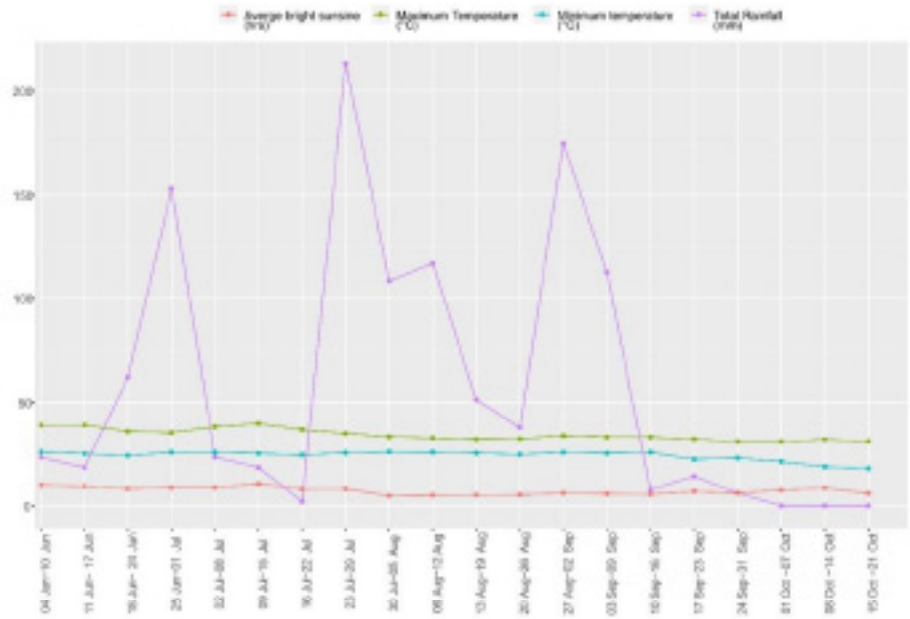

Fig.1. Weekly meteorological data of crop season period from June 2020 to October 2020.

Table 2. Descriptive statistics of fourteen quantitative traits recorded in Finger Millet

Parameters	Mean	Range				SE(m)	CD	CV	Best check in desirable direction	Number of accessions over best check in desirable direction
		Maximum value	Genotype	Minimum value	Genotype					
Days to 50% flowering	77.17	98.00	GP2016/126	60.00	VL 347	2.59	7.37	5.82	VL 347	0
Flag leaf blade length (cm)	34.05	39.33	GP2016/131	27.93	GP2017/479	1.82	5.16	9.24	VL 352	1
Flag leaf blade width (cm)	0.93	1.13	GP2016/131	0.67	VL 315	0.08	0.21	13.99	VL 324	2
Peduncle length (cm)	19.87	23.47	GP2017/687	15.87	GP2017/502	1.06	3.02	9.27	VL 347	1
Ear head length (cm)	10.84	13.20	GP2016/193	7.93	VL 315	0.51	1.45	8.15	VL 149	2
Number of productive tillers/plant	2.60	3.20	GP2017/733	2.13	GP2016/191	0.17	0.49	11.58	VL 324	1
Finger number on main ear	8.01	9.47	VL 324	7.13	GP2017/479	0.43	1.23	9.36	VL 324	0
Finger length (cm)	8.61	10.30	GP2017/479	7.00	GP2016/198	0.57	1.62	11.46	VL 149	1
Finger width (cm)	0.80	0.90	GP2018/1237	0.63	GP2017/689	0.04	0.12	9.18	VL 315	3
Plant height (cm)	105.52	121.67	GP2018/1249	91.87	GP2017/888	3.60	10.22	5.90	VL 348	1
Days to maturity	108.02	130.00	GP2016/126	88.00	VL 347	4.79	13.61	7.68	VL 347	0
1000 grains weight (g)	2.12	2.81	VL 352	1.45	GP2018/1240	0.06	0.16	4.62	VL 352	0
Biological yield per plot (g)	646.29	1006.67	VL 324	387.33	GP2016/191	52.51	149.15	14.07	VL 324	0
Grain yield per plot (g)	113.17	207.67	GP2016/131	60.55	GP2017/529	9.42	26.75	14.41	VL 149	3

