



Assessing the genetic diversity of finger millet (*Eleusine coracana*) germplasm for agronomic traits

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ABSTRACT

A field experiment was conducted during the rainy (*kharif*) season of 2019 and 2020 at research farm of CCS Haryana Agricultural University Hisar, Haryana to assess the genetic diversity of finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm for agronomic traits. Experiment consisted of 150 accessions and 4 checks in augmented block design. The analysis of variance (ANOVA) divulged that test genotypes showed a highly significant difference ($P < 0.01$) for agronomic traits. A maximum (96.67) heritability (*h*BS) was observed for days to 50% flowering, followed by 1000-grains weight (94.93). The least *h*BS (68.37) was observed for flag leaf blade width. Genetic advance over mean (GAM) was the maximum for grain yield per plant (99.51), followed by harvest index (65.59) and ear head width (59.22), productive tillers (55.54), 1000-grains weight (36.74), flag leaf blade width (25.19) and plant height (24.92) while the other traits like day to 50% flowering, days to maturity, fingers number on the main ear, peduncle length and flag leaf blade width showed less than 20% of GAM. Principal Component Analysis (PCA) revealed that the first 5 PCs with eigenvalues greater than unity, hold 74.07% total variability. Hierarchical clustering was also carried and top 10 promising accessions were identified. Hence, the current research revealed that the selected finger millet accessions were highly diverse for grain yield and other studied agronomic traits, which favour selection and could be utilized in different breeding programs.

Keywords: Agronomic traits, Finger millet, Genetic diversity, Heritability

Lowering the water table, nutrient imbalance, soil degradation, salinity, pest resistance, environmental pollution, and declining farm income are the 2nd generation Indian agricultural problems. Continuous adoption of the wheat-rice/cotton system leads to loss of soil fertility and reduction in the water table, especially in the north-western states of India. Crop diversification has been an effective strategy for achieving the objectives of water resources, sustainable agricultural development, environmental improvement, nutritional security, and poverty alleviation (Yadav *et al.* 2017). Finger millet [*Eleusine coracana* (L.) Gaertn.] is the most esteemed for its nutritional superiority among cereals. It is allotetraploid ($2N = 4X = 36$, AABB), belonging to the family Poaceae. It contains around 65–75% starches, 15–20% dietary fiber, 5–8% proteins, 2.5–3.5% minerals, and 1–2% ether extractives (Chethan and Malleshi 2007). It is a rich source of Ca^{2+} (344 mg/100 g) (Kumar *et al.* 2016). Apart from calcium, finger millet also holds a good expanse of Fe^{2+} , amino acids, mainly methionine,

phytochemicals like polyphenols, and slowly digestible starch (Badigannavar and Ganapathi 2018). Due to its gluten-free and low fat, finger millet is easy to digest and non-allergic; that's why finger millet is also called "super cereal". It has high water use proficiency and exhausts 10–20% less water than sorghum. It requires 3–4 times less water than paddy (Baath *et al.* 2018). The wide range of genotypic variation in finger millet germplasm represents an excellent prospect for identifying and screening genotypes for stress adaptation. So, it is crucial to categorize and promote finger millet germplasm that could bear the pressure of water scarcity and produce gainful crops to mitigate the increasing food crisis.

Therefore, the study aims to determine the extent of heritability, variability and correlation of diverse traits to categorize the 154 genotypes based on cluster analysis. It also aims to find those traits that subsidize the foremost source of variation within the finger millet germplasm via principal component analysis (PCA) and assess the genetic diversity of the germplasm using agronomic traits.

MATERIALS AND METHODS

Germplasm particulars: A total of 150 finger millet

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accessions and 4 check varieties (KMR 301, GPU 67, ML 365, VR 847) were procured from ICAR-NBPGR (National Bureau of Plant Genetic Resources) Pusa Campus, New Delhi, and IIMR (Indian Institute of Millets Research) Rajendranagar, Hyderabad, India, respectively (Supplementary Table 1).

