JEB®
Journal of Environmental Biology
p-ISSN: 0254-8704 • e-ISSN: 2394-0379 • CODEN: JEBIDP
Journal website : www.jeb.co.in ★ **E-mail :** editor@jeb.co.in
Triveni Enterprises
(Educational Services Set-up)

Original Research

DOI : http://doi.org/10.22438/jeb/43/4/MRN-2052

Genetic diversity, trait association and cause effect analysis in selected genotypes of finger millet [*Eleusine coracana* (L.) Gaertn.]

N. Sharma[1], B.B. Bandyopadhyay[1], S. Chand[1,2]*, P.K. Pandey[1], D.C. Baskheti[1] and B.K. Alam[3]

[1]Department of Genetic and Plant Breeding, G.B. Pant University of Agriculture and Technology, Pantnagar-263 145, India
[2]ICAR-Indian Grassland and Fodder Research Institute, Jhansi-284 003, India
[3]ICAR-National Research Centre for Orchids, Pakyong-737 106, India

***Corresponding Author Email :** subhashchand5415@gmail.com

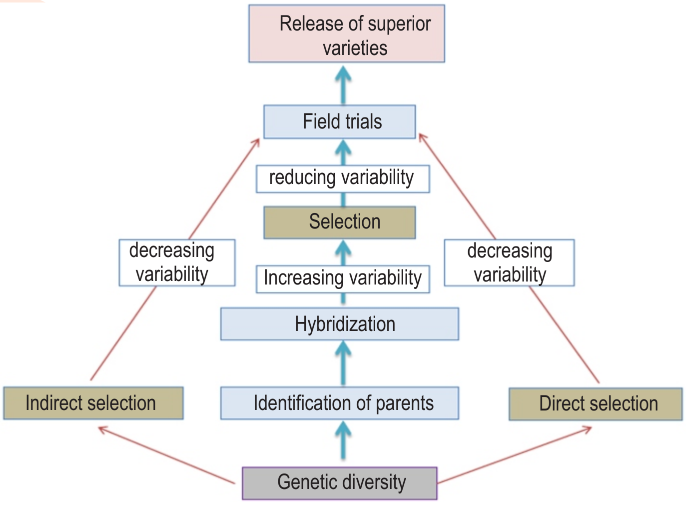
Received: 01.07.2021 *Revised*: 06.09.2021 *Accepted*: 17.11.2021

Abstract

Aim: The present investigation was planned to evaluate the finger millet genotypes for genetic variability, genotypic relatedness, an association between traits, and their direct effect on increasing grain and fodder yield.

Methodology: The experimental material used in the present investigation comprised thirty-one finger millet genotypes collected from different sources in India. The experiment was conducted in a randomized complete block design (RCBD) with three replications and analyzed for thirteen yield and its ancillary traits. In addition, the pre-existing variability, genetic parameters, inter-trait association, and direct and indirect contribution to grain yield were analyzed using OPSTAT Software. The principal component analysis (PCA), heat map and agglomerative hierarchical clustering were done using R software version3.6.1.

Results: Analysis revealed a high genotypic coefficient of variation (GCV) to the number of productive tillers per plant (57.98%), grain yield per plot (49.38%), number of heads per plot (49.27%) and number of fingers per head (45.54%). High heritability coupled with high genetic advance as percent of mean was observed for the number of heads per plot. Grain yield exhibited a significantly high positive correlation with fodder yield per plant (r_g: 0.98), number of heads per plot (r_g: 0.89) and harvest index (r_g: 0.78). Fodder yield per plant, harvest index, single head weight, number of heads per plot and days to final harvest had a high direct positive effect on grain yield. The PCA separated total genetic variation into six components and covered almost 85.0% of genetic variation. Genotypes were grouped into four main groups and several subgroups based on Euclidean distances.



Interpretation: The higher magnitude of GCV, heritability coupled with high genetic advance for a trait of interest; strong correlation between dependent and independent traits would be desirable for productivity enhancement in finger millet. The additive gene effect would also be rewarding by direct phenotypic selection.

Key words: Finger millet, Genetic diversity, Principle component analysis

How to cite : Sharma, N., B.B. Bandyopadhyay, S. Chand, P.K. Pandey, D.C. Baskheti and B.K. Alam: Genetic diversity, trait association and cause effect analysis in selected genotypes of finger millet [*Eleusine coracana* (L.) Gaertn.]. *J. Environ. Biol.*, **43**, 551-561 (2022).

Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn; 2n=4x=36, also called ragi] represents one of the major crops among the six-member group of minor millets *viz.,* finger millet, little millet, foxtail millet, proso millet, barnyard millet and kodo millet (Mundada *et al.,* 2019). This crop has local and regional importance because of its unique endurance capacity to survive under harsh or unfavourable nerve-racking climatic conditions (Seethatram, 1989). The crop provides food and fodder security of disadvantaged regions and rich in nutritional value (Panda *et al.,* 2020) compared to extraordinarily superior to many privileged crops like rice and wheat. The finger millet seeds are consumed as food for humans, and the crop foliage is used as forage for livestock. The seed consumption helps stave off anaemia, celiac disease, and diabetes in children, large urban and rural working men, women and vulnerable sections of the population (Devi *et al.,* 2014; Banerjee *et al.,* 2020). To increase awareness of the health benefits of millets and their suitability for cultivation in tough conditions, United Nations General Assembly (UNGA) adopted a resolution declaring 2023 as the International Year of Millet (Kumar, 2021).

In an initiative towards the success of international recognition and to promote the nutritional and ecological benefit of millet to the world as a key component of the food basket, Uttarakhand Agriculture Produce Marketing Board (UKAPMB), in collaboration with Agricultural and Processed Food Product Export Development (APEDA) and Just Organik (an exporter) consign an agreement of effect policy changes for exporting organic finger millet and barnyard millet direct from farmers' field of Uttarakhand state to Denmark. Finger millet, in Uttarakhand state, grows at a different level of altitude of hills in the Himalayas and rainfed conditions under traditional cropping system (Bandyopadhyay, 1998; Trivedi *et al.,* 2018). Poor crop competitive ability, low crop productivity compared to major cereal crops, decreasing demand, low price for produce, and the declining trend of cultivation are the major constraints towards gaining decent revenues by capitalizing on the crop at the national and international level (Seethatram, 1989). In pursuance of filling the most desire ambitious project and mitigating the above constraints, there is a dire need to focus on the crop production aspects by increasing the area and productivity.