SE(m) is the standard error of mean, CD is critical difference, CV is coefficient of variation,

GP 2018/1237 (0.90 cm) for finger width, GP 2017/888 (91.87 cm) for plant height, GP 2016/131 (96 days) for days to maturity, GP 2016/126 (2.62 g) for 1000 grain weight, GP 2016/126 (956.33 g) for biological yield per plot and GP 2016/131 (207.67 g) for grain yield per plot. Accessions with desirable mean performance could be selected as donor parents in future breeding programs. Sharma *et al.* (2018) and Bastola *et al.* (2015) also reported similar significant genetic variation as indicated by mean and range for yield and yield attributing traits in finger millet landraces of Uttarakhand (India) and Nepal, respectively.

The GCV and PCV, genetic advance, and GA as % mean were calculated along with heritability for all the traits (**Fig. 2**). As per the scale suggested by Sivasubramanian and Madhavamenon (1973) high (> 20 %) GCV and PCV were observed for grain yield per plot (37.33 % and 40.02 %, respectively) and biological yield per plot (26.21 % and 29.75 %, respectively), indicating large variability of these traits in the finger millet accessions. Similarly, GCV and PCV estimates were registered low (<10 %) for plant height (5.39 % and 7.99 %, respectively) implying lesser variability this trait. Moderate (10 % to 20%), GCV and PCV was found for 1000 seed weight (16.68 % and 17.31 %, respectively), days to 50% flowering (15.84 % and 16.88 %, respectively), ear head length (11.36 % and 13.98 %, respectively) and days to maturity (10.06 % and 12.66 %, respectively). The rest of the traits showed either mix of moderate and low or low estimates for GCV and PCV. The estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters. The difference between PCV and GCV estimates was least for 1000 grains weight and days to 50% flowering indicating a strong genetic expression in these traits. While, the flag leaf blade, finger width and finger length displayed a wider distance between PCV and GCV values, this corresponds to the considerable influence of environment on these traits. Selection is effective for a trait that has variability bearing fewer fluctuations caused by the environment. 1000 grain weight is an essential selection criterion because it has moderate variability and the smallest differences in PCV and GCV.

The estimates of broad-sense heritability and Genetic advance as per cent of mean (GAM) are classified as suggested by Robinson (1966) and Johnson *et al.* (1955), respectively. Highly heritable (>60 %) with high GAM (>20%), traits included1000 grains weight (92.86 % and 33.12 %, respectively), Days to 50% flowering (88.10 % and 30.63 %, respectively), Grain yield per plot (87.03 % and 71.74 %, respectively) and biological yield per plot (77.63 % and 47.57 %, respectively). The best conditions for selection are high genetic progress combined with high heritability estimates. It also indicates the predominance of additive gene action in the trait, implying that crop improvement can be achieved by selecting these traits (Ogunniyan and Olakojo, 2014). Low heritability