Experimental details: The crop was sown at research farm of CCS Haryana Agricultural University, Hisar (29.14°N 75.70°E), Haryana during the rainy (*khari*) season of 2019 and 2020. Received annual rainfall ranging from 264.0 to 285.6 mm, with mean minimum and maximum temperatures of 17.8°C and 30.6°C, respectively during the experimental years. The experiments were in an augmented block design having a single row of 2 m length with 20 cm inter-row spacing and 15 cm plant-to-plant distance. The standard packages and practices for cultivation were followed.

Phenotyping of agronomic traits: Data for 13 agronomic traits, viz. ear head length (EHL), ear head width (EHW), fingers number on the main ear (FN), flag leaf blade length (FLBL), flag leaf blade width (FLBW), peduncle length (PL), productive tillers (PT), plant height (PH), grain yield per plant (GYPP), days to 50% flowering (DF), days to maturity (DM), thousand grains weight (TGW), and harvest index (HI) were noted and equated for the response on diversity study.

Statistical analysis: The analysis of variance (ANOVA), adjusted means, descriptive statistics, genetic variability, correlation coefficient, principal component analysis (PCA), and hierarchical clustering were computed using the R studio.

RESULTS AND DISCUSSION

Variance and mean comparison: Genetic variability in the initial germplasm is a prerequisite for breeding programmes. A significant genotypic variation ($P < 0.01$)

was detected among treatments (Table 1). In the present study, the values of PCV were marginally higher than the conforming GCV values, which indicates the minor effect of environmental variance. The PCV and GCV were high for ear head width, productive tillers, grain yield per plant, and harvest index, indicating additive gene effects. Grain yield per plant showed the highest PCV (52.74), while flag leaf blade width showed the least PCV (5.93). The phenotypic and genotypic coefficient variation in Ethiopian finger millet landraces varied from 8.05–31.23% and 6.52–24.21% for days to maturity and grain yield per plant, respectively (Bezawele et al. 2006). Panda and co-workers (2022), explored the genetic variability of panicle characteristics in 33 indigenous finger millet genotypes and the yield reported varied from 13.2 to 32.4 q/ha. The actual heritable variation can not be genuinely estimated from the genotypic coefficient of variance. In addition, GCV and heritability would provide calculable statistics on the magnitude of the genetic advance anticipated from the selection. High heritability estimates for agronomic traits indicated no environmental effect. A maximum (96.67) *hBS* was noticed for days to 50% flowering, followed by 1000-grains weight, while the least *hBS* (68.37) was observed for flag leaf blade width (Table 1). Genotype selection created on specific traits with high *hBS* will prime the earlier and higher gains in the progeny compared to low *hBS* traits (Ganapathy et al. 2011). High heritability with high genetic advance revealed that the recorded traits are influenced by additive gene action and can be improved by assortment (Mahanthesh et al. 2017). Genetic advance over mean (GAM) was the maximum for grain yield per plant (99.51), followed by harvest index (65.59) and ear head width (59.22), productive tillers (55.54), 1000-grains weight (36.74), flag leaf blade width (25.19) and plant height (24.92) while the other traits like days to 50% flowering, days to maturity, fingers number on the

Table 1 Analysis of variance (ANOVA), mean, genetic variability and heritability for agronomic traits