The genetic variability in a gene pool is crucial to increase genetic crop potential using suitable breeding programs such as phenotypic selection and hybridization (Anteneh *et al.,* 2019; Panda *et al.,* 2021). However, magnitude of additive gene effect in heritable variance decides the success of selection (Dabholkar, 1992; Gaoh *et al.,* 2020).The premier CGIAR institute, *i.e.,* ICRISAT alone has 5949 finger millet accessions in India out of 8000 cultivable genotypes available globally (Reddy *et al.,* 2009; Ramakrishnan *et al.,* 2016). Grain yield is a complex quantitative trait and is expressed as a function of various yield attributing component traits of the plant. The genetic improvement primarily depends on the availability of diverse germplasm and genetic variability at various levels (Bandyopadhyay *et al.,* 2017; Lule *et al.,* 2018). The untapped genetic variability in finger millet could be channelized employing the dearth of knowledge of conventional and non-conventional tools of plant breeding (Panda *et al.,* 2021) Thus, understanding the genetic base of yield and related traits with genetic variation and genotypic relationship is required to exploit the preexisting genetic variability and its substantial use in future breeding programs. The population diversity in finger millet obliges its suitability in different agro-climatic conditions due to crop adaptation to marginal land (Trivedi *et al.,* 2018). Maintenance and management of diversity are associated with the livelihood of farmers. Therefore, the present investigation in finger millet revealed different conventional breeding approaches to harness the suitable genotypes having high yield potential and the selected genotype would be beneficial for further breeding programs.

Materials and Methods

Study site: The accessed genotypes were evaluated at N. E. Borlaug Crop Research Center of G.B. Pant University of Agriculture and Technology, Pantnagar during *Kharif*-2018. The testing site received a mean annual rainfall of 600mm with average minimum and maximum temperature of 23ºC and 32ºC, respectively. The experimental area is characterized by silty loam in texture, moderate phosphorous availability, and potassium with soil pH 7.4 to 7.6.

Plant materials: The experimental material used in the present investigation comprised a set of 31 finger millet genotypes collected from different sources *viz.,* eight from ICRISAT (Patancheru, Hyderabad, India), five from VPKAS (ICAR-Almora, Uttarakhand), twelve from PCPGR (Pantnagar, Uttarakhand), three local landraces from Pithoragarh, Uttarakhand and three (one advanced line and two released varieties) from GBPUA&T, Pantnagar, Uttarakhand. The collected seeds were cleaned manually and warehoused in airtight plastic bottles at room temperature to avoid excess moisture and insects and pests infestation.

Experimental design and layout: The experiment was planned in a randomized complete block design (RCBD) with three replications. Each replication had an area of 3 m length and 1 m width with three consecutive rows. The seeds were sown in 1st week of June 2018 with a spacing of 30 cm between two rows and 10 cm between two plants within a row. The genotypes were irrigated at regular intervals for stress-free environment using surface furrow irrigation till crop physiological maturity. The recommended dose of fertilizer [50:40:25; NPK (Kg ha^{-1})] was used during crop growth. Urea as a source of nitrogen was applied twice at sowing and tillering stage whereas both phosphorous and potassium were used in the form of di-ammonium phosphate and muriate of potash, respectively, at sowing only. All the recommended agronomic practices were followed during crop season for better growth and crop stand.

Data collection: The realization of a crop's total physiological production capacity predominantly depends on the full expression of morphological characters under prevalent climatic conditions at growing site. In this study, 13 morphological characters were analyzed for recording data at appropriate crop growth stages on the field. Ten representative plants were randomly selected and tagged from each replication for recording further observations. The morphological characters such as days to 50% flowering, number of heads per plot, days to final harvest, harvest index (%), and grain yield per plot (kg) were observed on the entire field in all replications. For remaining morphological characters such as plant height (cm), number of productive tillers per plant , leaf area (cm^2), number of fingers per head, number of spikes per finger, single head weight (g), seed volume (seeds cm^{-2}; measured as the number of seeds occupy the space of one square centimeter area) and fodder yield per plant (kg) were recorded on individual plant basis using ten randomly selected plants in each replication.

Data analysis: The pre-existing variability in observed data was subjected to analysis through analysis for variance using OPSTAT software (Sheoran *et al.,* 1998). A standard statistical procedure was followed to measure the variability and estimate genetic parameters of the individual trait and included phenotypic variance (σ^2p), genotypic variance (σ^2g), error or environmental variance (σ^2e). The phenotypic and genotypic coefficient of variation (PCV and GCV) was determined as per the procedure of Burton and Devane (1993). Broad sense heritability (h_b^2), genetic advance (GA), genetic gain over percent of mean (GG) were computed as per Johnson *et al.* (1955). The relationship between two individual variable traits and their contribution to grain yield was determined through correlation coefficient and path coefficient analysis, respectively, using OPSTAT software (Sheoran *et al.,* 1998). The Principal Component Analysis (PCA) and agglomerative hierarchical clustering were done using R software version 3.6.1. The PCA was used to determine the contribution of individual genotypes and traits to total variation. Heat map was also plotted using eigenvalues to visualize distances amongst the genotypes.

Results and Discussion

Analysis of variance revealed significant genotypic differences ($P<0.05$) for grain yield and its component attributing characters among thirty-one finger millet genotypes (Table 1). It suggests that substantial variation for respective trait exists in finger millet genotypes, which offers opportunities for genotypic improvement through phenotypic direct selection under the prevailing environmental condition at growing site. The higher magnitude of genetic variance (σ^2g) over environmental variance (σ^2e) for studied traits indicated that trait expression is highly influenced by genetic constitution than environmental variations (Table 2). Fodder yield per plant, grain yield per plant and number of heads per plot registered high value of genetic variance, while single head weight exhibited the lowest value. Single head weight, productive tillers per plant, and harvest index showed minimal gap between phenotypic and genotypic variance suggesting traits are stable and least influenced by prevailing environmental regimes. The higher phenotypic variance was also reported for days to 50% heading, days to 50% maturity, productive tillers, plant height, fingers per head, and grain yield per plant (Lule *et al.*, 2012; Anteneh *et al.*, 2019).

The magnitude of genetic and environmental effects involved in the expression of different characters is determined by GCV and PCV. In this study, the values of PCV recorded high correspond to its GCV value for each trait (Table 2). It indicates

Table 1: Analysis of variance (ANOVA) and simple descriptive variability parameters for yield and its contributing traits among thirty-one finger millet genotypes

Characters[#]	Mean sum of squares[@]			Variable parameters[$]					
	Replication (2)	Genotype (30)	Error (60)	Range	Mean	±SE (m)	± SE (d)	CD	CV
DTF	0.90	216.95*	32.07	62-97	72.13	3.27	4.62	9.27	7.85
PH	0.52	588.59*	30.85	57-117	96.74	3.21	4.54	9.09	5.74
PT/P	0.42	13.91*	2.56	1.0-12	3.35	0.92	1.31	2.62	47.70
LA	0.05	106.98*	3.70	5.54-31.85	21.09	1.11	1.57	3.15	9.12
F/H	1.22	36.42*	7.33	1.0-15	6.84	1.56	2.21	4.43	39.58
S/F	1.39	82.94*	28.95	28-50	38.23	3.11	4.39	8.81	14.08
DFH	2.88	775.57*	20.61	96-158	144.98	2.62	3.71	7.43	3.13
H/P	6.71	17758.00*	31.94	18-262	156.00	3.26	4.62	9.25	3.62
SHW	0.03	1.52*	0.04	2.19-5.19	3.51	0.12	0.17	0.33	5.81
SV	2.36	71.97*	22.08	31-54	39.72	2.71	3.84	7.70	11.83
FY/P	0.00	0.85*	0.00	0.45-2.49	1.35	0.03	0.04	0.08	3.72
HI	0.24	204.24*	4.28	12.17-47.77	37.00	1.20	1.69	3.39	5.59
GY/P	0.00	0.21*	0.00	0.06-1.19	0.53	0.03	0.04	0.08	9.48