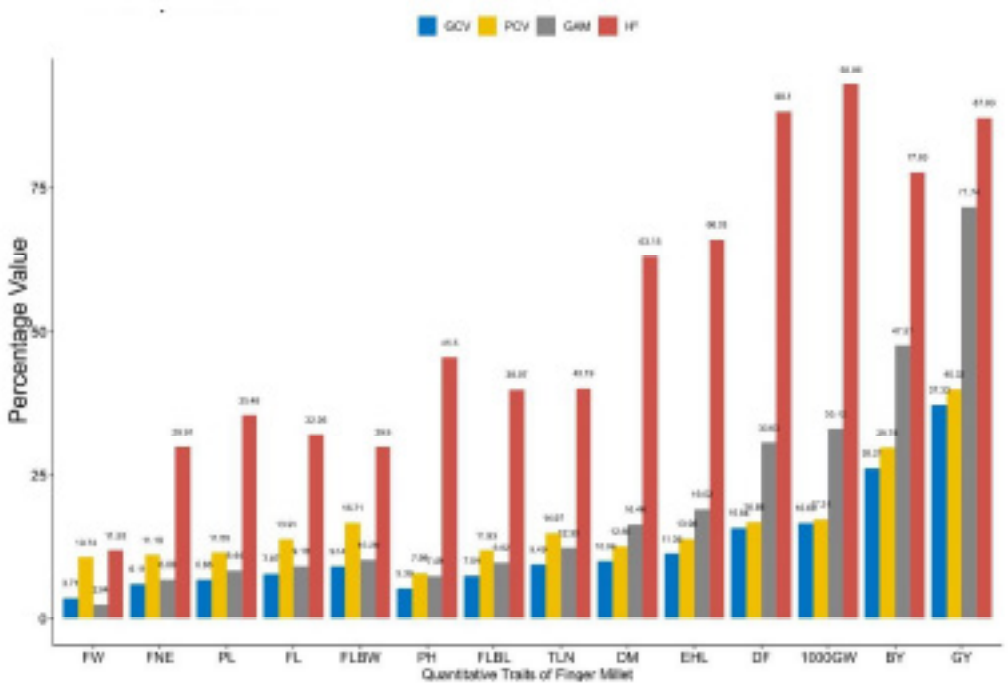

Fig. 2. Genetic and phenotypic coefficients of variation (GCV and PCV), genetic advance as percentage of mean (GAM) and heritability in broad-sense (H^2) estimated for the fourteen traits studied.

(< 30) % and low GAM (<10%) were recorded for finger width (11.93 % and 2.64 %, respectively) and finger number on main ear (29.91 % and 6.89 %), indicating a significant influence of environment on the trait which requires cautious selection in the future. Plant height had a moderate heritability (45.50%) and a low GAM (7.49%), indicating the presence of moderate non- additive gene action in a fraction of the population. Overall, high heritability (>60%), GAM (>20%), PCV (>20%), and GCV (>20%) were found in the traits like 1000 grains weight, days to 50% flowering, Grain yield per plot and biological yield per plot. Similar cases were reported for the traits- days to 50% flowering, Plant height and grain yield (Ravikanth and Sarma, 2017), for 1000 grains weight (Lule *et al.,* 2012), for plant height, finger length, finger width and grain yield (Das *et al.,* 2016) and for days to 50% flowering, the number of productive tillers, plant height and grain yield (Jyothsna *et al.,* 2016).

The D^2 values, derived from phenotypic data for all fourteen variables, ranged from 5.31 to 464.30, indicating significant diversity in the experimental material. Genotypes were divided into eight clusters based on D^2 values. Cluster II had twelve genotypes, Cluster III had four genotypes, Cluster I had four genotypes, Cluster IV had three genotypes, Cluster VI had two genotypes, and Cluster V, VII, and VII had only one genotype each. Cluster II was the largest cluster having twelve genotypes including three checks viz. VL 348, VL 347 and VL 149 along with nine landraces, six of which were from Pithoragarh district, two from Bageshwar district and one from Pauri Garhwal. Check VL 315 was grouped with two germplasm accessions in cluster I. Check varieties VL 324 and VL 352 form two separate clusters viz., Clusters VII and VIII, respectively, indicating their divergence from other varieties and accessions. Clustering showed that the geographical distribution by districts was not responsible for genetic diversity in the germplasm as shown in **Fig. 3.** The division of accessions from the same geographical origin into multiple clusters indicates the broad genetic base in genotypes of that origin. These findings demonstrated that finger millet has abundant genetic variation in Uttarakhand's Himalayan areas. Checks, VL 324 and VL 352 were found diverse from the germplasm material included in the study, which could be owing to earlier germplasm selection during the development of these varieties.

In the perusal of D^2 statistics, the distance between clusters, inter-cluster D-values ranged from 7.45 to 19.80 (**Fig. 4**). The inter-cluster D-value was highest (19.80) between cluster I and cluster VIII, followed by cluster I and cluster VII (18.72) and between cluster I and cluster III (17.68). Cluster I was common in the first three highly divergent clusters. The magnitude of high inter cluster D-values indicates extent of genetic non-relatedness between the genotypes present in the cluster pairs. In future finger millet breeding attempts, intercrossing Cluster I genotypes