Trait	ANOVA	Mean	SE	Min	Max	GCV	PCV	ECV	CV	<i>hBS</i>	GAM
EHL	2.24**	9.16	0.11	5.88	12.57	12.5	14.45	6.61	6.58	79.08	23.57
EHW	5.05**	7.24	0.17	4.39	17.17	29.56	30.44	7.26	7.22	94.31	59.22
FN	0.68**	7.02	0.07	4.65	10.27	10.16	11.63	5.65	5.62	76.35	18.32
FLBL	17.74**	29.98	0.34	18.09	55.03	13.2	14.28	5.43	5.43	85.52	25.19
FLBW	0.01**	1.11	0.01	0.87	1.31	4.91	5.93	3.34	3.31	68.37	8.37
PL	3.92**	16.84	0.16	11.2	21.3	10.47	11.74	5.31	5.31	79.54	19.26
PT	3.79**	6.25	0.16	2.94	14.69	28.76	30.67	10.72	10.86	87.78	55.54
PH	154.05**	97.81	1.03	57.03	124.51	12.41	12.75	2.92	2.94	94.74	24.92
GYPP	145.63**	19.22	0.8	4.14	71.57	50.44	52.74	15.4	14.06	91.47	99.51
DF	77.85**	95.99	0.7	64.73	117.23	8.93	9.08	1.66	1.66	96.67	18.11
DM	105.41**	133.75	0.8	93.29	160.29	7.29	7.55	1.97	1.97	93.21	14.51
TGW	0.21**	2.24	0.04	1.22	3.28	18.28	18.76	4.23	4.13	94.93	36.74
HI	48.57**	16.14	0.47	4	30.32	33.65	35.63	11.69	10.86	89.24	65.59

ns $P > 0.05$; * $P < 0.05$; ** $P < 0.01$. SE, Standard Error; GCV, Genotypic Coefficient of Variability; PCV, Phenotypic Coefficient of Variability; ECV, Environmental Coefficient of Variability; CV, Coefficient of Variance; *hBS*, Broad Sense Heritability; GAM, Genetic Advance over Mean.

Refer to the methodology for trait details.

main ear, peduncle length and flag leaf blade width showed less than 20% of GAM (Table 1). The highest coefficient of variation was portrayed by grain yield per plant (14.06%), followed by harvest index (10.86%) (Table 1). In the given study, high heritability associated with high genetic advance was recorded for the traits, ear head length, ear head width, flag leaf blade length, productive tillers, plant height, grain yield per plant, test weight of 1000-grains, and harvest index which indicates lesser environmental influence on these traits and a role of an additive gene effect.

Correlation among agronomic traits: A robust positive correlation close to unity among the attributes illustrated as red blocks and blue blocks showed a negative correlation (Fig 1). Grain yield per plant had a highly significant ($P<0.001$) positive correlation with harvest index (0.72***), productive tillers (0.54***), test weight of 1000-grains (0.48***), plant height (0.35***), and flag leaf blade length (0.26***); however, a highly significant ($P<0.001$) negative correlation with days to 50% flowering (-0.35***), and days to maturity (-0.28***), were observed. The correlation between grain yield and other agronomic traits assists in refining selection proficiency. The correlation between traits is contingent on the association of loci or significant QTLs, which governs the variability for traits located on identical chromosomes. A significant positive correlation had been reported between grain yield and finger width ($rg=0.876$), threshing percent ($rg=0.677$), grains per spikelet ($rg=0.623$), panicle exertion ($rg=0.571$) and peduncle length ($rg=0.517$) (Eric *et al.* 2016). In the present study, a highly significant correlation between grain yield per plant and plant height is justifiable. Usually, the taller finger millet plant has several leaves, increasing total biomass production through improved carbon fixation and eventually yielding to reproductive organ establishment. Grounded on these verdicts, a high-yielding finger millet plant is tall. It is accomplished by sustaining maximum leaf area and bearing a bulky ear head to embrace as many grains as conceivable. Henceforth, assortment standards founded on desired values traits like plant height, flag leaf blade length, ear head length, and grain yield per plant will be more beneficial than along a single desired trait grain yield per plant.