[@]Figure under parenthesis represents degree of freedom; * Significant at 5% level of significance; [#] DTF-Days to 50% flowering, PH-Plant height, PT/P-Productive tillers per plant, LA-Leaf area, F/H-Fingers per head, S/F-Spikes per finger, DFH-Days to final harvest, H/P-Heads per plot, SHW-Single head weight, SV-Seed volume, FY/P-Forage yield per plant, HI-Harvest index, GY/P-Grain yield per plot; [$] CD-Critical difference at 5% level of significance, SE (m)-Standard error of mean, SE (d)-Standard error of difference, CV-Coefficient of variation

Table 2: Estimation of genetic parameters of variability for yield and its contributing traits in thirty-one finger millet genotypes

Parameter*	Morphological traits[#]												
	DTF	PH	PT/P	LA	F/H	S/F	DFH	H/P	SHW	SV	FY/P	HI	GY/P
σ^2g	61.63	185.91	3.78	34.43	9.70	18.00	251.65	5908.69	0.49	16.63	282940.75	66.65	68251.40
σ^2p	93.70	216.76	6.34	38.12	17.02	46.95	272.27	5940.63	0.53	38.72	285455.43	70.94	70766.08
GCV (%)	10.88	14.09	57.98	27.82	45.54	11.10	10.94	49.27	19.97	10.27	39.45	22.06	49.38
PCV (%)	13.42	15.22	75.08	29.28	60.33	17.93	11.38	49.41	20.80	15.67	39.62	22.76	50.28
ECV (%)	2.54	1.13	17.10	1.46	14.80	6.83	0.44	0.13	0.83	5.40	0.18	0.70	0.90
h^2 (b) (%)	65.77	85.77	59.63	90.30	56.97	38.33	92.43	99.46	92.19	42.95	99.12	93.96	96.45
GA (%)	13.12	26.01	3.09	11.49	4.84	5.41	31.42	157.92	1.39	5.51	1.09	16.30	0.53
GG_M (%)	18.18	26.89	92.22	54.46	70.80	14.15	21.67	101.23	39.50	13.86	80.91	44.06	99.89

*σ^2g-Genotypic variance, σ^2p-Phenotypic variance, PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h^2b-Heritability in broad sense, GA-Genetic advance, GG_M-Genetic gain over per cent of mean; [#]as indicated in Table 1

Table 3: Correlation coefficient of thirteen morphological traits of thirty-one finger millet genotypes at phenotypic (r_p) and genotypic (r_G) level

Parameter	Morphological traits[#]												
	Correlation	PH	PT/P	LA	F/H	S/F	DFH	H/P	SHW	SV	FY/P	HI	GY/P
DTF	r_P	0.33**	0.14	0.23*	0.12	0.35**	0.01	-0.20	-0.12	0.19	-0.30**	-0.07	-0.26*
	r_G	0.17	-0.31**	0.08	-0.35**	-0.13	-0.18	-0.29**	-0.29**	-0.39**	-0.43**	-0.26*	-0.50**
PH	r_P		0.09	0.17	0.17	0.33**	0.27**	0.20	-0.32**	0.31**	0.04	-0.02	0.06
	r_G		-0.17	0.08	-0.04	0.13	0.20	0.19	-0.43**	0.11	0.01	-0.12	-0.01
PT/P	r_P			0.26*	0.29**	0.33**	0.34**	-0.11	0.33**	0.51**	-0.02	-0.14	-0.02
	r_G			0.11	-0.10	-0.20	0.26*	-0.19	0.31**	0.23*	-0.09	-0.37**	-0.16
LA	r_P				0.27**	0.32**	0.15	0.02	0.32**	0.07	0.122	0.06	0.12
	r_G				0.15	0.19	0.08	0.01	0.30**	-0.19	0.10	-0.01	0.08
F/H	r_P					0.30**	0.04	-0.06	0.22*	0.43**	0.03	-0.05	0.07
	r_G					-0.28**	-0.14	-0.13	0.14	0.06	-0.03	-0.27**	-0.05
S/F	r_P						0.19	0.13	0.18	0.43**	0.19	0.13	0.21*
	r_G						-0.00	0.13	0.10	-0.18	0.21*	-0.07	0.14
DFH	r_P							0.32**	0.10	-0.08	0.40**	0.20	0.40**
	r_G							0.32**	0.05	-0.41**	0.40**	0.15	0.37**
H/P	r_P								-0.33**	-0.09	0.88**	0.76**	0.89**
	r_G								-0.36**	-0.22*	0.88**	0.77**	0.89**
SHW	r_P									-0.02	0.08	-0.05	0.09
	r_G									-0.19	0.07	-0.10	0.05
SV	r_P										-0.19	-0.13	-0.13
	r_G										-0.37**	-0.47**	-0.39**
FY/P	r_P											0.69**	0.98**
	r_G											0.70**	0.98**
HI	r_P												0.78**
	r_G												0.78**

*Significant at 5% and **significant at 1% level of significance; [#]as indicated in Table 1

the influence of environmental variables on the phenotypic expression of these traits. The highest value for PCV and GCV were recorded for number of productive tillers per plant, followed by number of fingers per head, grain yield per plant and number of heads per plot. A close association between PCV and GCV values was observed in traits *viz.,* number of heads per plot, fodder yield per plant, harvest index and grain yield per plant. The lowest value of PCV and GCV was found in days to final harvest and days to 50% flowering, respectively. It indicates that the environment exerted a little influence on the manifestation of its phenotypic variability, and selection would effectively improve these economically important traits. The high PCV and GCV were

Table 4: Partitioning of direct and indirect effects of morphological traits of thirty-one finger millet genotypes at phenotypic (P) and genotypic (G) level by path coefficient analysis