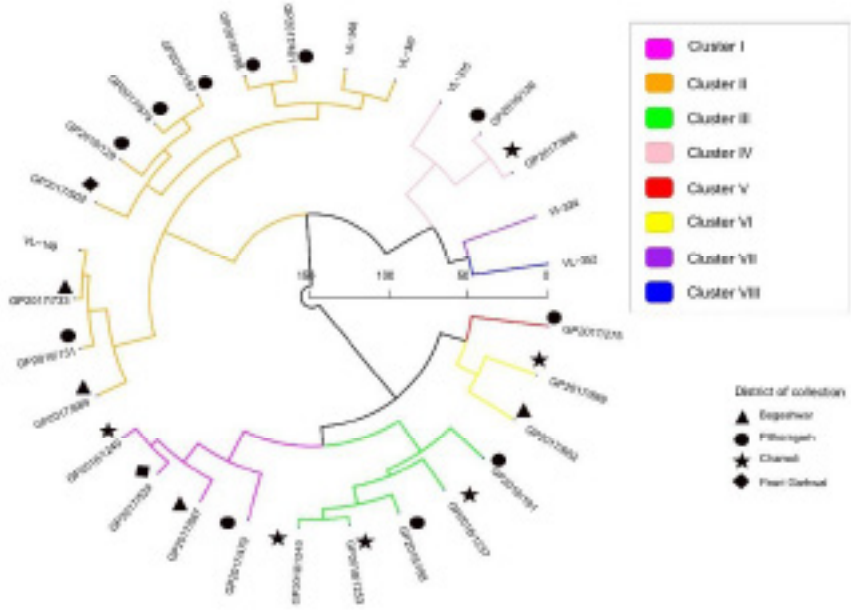

Fig. 3. Dendrogram showing clustering of twenty-nine genotypes based on Mahalanobis's distance and the UPGMA algorithm, showing eight clusters along with geographical distribution

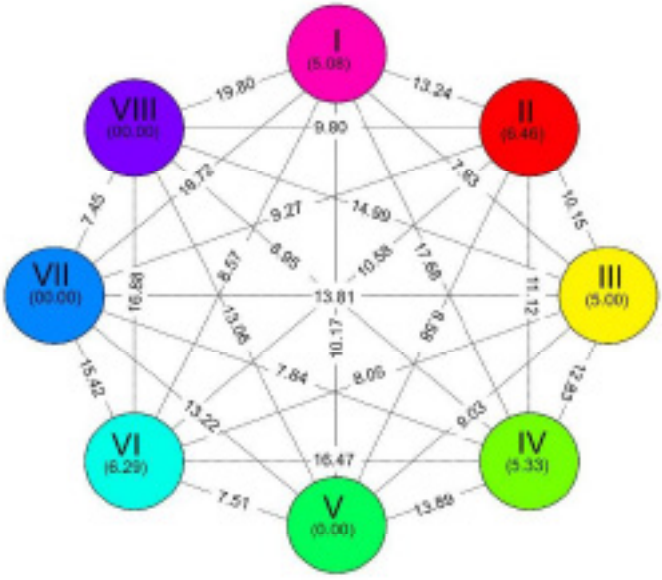

Fig. 4. Intra and inter-cluster distance based on D-value for landraces and genotypes of finger millet.

with Cluster VII, VIII, III, and Cluster VI genotypes with Cluster VIII and IV genotypes may result in the release of *de-novo* variability, throwing transgressive segregants or superior heterotic combinations of genes. Minimum inter cluster D-value was found between cluster VII and cluster VIII (7.45) followed by cluster V and cluster VI (7.51). Crosses between genotypes from clusters separated by a small inter-cluster distance are more likely to be non-fruitful. Intra-cluster D-distance (D) revealed that cluster II registered maximum intra-cluster distance (6.46) followed by cluster VI (6.29), cluster IV (5.33), cluster I (5.08) and cluster V (5.00). Clusters V, VII, and VIII, on the other hand, each had a single genotype and showed no intra cluster distance. Cluster II showed maximum intra cluster distance and had maximum genotypes (12) however this relation of high intra-cluster value to the number

of cluster members was not true for other clusters. Suryanarayana *et al.* (2014) reported a similar range of inter and intra cluster D values with 35 finger millet genotypes, Bendi *et al.* (2017) and Negi *et al.* (2017) with 55 and 35 finger millet genotypes, respectively, and Mahalle *et al.* (2020) with 50 finger millet genotypes.