Principal component analysis (PCA): PCA provides the most appropriate and explicit understanding of the degree of relatedness among various contributing traits and genotypes used in the experimental setup. PCA resulted in 13 independent principal components (PCs), among which the first five PCs with eigenvalues greater than unity accounted for 74% of the total variability. PC1 holds 26.49% of the total variation. The traits which positively contribute to PC1 were grain yield per plant (0.79), productive tillers (0.68), harvest index (0.63), test weight of 1000-grains (0.61), plant height (0.60), flag leaf blade length (0.55), peduncle length (0.41), ear head length (0.08) and fingers number on the main ear (0.06) whereas traits days to 50% flowering, days to maturity, ear head width and flag leaf blade width contributed negatively for PC1 (Fig 2). PC2 holds 17.76% of the total variation, and the traits which govern the highest

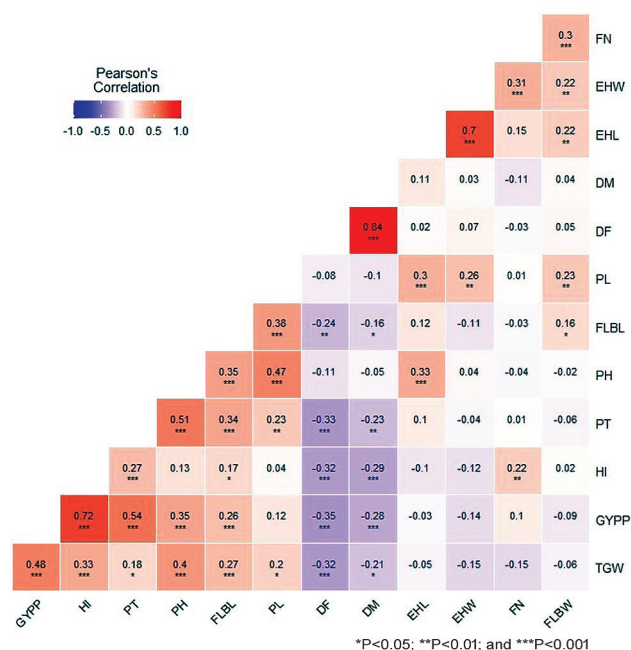


Fig 1 Correlation among agronomic traits of finger millet germplasm.

interpretation of PC2 were ear head length (0.83), ear head width (0.78), and peduncle length (0.56). The contributing agronomic traits in PC1 and PC2 are shown in the PCA biplot (Fig 2). Suman and co-workers (2019) studied the genetic diversity of 55 finger millet accessions using PCA and found that the first four PCs with eigenvalues greater than 1.33 contributed 66.54% of the total variation (Suman *et al.* 2019). In the present study, grain yield per plant, 1000-grains weight, and harvest index had a slight angle with each other, indicating a positive correlation. Similarly, days to 50% flowering and days to maturity had positive correlations with each other and negative correlations to

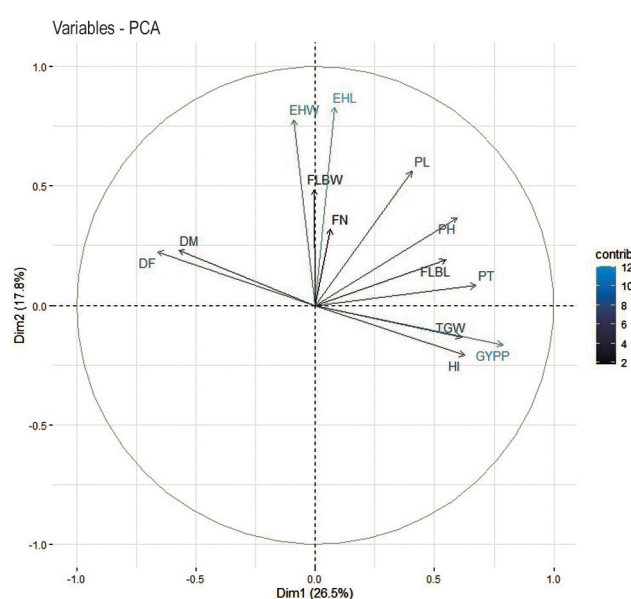


Fig 2 PCA biplot of variables showing the contribution of various traits to variation in PC1 and PC2.