Parameter		Morphological traits$^{\#}$												
		DTF	PH	PT/P	LA	F/H	S/F	DFH	H/P	SHW	SV	FY/P	HI	GY/P
DTF	P	0.01	0.01	-0.01	-0.01	0.01	0.00	0.00	-0.04	-0.02	0.01	-0.20	-0.01	-0.26*
	G	0.04	0.00	0.01	0.00	-0.02	0.00	-0.01	-0.04	-0.03	-0.03	-0.32	-0.05	-0.45**
PH	P	0.00	0.02	0.00	0.00	0.01	0.00	0.01	0.04	-0.04	0.01	0.02	0.00	0.06
	G	0.01	0.01	0.01	0.00	0.00	0.00	0.01	0.02	-0.05	0.01	0.00	-0.02	-0.01
PT/P	P	0.00	0.00	-0.04	-0.01	0.01	0.00	0.01	-0.02	0.04	0.02	-0.01	-0.02	-0.02
	G	-0.01	0.00	-0.04	0.00	-0.01	0.00	0.01	-0.02	0.04	0.02	-0.06	-0.08	-0.16
LA	P	0.00	0.00	-0.01	-0.03	0.01	0.00	0.01	0.00	0.04	0.00	0.08	0.01	0.12
	G	0.00	0.00	0.00	-0.03	0.01	0.00	0.00	0.00	0.03	-0.01	0.08	0.00	0.08
F/H	P	0.00	0.00	-0.01	-0.01	0.04	0.00	0.00	-0.01	0.03	0.02	0.02	-0.01	0.07
	G	-0.01	0.00	0.00	0.00	0.05	0.00	-0.01	-0.02	0.02	0.00	-0.02	-0.06	-0.05
S/F	P	0.00	0.01	-0.01	-0.01	0.01	-0.01	0.01	0.03	0.02	0.02	0.13	0.02	0.21*
	G	0.00	0.00	0.01	-0.01	-0.01	0.00	0.00	0.02	0.01	-0.01	0.16	-0.01	0.14
DFH	P	0.00	0.00	-0.02	0.00	0.00	0.00	0.03	0.06	0.01	0.00	0.27	0.03	0.40**
	G	-0.01	0.00	-0.01	0.00	-0.01	0.00	0.05	0.04	0.01	-0.03	0.29	0.03	0.37**
H/P	P	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.20	-0.04	0.00	0.60	0.13	0.89**
	G	-0.01	0.00	0.01	0.00	-0.01	0.00	0.02	0.13	-0.04	-0.02	0.66	0.16	0.89**
SHW	P	0.00	-0.01	-0.01	-0.01	0.01	0.00	0.00	-0.07	0.13	0.00	0.06	-0.01	0.10
	G	-0.01	0.00	-0.01	-0.01	0.01	0.00	0.00	-0.04	0.12	-0.01	0.05	-0.02	0.06
SV	P	0.00	0.01	-0.02	0.00	0.02	-0.01	0.00	-0.02	0.00	0.04	-0.13	-0.02	-0.13
	G	-0.01	0.00	-0.01	0.01	0.00	0.00	-0.02	-0.03	-0.02	0.07	-0.28	-0.10	-0.39**
FY/P	P	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.17	0.01	-0.01	0.68	0.12	0.98**
	G	-0.02	0.00	0.00	0.00	0.00	0.00	0.02	0.11	0.01	-0.03	0.74	0.14	0.98**
HI	P	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.15	-0.01	-0.01	0.47	0.17	0.78**
	G	-0.01	0.00	0.02	0.00	-0.01	0.00	0.01	0.10	-0.01	-0.03	0.52	0.21	0.78**

Residual is equal (0.01) for both phenotypic (P) and genotypic (G) level; * Significant at 5% and ** significant at 1% level of significance; $^{\#}$ as indicated in Table 1

reported for productive tillers per plant (Priyadharshini *et al.*, 2011; Patil and Mane, 2013), moderate for plant height, fingers per head, and ear length (Patil and Mane, 2013), and low for days to 50% flowering and days to maturity (Anuradha *et al.*, 2017).

The estimates of heritability ranged between 99.46% (number of heads per plot) to 38.33% (number of spikes per finger). High heritability (>80%) was recorded for number of heads per plot, fodder yield per plant, grain yield per plant, harvest index, days to final harvest, single head weight, leaf area and plant height indicating that inheritance of these characters was controlled by genetic variation of traits and less influenced by the environment. Moderate to low heritability was registered for days to 50% flowering, number of productive tillers per plant, number of fingers per head, number of spikes per finger and seed volume. In previous studies also, high broad sense heritability (>80%) was conveyed for grain yield per plant, harvest index, days to final harvest, leaf area (Kumari and Singh, 2015), fodder yield, number of heads per plant and plant height (Anteneh *et al.,* 2019). Heritability coupled with high genetic gain substantially decides the effectiveness of selection and helps to improve trait of interest in the breeding program (Johnson *et al.,* 1955; Nyquist and Baker, 1991). The maximum and minimum values for genetic advance were registered for the number of heads per plot and grain yield per plant, respectively. Days to final harvest, plant height and harvest index exhibited moderate value for genetic advance. The higher magnitude of genetic advance, the more the expected improvement of genetic progress per cycle of selection for a particular trait, and it measures stability under selection pressure.

The genetic gain over percent of mean registered high for the number of heads per plot followed by grain yield per plant, number of productive tillers per plant, fodder yield per plant and number of fingers per head. However, moderate to low genetic gain was registered for leaf area followed by harvest index, single head weight, plant height, days to final harvest, spikes per finger and seed volume. Likewise, high magnitude of genetic advance as per cent of mean was observed for grain yield per plant and harvest index (Kumari and Singh, 2015). However, Anteneh *et al.* (2019) reported low genetic advance as per cent of mean for grain yield per plant, fodder yield, finger per head, productive tillers per plant and days to maturity. High magnitude of heritability coupled with high values for GCV, genetic advance and genetic gain over per cent of mean for number of heads per plot suggested that direct selection would be rewarding due to additive gene effect and would respond very well to continuous selection. Direct

Table 5: Eigenvalues, standard deviation, proportion of variance, cumulative variance and eigenvectors of thirteen agronomically important traits in finger millet genotypes

Characters	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	0.35	-0.35	-0.38	0.57	-0.05
Plant height	-0.05	-0.20	-0.84	-0.04	0.08
Number of productive tillers per plant	0.17	0.68	-0.15	-0.16	0.51
Leaf area	-0.07	0.49	-0.30	0.50	-0.32
Number of fingers per head	0.11	0.43	-0.12	-0.31	-0.49
Number of spikes per finger	-0.15	0.30	-0.53	0.19	-0.27
Days to final harvest	-0.44	0.27	-0.24	0.21	0.64
Number of heads per plot	-0.93	-0.17	-0.19	-0.18	-0.01
Single head weight	0.05	0.77	0.39	0.29	-0.09
Seed volume	0.37	0.22	-0.40	-0.68	-0.08
Forage yield per plant	-0.96	0.16	-0.01	-0.05	-0.04
Harvest Index	-0.83	-0.18	0.15	0.03	-0.14
Grain yield per plot	-0.97	0.13	0.01	-0.06	-0.07
Eigenvalues	3.94	1.95	1.68	1.36	1.14
Standard deviation	1.98	1.40	1.29	1.16	1.07
Proportion of variance (%)	30.33	15.04	12.91	10.47	8.76
Cumulative proportion (%)	30.33	45.36	58.27	68.73	77.50

selection would be fixable and predictable. Plant height, leaf area, days to final harvest, single head weight, fodder yield per plant, harvest index and grain yield per plant showed high values of heritability estimates but registered moderate to low values for the GCV, genetic advance and genetic gain over per cent of mean. It suggests that the non-additive gene effect controlled these characters. An improvement of these characters, therefore, can be achieved through exploiting the dominance effect. The non-additive gene effect for grain yield per plant, fodder yield per plant and number of productive tillers per plant were supported by the earlier workers in finger millet (Anuradha *et al.,* 2017; Chavan *et al.,* 2020). Additive gene effect for grain yield was observed by Bandyopadhyay (1998), suggesting that exposure to sub-optimal low-temperature stress condition at high altitude direct selection of finger millet cultivar for grain yield would respond well.