The relative contribution of traits towards total divergence is depicted in **Fig. 5**. Among all the characters undertaken, the top five traits that contributed most towards the total divergence were 1000 grains weight (36.54%) followed by days to 50% flowering (13.79 %), grain yield per plot (13.59 %), biological yield per plot (8.43%) and ear head length (5.03%). The bottom two traits that contributed least towards divergence were finger leaf blade width (1.79%) and days to maturity (0.48%). During hybridization and selection, traits having a large contribution to total divergence should be prioritized. As a result, the current population could be further selected based on traits like 1000 grain weight, days to 50 % flowering, grain yield per plot, biological yield per plot, and ear head length. Earlier similar reports were given for days to 50% flowering, ear head length, and biological yield (Negi *et al.,* 2017), days to 50% flowering and grain yield (Kumari and Singh, 2015), ear head length (Devaliya *et al.,* 2017; Patel *et al.,* 2020), grain yield (Suryanarayana *et al.,* 2014; Mahanthesha *et al.,* 2017) and 1000 grain weight (Mahalle *et al.,* 2020).

Cluster means for different characters also supported the genetic difference among genotypes (**Table 3**). Cluster VIII containing a single genotype, VL 352 was the earliest to flower (62.00 days) and mature (96.00 days). It possessed the longest flag leaf blade length (39.07 cm), highest 1000 grains weight (2.81 g), the second highest finger number per ear (9.47) and finger width (0.83 cm)

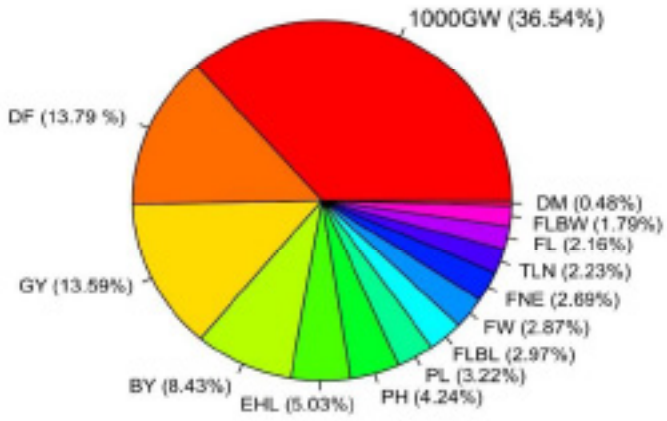

Fig. 5. Pie chart depicting relative contribution of fourteen traits towards total divergence

Table 3. Cluster means of fourteen quantitative traits in 29 genotypes of finger millet

Cluster	Number of genotypes	DF	FLBL	FLBW	PL	EHL	TLN	FNE	FL	FW	PH	DM	1000GW	BY	GY
I	4	92.67	30.65	0.98	21.57	10.63	2.43	7.38	8.98	0.82	101.01	120.00	1.58	445.08	66.16
II	12	67.83	36.59	0.98	19.83	11.84	2.79	8.32	8.74	0.77	106.44	98.00	2.23	648.39	144.17
III	5	88.67	32.19	0.82	18.98	10.00	2.44	7.79	8.40	0.87	111.55	119.07	1.98	567.13	73.63
IV	3	92.00	32.18	0.88	19.33	9.47	2.34	7.23	7.98	0.77	97.93	122.89	2.64	871.56	118.63
V	1	64.67	30.33	0.97	21.80	11.07	2.20	8.73	9.47	0.83	97.13	108.67	1.92	659.00	84.60
VI	2	69.17	32.00	0.80	20.50	10.23	2.50	7.53	8.70	0.80	112.70	106.00	1.69	738.50	91.50
VII	1	69.00	34.87	1.07	16.40	10.00	3.13	9.47	8.27	0.80	104.93	96.00	2.44	1006.67	171.97
VIII	1	62.00	39.07	0.90	19.93	9.67	2.67	9.13	7.73	0.83	105.53	96.00	2.81	588.33	123.67

DF=days to 50% flowering, FLBL=flag leaf blade length (cm), FLBW=flag leaf blade width (cm), PL=peduncle length (cm), EHL=ear head length (cm), TLN=number of productive tillers per plant, FNE=finger number on main ear, FL=finger length (cm), FW=finger width (cm), PH=plant height (cm), DM=days to maturity, 1000GW=1000 grains weight (g), BY=biological yield per plot (g), GY=grain yield per plot (g).