Table 2 Mean comparison between 5 clusters for agronomic traits

Trait	Cluster 1 (8)		Cluster 2 (10)		Cluster 3 (43)		Cluster 4 (26)		Cluster 5 (67)	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
EHL	8.93	6.71-10.92	9.23	6.75-11.28	8.47	6.44-10.76	8.24	5.80-10.04	10.87	8.81-12.21
EHW	6.41	5.12-8.50	7.01	5.76-11.18	6.17	4.82-7.40	6.60	4.65-9.94	10.61	7.73-17.31
FN	6.55	5.0-7.5	7.36	6.5-8.5	7.06	6.0-8.5	7.05	5.5-8.5	7.72	6.5-10.5
FLBL	29.07	22.78-31.31	31.12	26.26-37.88	31.19	22.77-53.05	24.44	19.70-28.42	28.39	18.71-36.06
FLBW	1.09	0.91-1.23	1.14	1.06-1.31	1.08	0.95-1.17	1.10	1.02-1.28	1.15	1.00-1.24
PL	16.97	14.21-21.87	17.77	13.66-20.86	17.06	15.15-18.41	14.04	10.96-17.22	17.66	13.84-20.85
PT	6.10	4.0-10.5	7.10	4.0-12.5	7.57	5.0-15.0	4.70	3.0-6.5	5.82	4.0-8.5
PH	102.41	82.58-122.52	101.91	86.11-112.93	99.42	58.53-113.24	77.42	54.82-94.00	98.66	80.12-126.34
GYPP	16.88	2.85-27.55	18.76	6.00-29.40	34.86	17.45-74.80	9.37	2.45-19.85	16.99	4.70-29.85
DF	98.66	88.5-111.0	83.60	64.0-93.5	90.35	73.5-103.0	101.78	92.0-116.0	100.78	93.0-116.5
DM	137.08	119.0-149.0	119.45	94.0-141.5	127.21	114.5-141.0	140.98	127.0-155.0	138.37	128.0-161.0
TGW	2.39	1.56-3.26	2.23	1.43-2.57	2.58	2.06-3.01	1.67	1.25-2.23	2.05	1.40-2.63
HI	13.91	6.47-25.45	15.77	6.52-24.37	24.45	16.53-32.75	13.51	4.14-27.15	15.26	8.08-26.76

Refer to the methodology for trait details.

yield contributing traits, viz. grain yield per plant, harvest index, and thousand grains weight. Hence, selecting parent genotypes with the help of a PCA biplot would be rewarding for future breeding programmes.

Cluster analysis: The current study focused on identifying finger millet accessions with high yield coupled with desirable agronomic traits via hierarchical clustering analysis (HCA). The finger millet germplasm was grouped into five distinct clusters diverged from 8 (cluster 1) to 67 (cluster 5) (Table 2). Cluster 2 accessions matured early (119.45 days), while cluster 5 accession were late matured (138.37 days) (Table 2). The average phenotypic distance within a group was higher in cluster 2 (4.428), followed by cluster 3 (4.327), while lowest in cluster 5 (3.238). The highest average distance between all the objects belonging to two different groups was observed within clusters 3 and 5 (7.779), followed by clusters 4 and 5 (7.435), and the lowest between clusters 1 and 2 (4.645). The checks genotype KMR 301 and ML 365 of finger millet lie in cluster 3, while GPU 67 and VR 847 were categorized in cluster 4. Based on mean cluster values, selecting genotypes with more than one required trait is always valuable whether it belongs to, unlike clusters. Therefore, it is proposed that 10 accessions assembled in cluster 2 are noticed as the genotypes with high grain yield per plant and early maturity. These genotypes can form the genetic base for developing high-grain-yielding and early-maturing varieties to create inbred