A perusal of correlation data revealed that days to 50% flowering registered significant negative association with fodder yield per plant and grain yield per plant both at the phenotypic and genotypic level (Table 3). The correlation coefficient values of days to 50% flowering showed a significant positive association with number of spikes per finger and plant height at the phenotypic level while established significant inverse relation with seed volume, number of finger per head, number of productive tiller per plant, number of heads per plot, single head weight and harvest index at the genotypic level. It can be due to a normal physio-biochemical activities of the plant, effective partitioning of photosynthates into the growth of structural compound of vegetative organ and non-structural compound of in reproductive state was more important to promote both fodder yield and grain yield among finger millet cultivars. A significant positive association of grain yield per plant with days to final harvest, number of heads per plot, fodder yield per plant and harvest index was observed both at the phenotypic and genotypic level. However, grain yield per plant revealed a significant negative correlation with seed volume at the genotypic level and a significant positive correlation with number of spikes per finger at the phenotypic level. Grain yield per plant showed a positive association with biological yield per plant, harvest index, tillers per plant (Negi *et al*., 2017), plant height, ears per plant, and fingers per ear (Wolie and Dessalegn, 2011). An increase in spikes per finger and harvest index indicates the influence of floret site utilization, while decreases in seed volume suggest increasing competition to sustain seed growth at the pollinated site. It elucidated that the better the physio-anatomical development of crop higher would be its grain and fodder yield under prevailing environment condition at growing site.

Finger millet cultivars, when grown at high altitude, exhibited significant negative and non-significant association of grain yield with days to maturity and days to head emergence, respectively (Bandyopadhyay, 1998), indicating that early maturity (*i.e.,* early development of seed) is essential for augmenting the grain yield at low-temperature stress condition of high altitude instead of its early head emergence. Fodder yield per plant also revealed an identical relation as recorded with grain yield per plant for days to final harvest, number of heads per plot, and harvest index, both at the phenotypic and genotypic level and constituted significant negative correlation with seed volume at genotypic level. The number of heads per plot was significantly positively correlated with days to final harvest and harvest index but established significant inverse relation with single head weight both at the phenotypic and genotypic level and with seed volume at the genotypic level. A reduction in single head weight might emanate through greater competition and insufficient supply of assimilating for seed growth. It is, therefore, apparent that selection for the greater physiological production capacity of finger millet genotypes is determined by early initiation of

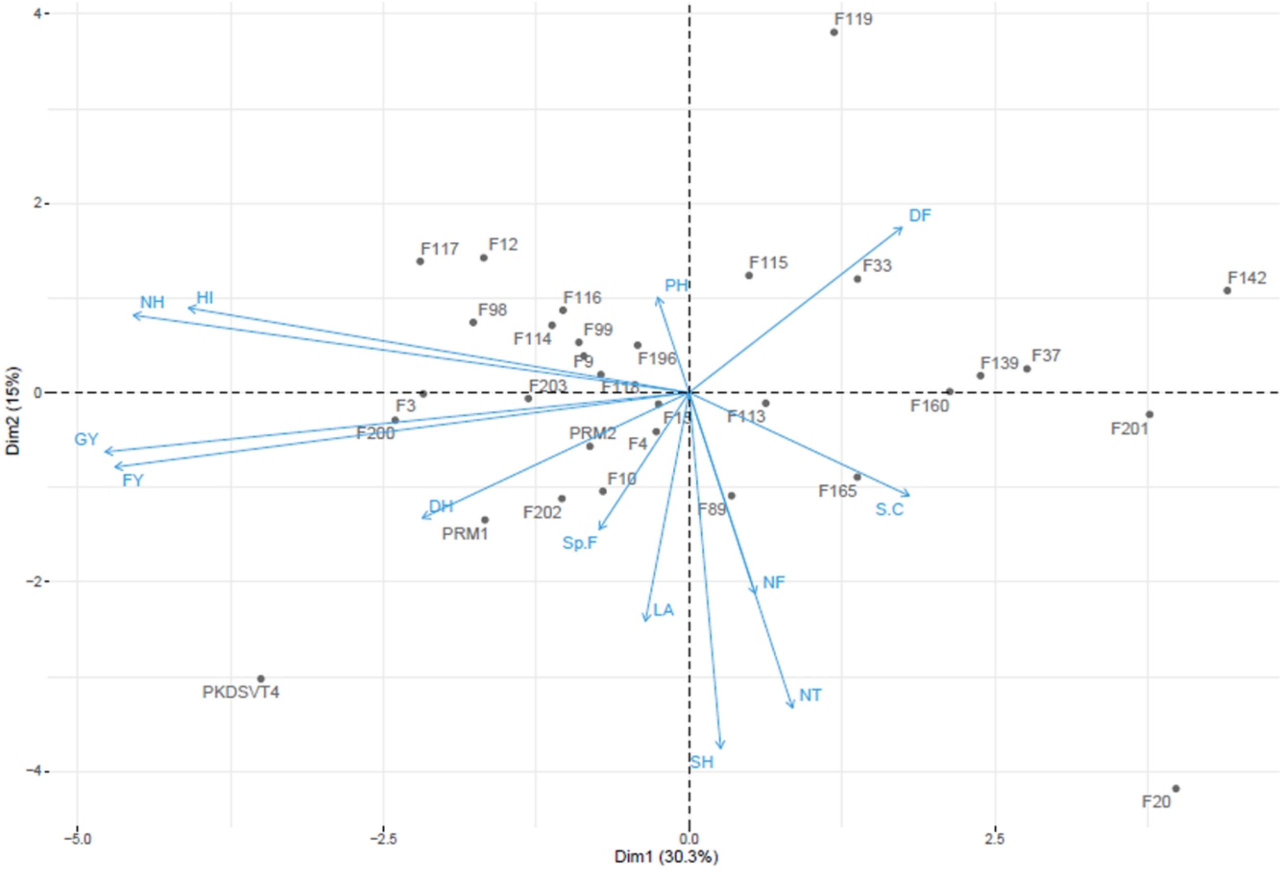


Fig. 1: The principal component analysis (PCA) bi-plot shows eigenvectors of each of the 13 morphological traits (green arrows) and PCA scores for combined phenotypes of 31 genotypes (represented by dots). The magnitude of the vector displays the weightage of their contribution to each PC. Vectors pointing in similar directions indicate positively correlated traits, whereas vectors pointing opposite directions indicate negatively correlated variables, and vectors at right angles indicate low or no correlation. Here, Dim 1 and Dim 2 represent PC1 and PC 2, respectively.

flowering in finger millet, coupled with an increase in the number of heads per plot, delayed in final harvest, high harvest index and high biomass content. The result, however, did not accord to the study on finger millet conducted at high altitude (Bandyopadhyay, 1999), where due to eco-physiological constraint at growing site, harvest index appeared as the only component trait established a significant positive correlation with grain yield.