and the third in grain yield per plot (123.67 g) with this combination it stood separate from other clusters. Cluster VII with a single genotype, VL 324 had the highest cluster mean for biological yield per plot (1006.67 g) and grain yield per plot (171.97 g). It was also found best for the number of fingers on main ear (9.47), the number of tillers per plant (3.13), and flag leaf blade width (1.07 cm). It possessed the smallest peduncle length (16.40 cm). Cluster II with maximum members including three checks had the highest cluster mean value for ear head length (11.84 cm), the second in grain yield per plot (144.17 g), the number of tillers per plant (2.79), flag leaf blade length (36.59 cm) and flag leaf blade width (0.98 cm). Overall, cluster VIII was identified as a donor for earliness and early maturity and high 1000 grain weight. While, cluster VII was identified as a donor for enhancing biological yield per plot and grain yield per plot. Cluster II was identified as a suitable donor for ear head length. The highest yielding top three genotypes *viz.* GP2016/131, GP2017/733 and GP2017/689 were contained in cluster II. Therefore, the genotypes from clusters II, VII and VIII can be utilized as superior donors for further yield increments and genetic diversification through hybridization in finger millet.

Grain yield per plot and biological yield per plot showed high GCV, heritability and GAM, these two characters would be used for direct selection in the breeding programme. GP 2016/131 topped the mean performance among entries for four quantitative traits *viz.* flag leaf blade length, flag leaf blade width, days to maturity and grain yield per plot. Therefore, this genotype can be used as a donor of these traits. Finger millet genotype having the most divergence range of days to 50% flowering followed by the 1000 grain weight, ear head length, plant height and grain yield per plot had contributed towards diversity. The outstanding checks were VL 352 and VL 324, while the best entries in the trail were accessions GP2016/131, GP2017/733, and GP2017/689. These accessions could be utilized for the development of varieties after proper multilocation testing or as a donor for a hybridization programme to get transgressive segregants in future generations.

ACKNOWLEDGEMENT

The authors are thankful to the Department of Science and Technology (DST), New Delhi for the financial assistance through the project under the TIME-LEARN programme of SEED division.

REFERENCES

Bastola, B. R., Pandey, M. P., Ojha, B. R., Ghimire, S. K. and Baral, K. 2015. Phenotypic diversity of Nepalese finger millet (*Eleusine coracana* (L.) Gaertn.) accessions at IAAS, Rampur, Nepal. *International Journal of Applied Sciences and Biotechnology*, **3**(2): 285-290. [Cross Ref]

Bendi, R. and Sarma, N. D. R. K. 2017. Genetic variability and diversity studies on yield and quality traits in finger millet (*Eleusine coracana* (L.) Gaertn.). *Environment and Ecology*, **35**(1): 185-188.

Bharathi, A. 2011. Phenotypic and genotypic diversity of global finger millet (*Eleusine coracana* (L.) Gaertn.) composite collection. PhD Thesis, Tamil Nadu Agricultural University, TamilNadu.

Bhat, B.V., Arunachalam, A., Kumar, D., Tonapi, V. A. and Mohapatra, T. 2019. Millets in the Indian Himalaya, Indian Council of Agricultural Research, New Delhi. 84p.

Bisht, M. S. and Mukai, Y. 2002. Genome organization and polyploid evolution in the genus *Eleusine* (Poaceae). *Plant Systematics and Evolution*, **233**(3): 243-258. [Cross Ref]

Da Silva, A.R. 2021. *biotools: Tools for Biometry and Applied Statistics in Agricultural Science*. R package version 4.2, https://cran.r-project.org/package=biotools.

Das, R., Sujatha, M. and Pandravada, S. R. 2016. Assessment of variability, heritability, genetic advance in finger millet (*Eleusine coracana* Gaertn) germplasm lines. *Environment and Ecology*, **34**(4A): 1829-1833.