lines for use in the breeding programmes. The genotypes of cluster 2 and cluster 1 can aid as a base material when the breeding objective is to accumulate the weight of the grain, as cluster 3 genotypes have the highest 1000-grains weight (2.58 g), which is positively correlated with plant height and flag leaf blade length and cluster 1 genotypes dominate in plant height. Breeders can choose exceedingly divergent genotypes from particular clusters based on cluster mean values in breeding experiments. Recently, the finger millet germplasm of Uttarakhand hills was sorted into eight groups using Mahalanobis D statistics (Soe *et al.* 2022). Similarly, 31 finger millet genotypes collected from different germplasm storage units in India were grouped into four clusters based on Euclidean distances (Sharma *et al.* 2022). Thus, generating genotypes into collections is a big step toward characterizing these genotypes and forming a part of vital genetic resources for finger millet improvement.

Promising yield-specific accessions: The top 10 promising accessions with desirable trait values as well as a significant correlation with grain yield per plant are given in Table 3. Sharma *et al.* (2022) identified two diverse and complementary genotypes that possessed the complementary traits, viz. number of spikes, number of tillers per plant, bold seed, grain yield, single head weight and harvest index. Accession IC406600 was the most promising yield-specific accession having a 71.57 g grain yield per plant. VR 847 was the top-performing check for grain yield per plant, i.e.

Table 3 Top 10 accessions of desirable traits

Trait	Class	Top 10 accessions	Range	Top-performing check
GYPP	High	IC406600, IC71581, IC87514A, IC203761, IC87518, IC71410, IC49946A, IC49974E, IC382774, IC49979B	71.57-32.12 gm	VR847 (48.18 gm)
FLBL	High	IC49946A, IC4992, IC340142, IC50019, IC50009, IC71395, IC87502, IC71419A, IC71395A, IC45867	55.03-34.26 cm	GPU67 (33.93 cm)
PT	High	IC406600, IC73542, IC87319, IC203761, IC49946A, IC50019, IC66172, IC71581, IC71419A, IC87514A,	14.69-9.81	VR847 (6.92)
PH	High	IC65632A, IC71330, IC87530, IC83483, IC71399, IC71400A, IC82522, IC87319, IC71342, IC71408	124.51-115.07 cm	KMR301 (97.52 cm)
TGW	High	IC71413, IC87526, IC49979B, IC71400A, IC49981, IC71399, IC71410, IC204143, IC382774, IC49990B	3.28-2.88 gm	GPU67 (2.88 gm)
HI	High	IC340127, IC71400A, IC84534, IC51458, IC203978, IC50000, IC49946A, IC204137, IC49947A, IC340142	30.32-26.91	VR847 (28.04)
DF	Low*	IC45977B, IC71581, IC206162, IC73542, IC73541A, IC87458A, IC204141, IC73581, IC71419A, IC49949A	64.73-84.73 days	GPU67 (86.67 days)
DM	Low*	IC45944B, IC206166, IC73542, IC206162, IC73581, IC71581, IC206165, IC49947, IC34779, IC45878	93.29-118.29 days	GPU67 (122.75 days)

*Low agronomic values are desirable.

Refer to the methodology for trait details.

48.18 g. Accession IC49946A has been acknowledged for its longest flag leaf blasé length (55.03 cm) because of the importance of flag leaf in increasing the content of photo-assimilates and minerals accumulation in the reproductive parts of plants. In terms of early mature germplasm, accession IC45944 showed maturity in 93.29 days. Early maturing crop varieties help to reduce the risk of crop loss and enhance crop resilience to disease and harsh climatic conditions.

Genetically diverse and superior genotypes are the ultimate aim for plant breeders in population and heterosis breeding programmes. The present research revealed highly diverse finger millet germplasm for grain yield and other agronomic traits which favour selection and utilization in different breeding programmes. The critical analysis of results obtained from descriptive statistics, correlation studies, and PCA indicated that productive tillers, plant height, flag leaf blade length, and peduncle length should be given priority when selecting for high grain yield per plant in establishing the core collection. Flag leaf blade length stood out as the character with the highest significant positive correlation with peduncle length, productive tillers and plant height. This suggests that flag leaf blade length could be used as an indirect selection toward increasing grain yield per plant in finger millet germplasm. For the expansion of trait-specific heterotic gene pools, promising trait-specific superior genotypes of finger millet will assist as donors for crop improvement, nutritional security and crop diversification.