Path coefficient analysis splits the observed correlation coefficients (Wright, 1921; Dewey and Lu, 1959) and provides specific information about the direct and indirect contribution of independent component traits on major dependable variable traits like grain yield. The path coefficient analysis revealed that fodder yield per plant, number of heads per plot, harvest index and single head weight contributed major direct positive effect on grain yield both at phenotypic and genotypic level indicating that phenotypic selection for these traits would be effective for grain yield improvement (Table 4). Fodder yield per plant, number of heads per plot and harvest index also appeared as a major indirect contributor for other component traits towards achieving desire correlation with grain yield. Residual effect both at phenotypic (0.01) and genotypic (0.01) level suggested that the characters considered for this study could explain the variability (98.78, 98.89%), respectively. Previously, it has been reported that fingers per ear, ears per plant (Wolie and Dessalegn, 2011; Kumar *et al*., 2014), productive tillers per plant, harvest index (Negi *et al*., 2017; Chavan *et al*., 2020) exerted a positive direct effect on grain yield per plant, whereas plant height, days to heading, and days to maturity (Wolie and Dessalegn, 2011) had a negative direct effect. This study, therefore, suggested that fodder yield per plant appeared as major selection criteria for enhancing the productivity of grain yield in finger millet, however the importance of number of heads per plot and high harvest index cannot be ignored. Principal component analysis separated the total genetic variations into five main principal components based on eigenvalues (≥1.0) and covered almost 77.50% of genetic variation (Table 5).

The first principal component (PC1) accounted for the highest variance (30.33%) of total variance, and attributes such

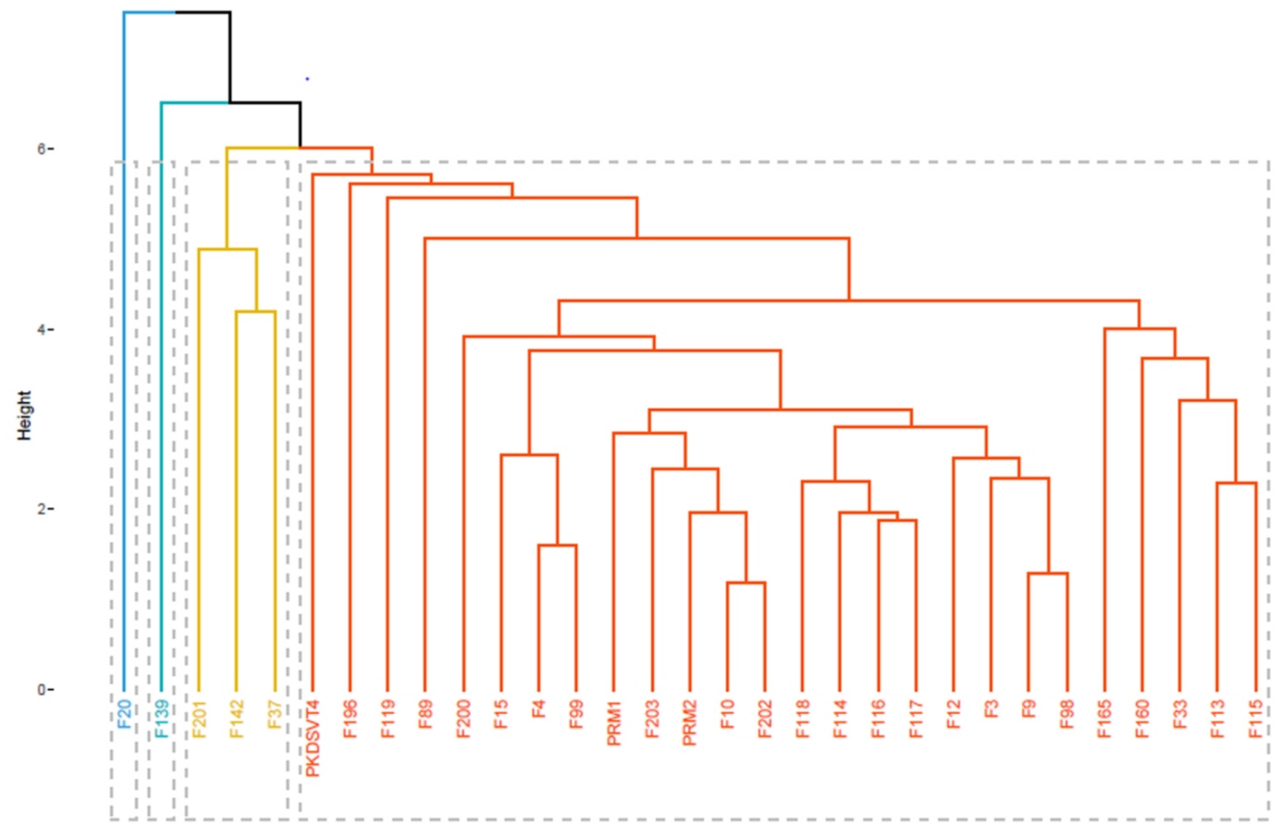


Fig. 2: Dendrogram and average hierarchical clustering of 31 genotypes of finger millet based on Euclidean distances. Genotypes with the same color are separated by dotted lines and grouped in the corresponding cluster.

as seed volume and days to 50% flowering contributed significantly to the total genetic variability. In contrast, grain yield per plot, forage yield per plant, harvest index and heads per plot had significantly contributed to PC1 in negative direction. Subsequently, PC2 accounted for 15.04% of total variability and characters such single head weight, productive tillers per plant and fingers per head significantly and positively contributed to genetic variability. Single head weight and harvest index had contributed positively for PC3, accounting for 12.91% of the total variability. The PC4 accounted for 10.47% of total variability originated primarily due to days to 50% flowering, leaf area, days to final harvest, single head weight, and spikes per finger.