De Wet, J. M. J., Rao, K. P., Brink, D. E. and Mengesha, M. H. 1984. Systematics and evolution of *Eleusine coracana* (Gramineae). *American journal of Botany*, **71**(4): 550-557. [Cross Ref]

Devaliya, S. D., Singh, M. and Intawala, C. G. 2017. Genetic divergence studies in finger millet [*Eleusine coracana* (L.) Gaertn.]. *International Journal of Current Microbiology and Applied Sciences,* **6**(11): 2017-2022. [Cross Ref]

Devi, P. B., Vijayabharathi, R., Sathyabama, S., Malleshi, N. G. and Priyadarisini, V. B. 2014. Health benefits of finger millet (*Eleusine coracana* L.) polyphenols and dietary fiber: a review. *Journal of food science and technology*, **51**(6): 1021-1040. [Cross Ref]

Dida, M. M. and Devos, K. M. 2006. Finger millet. In *Cereals and millets*). Springer, Berlin, Heidelberg. Pp. 333-343. [Cross Ref]

Directorate of Economics and Statistics. 2021. Agricultural statistics at a glance 2021, Department of Agriculture, Co-operation and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India.

Galili, T. 2015. dendextend: An R package for visualizing, adjusting and comparing trees of hierarchical clustering. *Bioinformatics,* **31**: 3718–3720. [Cross Ref]

Goron, T. L. and Raizada, M. N. 2015. Genetic diversity and genomic resources available for the small millet

crops to accelerate a New Green Revolution. *Frontiers in plant science*, **6**: 157. [Cross Ref]

Gu, Z., Gu, L., Eils, R., Schlesner, M. and Brors, B. 2014. Circlize implements and enhances circular visualization in R. *Bioinformatics*, **30**: 2811–2812. [Cross Ref]

Gull, A., Jan, R., Nayik, G. A., Prasad, K. and Kumar, P. 2014. Significance of finger millet in nutrition, health and value-added products: a review. *Magnesium (mg)*: **130(**32):120.

Gupta, S. M., Arora, S., Mirza, N., Pande, A., Lata, C., Puranik, S. and Kumar, A. 2017. Finger millet: a "certain" crop for an "uncertain" future and a solution to food insecurity and hidden hunger under stressful environments. *Frontiers in plant science*, **8**: 643. [Cross Ref]

Hilu, K.W. and de Wet, J.M.J.1976. Domestication of *Eleusine* coracana. *Econ Bot,* **306**:199–208. [Cross Ref]

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**(7): 314-318. [Cross Ref]

Joshi, D. C., Sood, S., Gupta, A., Khulbe, R. K., Pandey, B. M., Pal, R. S. and Kant, L. 2021. VL Mandua 382: The first early maturing, white seeded finger millet cultivar suitable for rainfed organic agro-ecology of the Himalayan region. *Electronic Journal of Plant Breeding*, **12**(4): 1308-1313. [Cross Ref]

Jyothsna, S., Patro, T. S. S. K., Ashok, S., Rani, Y. S. and Neeraja, B. 2016. Studies on genetic parameters, character association and path analysis of yield and its components in finger millet (*Eluesine coracana* L. Gaertn*). International Journal of Theoretical and Applied Sciences*, **8**(1): 25.

Kumari, S. and Singh, S. K. 2015. Assesment of genetic diversity in promising finger millet [*Eleusine coracana* (L.) Gaertn] genotypes. *The bioscan*, **10** (2): 825-830.

Lovisolo, M. R. and Galati, B. G. 2007. Ultrastructure and development of the megagametophyte in *Eleusine* tristachya (Lam.) Lam. (Poaceae). *Flora-Morphology, Distribution, Functional Ecology of Plants*, **202**(4): 293-301. [Cross Ref]

Lule, D. and Tesfaye, K and Fetene, M and de Villiers, S. 2012. Inheritance and association of quantitative traits in finger millet (*Eleusine coracana* Subsp. Coracana) landraces collected from Eastern and South Eastern Africa. *International Journal of Genetics*, **2** (2): 12-21.