REFERENCES

- Baath G S, Northup B K, Gowda P H, Rocateli A C and Turner K E. 2018. Adaptability and forage characterization of finger millet accessions in U.S. southern great plains. *Agronomy* **8**: 177.
- Badigannavar A and Ganapathi T R. 2018. Genetic variability for mineral nutrients in indigenous germplasm lines of finger millet (*Eleusine coracana* Gaertn.). *Journal of Cereal Science* **84**: 1–6.
- Bezaweletaw K, Sripichitt P, Wongyai W and Hongtrakul V. 2006. Genetic variation, heritability and path-analysis in Ethiopian finger millet [*Eleusine coracana* (L.) Gaertn] landraces. *Agriculture and Natural Resources* **40**(2): 322–34.
- Chethan S and Malleshi NG. 2007. Finger millet polyphenols: Characterization and their nutraceutical potential. *American Journal of Food Technology* **2**(7): 582–92.
- Eric MO, Pangirayi T, Paul S, Mwangi G and Abhishek R. 2016. Correlations, path coefficient analysis and heritability for quantitative traits in finger millet landraces. *International Journal of Current Microbiology and Applied Sciences* **8**(1): 1020–27.
- Ganapathy S, Nirmalakumari A and Muthiah A R. 2011. Genetic variability and interrelationships analyses for economic traits in finger millet germplasm. *World Journal of Agricultural Sciences* **7**(2): 185–88.
- Kumar A, Metwal M, Kaur S, Gupta A K, Puranik S, Singh S, Singh M, Gupta S, Babu B K, Sood S and Yadav R. 2016. Nutraceutical value of finger millet [*Eleusine coracana* (L.) Gaertn.] and their improvement using omics approaches. *Frontiers in Plant Science* **7**: 934.
- Mahanthesha M, Sujatha M, Meena A K and Pandravada S R. 2017. Studies on variability, heritability and genetic advance for quantitative characters in finger millet [*Eleusine coracana* (L.) Gaertn] germplasm. *International Journal of Current Microbiology and Applied Sciences* **6**(6): 970–74.
- Panda D, Panda A, Prajapati H, Behera P K, Nayak J K, Lenka K C and Parida P K. 2022. Genetic variability of panicle architecture and nutritional parameters in indigenous finger millet genotypes from Koraput, Eastern Ghats of India. *Cereal Research Communications*.
- Sharma N, Bandyopadhyay B B, Chand S, Pandey P K, Baskheti D C and Alam B K. 2022. Genetic diversity, trait association and cause effect analysis in selected genotypes of finger millet

- [*Eleusine coracana* (L.) Gaertn.]. *Journal of Environmental Biology* **43**(4): 551–61.
- Soe W, Jeena A S, Pant U, Kumar A, Chaudhary R and Chaudhary D. 2022. Revealing genetic diversity in finger millet [*Eleusine Coracana* (L.) Gaertn] germplasm collected from Uttarakhand hills. *Electronic Journal of Plant Breeding* **13**(2): 633–44.
- Suman A, Surin S S and Ahmad E. 2019. Finger millet germplasm characterization and evaluation using principal component analysis. *International Journal of Chemical Studies* **7**(2): 1002.
- Yadav M R, Parihar C M, Jat S L, Singh A K, Kumar R, Yadav R K, Kuri B R, Parihar M D, Yadav B, Verma A P and Jat M L. 2017. Long term effect of legume intensified crop rotations and tillage practices on productivity and profitability of maize vis-a-vis soil fertility in North-Western Indo-Gangetic Plains of India. *Legume Research* **40**(2): 282–90.