The days to final harvest and productive tillers per plant had contributed positively to PC5, accounting for 8.76% of variability. In earlier studies also, genetic variation was grouped into three (Anuradha *et al.,* 2017), four (Ulaganathan *et al.,* 2015) and five (Anteneh *et al.,* 2019) PCs and covered maximum portion of genetic variation in finger millet. Biplot represents the distribution of genotypes, morphological traits, and relationships with each other using PCA scores on the X and Y axis (Fig. 1). The genotype by trait biplot also provides visual comparison between genotypes based on yield and ancillary traits. In this study, biplot revealed relatively long vectors for grain yield per plot, fodder yield per plant, heads per plot, harvest index, single head weight, days to 50% flowering, days to final harvest and productive tiller per plant, suggesting that these traits had contributed large dissimilarity among genotypes. However, plant height, leaf area and spikes finger^{-1} were the least discriminator (Table 5; Fig. 1). Anteneh *et al.* (2019) had reported significant influence of days to maturity and days to flowering in PC1 whereas grain yield and harvest index in PC2. Bi-plot also revealed significant positive contribution of genotypes such as F142, F20, F201, F37, and F139 using high weightage of days to 50% flowering and seed volume in PC1, whereas genotypes-F119, F12, F117, and F115 had contributed significantly using plant height and harvest index in PC2. Earlier, it has been reported that days to 50% flowering, straw yield, finger length (Nandini *et al.*, 2018), fingers per ear, and tillers per plant (Sharma *et al.*, 2018) had played a major role in contributing to total variability.

The dendrogram revealed four main groups and several subgroups based on fodder and seed yield contributing traits (Fig. 2). The study explained clusters I and II comprised only one genotype each, cluster III constituted three genotypes, and cluster IV composed 26 genotypes. The nature of clustering was non-

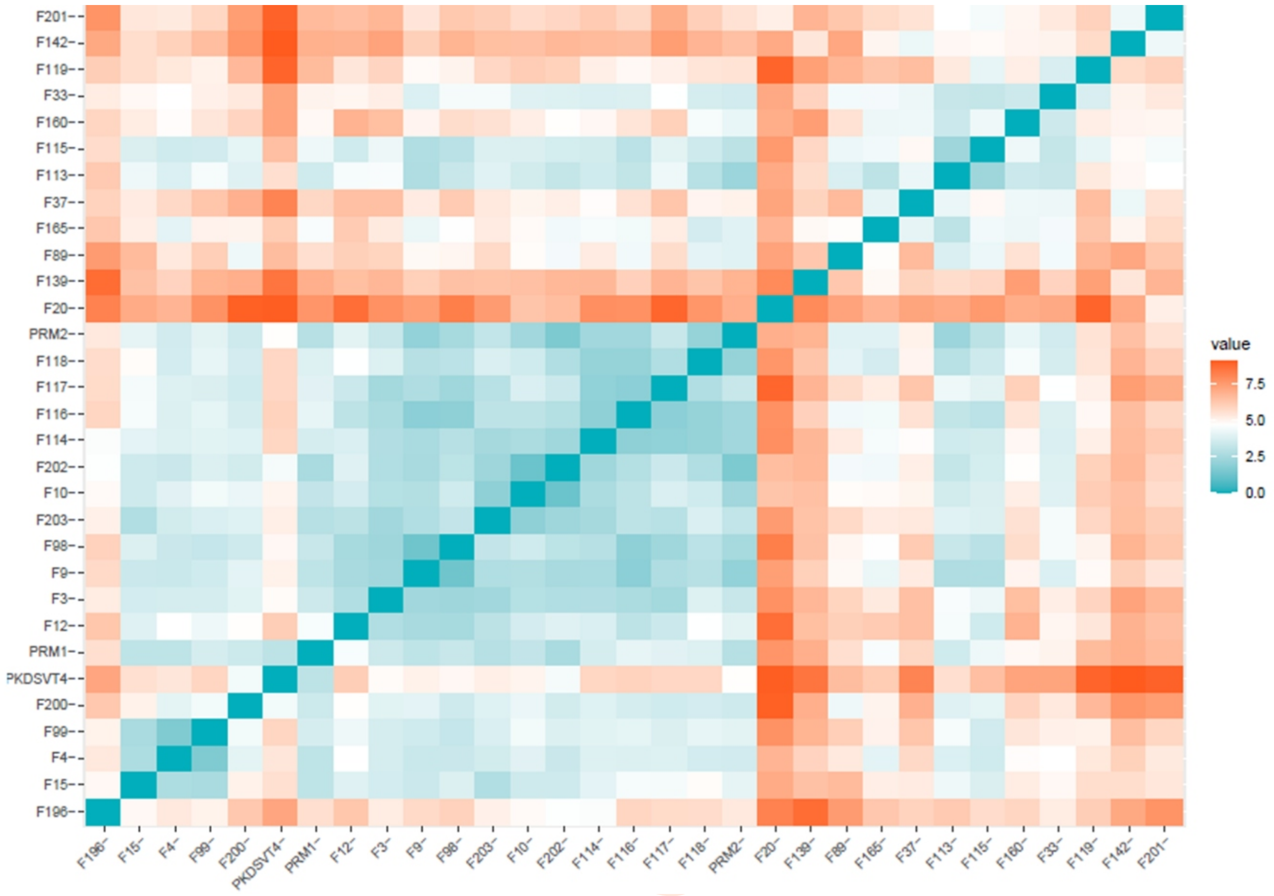


Fig. 3: Heat map of 31 genotypes based on Euclidean distances amongst them. Diagonal color (blue) represents zero intra-genotypic Euclidean distance. The Euclidean distances among genotypes are displayed by the intensity of color, where light and dark color intensity show less and high divergence between them, respectively.

overlapping, where individual genotypes shared a single cluster group only. Most of the genotypes accessed from different centers were clustered in the same group, indicating their similarities for agriculturally important traits. It also highlighted that the geographical distribution of genotypes might not be the single factor that leads to genetic diversity, which might be due to their common ancestral lineage or single source of origin and later delineation to different centers (Bandyopadhyay *et al.,* 2017). Thus, the selection of parents must be based on genetic divergence than geographical diversity for crop improvement programs. Moreover, genotypes constellated in the same cluster are more similar than genotypes in different groups. The more genetic distance between parents, the more will be level of heterosis and followed by a wide range of variability in segregating generation using a favorable combination of alleles (Singh *et al.,* 2018). The Euclidean distance was highest between F142 and PKDSVT4 genotypes, followed by F20 and PKDSVT4, F201 and PKDSVT4, F119 and PKDSVT4. Furthermore, the Euclidean heat map confirmed that the genotype F20 showed the highest Euclidean distance with other studied genotypes (Fig. 3). It also highlighted the existence of genetic distances between different genotypes and identified other genotypes *viz.,* F142, F201, F139, and F119, which also displayed higher genetic distance with other genotypes. This suggests that consideration of diverse genotypes belonged to different clusters like PKDSVT4, F20, F139 and F142 as a parent in crossing would be more rewarding for grain and fodder yield improvement in finger millet.