Mahalle, S. P., Lad, D. B. and Karad, S. R. 2020. Assessment of genetic diversity among finger millet (*Eleusine coracana* L. Gaertn.) genotypes during kharif season in Western Maharashtra (India). *International Journal of Scientific and Research Publications*, **10** (5): 803-807. [Cross Ref]

Mahanthesha, M., Sujatha, M., Pandravada, S. R. and Meena, A. K. 2017. Study of genetic divergence in finger millet (*Eleusine coracana* (L.) Gaertn) germplasm. *International Journal of Pure and Applied Bioscience*, **5**(3): 373-377. [Cross Ref]

Mirza, N. and Marla, S. S. 2019. Finger millet (*Eleusine coracana* L. Gartn.) breeding. In *Advances in plant breeding strategies: cereals* Springer, Cham. Pp. 83-132. [Cross Ref]

Nakarani, U. M., Singh, D., Suthar, K. P., Karmakar, N., Faldu, P. and Patil, H. E. 2021. Nutritional and phytochemical profiling of nutracereal finger millet (*Eleusine coracana* L.) genotypes. *Food Chemistry*, **341**: 128271. [Cross Ref]

Negi, S., Kumar, V. and Bhatt, A. 2017. Genetic diversity among Finger Millet [*Eleusine coracana* (L.) Gaertn] genotypes for yield and its contributing traits. *International Journal of Current Microbiology and Applied Sciences*, **6**(8): 3332-3337. [Cross Ref]

Ogunniyan, D. J. and Olakojo, S. A. 2014. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics*, **28**(2): 24-28. [Cross Ref]

Patel, S., Patil, H. E., Pali, V. and Patel, B. K. 2020. Genetic diversity analysis in finger millet [*Eleusine coracana* (L.) Gaertn.]. *Journal of Pharmacognosy and Phytochemistry*, **9**(1): 677-680.

Phillips, S.M. 1972. A survey of the genus *Eleusine* Gaertn. (Gramineae) in Africa. *Kew Bull,* **27**:251–270. [Cross Ref]

Popat, R., Patel, R. and Parmar, D. 2020. Variability: Genetic Variability Analysis for Plant Breeding Research**,** https://cran.r-project.org/web/packages/variability/variability.pdf

Ramakrishnan, M., Ceasar, S. A., Duraipandiyan, V., Al-Dhabi, N. A. and Ignacimuthu, S. 2016. Assessment of genetic diversity, population structure and relationships in Indian and non-Indian genotypes of finger millet (*Eleusine coracana* (L.) Gaertn) using genomic SSR markers. *SpringerPlus*, **5**(1): 1-11. [Cross Ref]

Rao, P. U. and Deosthale, Y. G. 1988. In vitro availability of iron and zinc in white and coloured ragi (*Eleusine* coracana): role of tannin and phytate. *Plant Foods for Human Nutrition*, **38**(1): 35-41. [Cross Ref]

Ravikanth, B. and Sarma, N. D. R. K. 2017. Genetic variability and diversity studies on yield and quality traits in finger millet (*Eleusine coracana* (L.) Gaertn.). *Environment and Ecology*, **35**(1): 185-188.

Robinson, H. F. 1966. Quantitative genetics in relation to breeding on centennial of Mendelism. In *Indian Journal of Genetics and Plant Breeding*, Indian Agriculture Res Inst, New Delhi, Pp. 171.

Sharma, D., Tiwari, A., Sood, S., Jamra, G., Singh, N. K., Meher, P. K. and Kumar, A. 2018. Genome wide association mapping of agro-morphological traits among a diverse collection of finger millet (*Eleusine coracana* L.) genotypes using SNP markers. *PloS one*, **13**(8): e0199444. [Cross Ref]

Singh, D. 1981. The relative importance of characters affecting genetic divergence. *Indian Journal Genetics & Plant Breeding,* **41**:237-245.

Singh, P. and Raghuvanshi, R. S. 2012. Finger millet for food and nutritional security. *African Journal of Food Science*, **6**(4): 77-84. [Cross Ref]

Sivasubramanian, S. and Menon, M. 1973. Heterosis and inbreeding depression in rice. *Madras Agricultural Journal,* **60**(7): 1139-1140.

Sood, S., Patro, T. S. S. K., Karad, S. and Sao, A. 2018. Graphical analysis of genotype by environment interaction of Finger millet grain yield in India. *Electronic Journal of Plant Breeding*, **9**(1): 82-89. [Cross Ref]

Suryanarayana, L., Sekhar, D. and Rao, N. V. 2014. Genetic variability and divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.). *International journal of current microbiology and applied sciences*, **3**(4): 931-936.

Wickham, H. 2016. *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York, https://ggplot2.tidyverse.org. [Cross Ref]