The present investigation highlighted substantial genetic diversity amongst the finger millet genotypes to be used in crop improvement programs through phenotypic selection and hybridization methods. Traits predominant with additive gene effect could be improved directly by phenotypic selection whereas traits showing non-additive gene effects by exploiting the dominance effect. The genetic enhancement of dependable variable (grain yield) is possible if independent variables have significant positive correlation and high direct effect with it. A wide range of genetic variability was witnessed in all the studied genotypes. The selected genotypes showed high genetic diversity could be used to improve finger millet using selection methods and/or hybridization followed by transgressive segregants.

Acknowledgments

The authors duly acknowledged the Vice Chancellor and Head of the Division, Department of Genetics and Plant Breeding, GBPUA&T, Pantnagar. We also thank different centers for providing study material and staff members of CRC for their assistance during experiment.

Add-on Information

Authors' contribution: N Sharma: Data collection, field management; **B. B. Bandypodhyay:** Experimental design, MS writing and revisions; **S. Chand:** Data analysis, MS writing and revisions; **P. K. Pandey:** Experimental design; **D.C. Baskheti:** Field management; **B.K. Alam:** Data analysis.

Research content: The research content of the manuscript is original and has not been published elsewhere.

Ethical approval: Not applicable.

Conflict of interest: No conflict of interests regarding this publication.

Data from other sources: Not applicable.

Consent to publish: All authors agree to publish the paper in the *Journal of Environmental Biology*.

References

Anteneh, D., F. Mekbib, T. Tadesse and Y. Dessalegn: Genetic diversity among lowland finger millet (*Eleusine coracana* (L) Gaertn) accessions. *Ethiopian J. Agricul. Sci.,* **29**, 93-108 (2019).

Anuradha, N., T.S.S.K. Patro, M. Divya, Y.S. Rani and U. Triveni: Genetic variability, heritability and association in advanced breeding lines of finger millet [*Eluesine coracana* (L.) gaertn.]. *Int. J. Chemi. Stud.,* **5**, 1042-1044 (2017).

Bandyopadhyay, B.B., S. Chand, M.K. Nautiyal and A.S. Jeena: Genetic Diversity analysis in Jatropha (*Jatropha curcas* L.) genotypes. *Elixir Int. J.,* **105**, 46169-46174 (2017).

Bandyopadhyay, B.B.: Selection criteria for grain yield improvement in finger millet at high altitude. *Indian J. Gene. Plant Bree.,* **59**, 535–538 (1999).

Bandyopadhyay, B.B.: Variability, heritability and inter-relationship of important quantitative characters in finger millet. *Ann. Agricul. Res.,* **19**, 173 – 176 (1998).

Banerjee, P., S. Maitra and P. Banerjee. The role of small millets as functional food to combat malnutrition in developing countries. *Indian J. Nat. Sci.,* **10**, 20412-20417 (2020).

Burton, G.W. and D.E. Devane: Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agron. J.,* **45**, 478-481 (1953).

Chavan, B.R., L.N. Jawale and A.V. Shinde: Correlation and path analysis studies in finger millet for yield and yield contributing traits (*Eleusine coracana* L. Gaertn). *Int. J. Chemi. Stud.,* **8**, 2911-2914 (2020).

Dabholkar, A.R.: Elements of Bio Metrical Genetics (revised And Enlarged Edition). Concept Publishing Company (1999).

Devi, P.B., R. Vijayabharathi, S. Sathyabama, N.G. Malleshi and V.B. Priyadarisini: Health benefits of finger millet (*Eleusine coracana* L.) polyphenols and dietary fiber: A review. *J. Food Sci. Technol.,* **51**, 1021-1040 (2014).

Dewey, D.R. and K. Lu: A Correlation and Path-Coefficient Analysis of components of crested wheatgrass seed production 1. *Agronomy*, J., **51**, 515-518 (1959).

Gaoh, B.S.B., P.I. Gangashetty, R. Mohammed, D.K. Dzidzienyo and P. Tongoona: Generation mean analysis of pearl millet [*Pennisetum glaucum* (L.) R. Br.] grain iron and zinc contents and agronomic traits in West Africa. *J. Cer. Sci.,* **96**, 103066 (2020).

Johnson, H.W., H.F. Robinson and R.E. Comstock: Estimates of genetic and environmental variability in soybeans 1. *Agron. J.,* **47**, 314-318 (1955).

Kumar, B.S.S.: United Nation declares 2023 International Year of Millet. The Hindu (Bengaluru, 27 April, 2021; 00:34 IST). https://www.thehindu. con>news (2021).

Kumar, D., V. Tyagi and B. Ramesh: Path coefficient analysis for yield and its contributing traits in finger millet. *Int. J. Adv. Res.,* **2**, 235-240 (2014).

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

Lule, D., K. Tesfaye, M. Fetene and S. De Villiers: Inheritance and association of quantitative traits in finger millet (*Eleusine coracana* Sub sp. Coracana) landraces collected from eastern and south eastern Africa. *Int. J. Gene.,* **2**, 12-21(2012).

Lule, D., S. de Villiers, M. Fetene, D.A. Odeny, A. Rathore, R.R. Das and K. Tesfaye: Genetic diversity and association mapping of Ethiopian and exotic finger millet accessions. *Crop Past. Sci.,* **69**, 879-891 (2018).

Mundada, P.S., S.D. Umdale, T.D. Nikam and M.L. Ahire: Genetic diversity using RAPD markers, mineral composition and their correlation in selected local landraces of finger millet [*Eleusine coracana* (L.) Gaertn.]. *Vegetos*, **32**, 1-10 (2019).

Negi, S., A. Bhatt and V. Kumar: Character association and path analysis for yield and its related traits in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes. *J. Appli. Natu. Sci.,* **9**, 1624-1629 (2017).

Nyquist, W.E. and R.J. Baker: Estimation of heritability and prediction of selection response in plant populations. *Criti. Revi. Plant Sci.,* **10**, 235-322 (1991).

Nandini, C., B. Sujata, V. Tippeswamy and T.V. Krishna: Characterization and evaluation of finger millet (*Eleusine coracana* L.) core set germplasm using principal component analysis. *Mysore J. Agricul. Sci.,* **52**, 49-56 (2018).

Panda, D., N.H. Sailaja, P.K. Behera, K. Lenka, S.S. Sharma and S.K. Lenka: Genetic diversity of under-utilized indigenous finger millet genotypes from Koraput, India for crop improvement. *J. Plant Bioche. Biotechnol.,* **30**, 99–116 (2020).

Panda, D., N.H. Sailaja, P.K. Behera, K. Lenka, S.S. Sharma and S.K. Lenka: Genetic diversity of under-utilized indigenous finger millet genotypes from Koraput, India for crop improvement. *J. Plant Bioche. Biotechnol.,* **30**, 99-116 (2021).

Patil, A.S. and V.A. Mane: Studies on the genetic variation of yield and contributing traits in finger millet [*Eleusine coracana* (L) Gaertn]. *Progre. Res.,* **8**, 526-528 (2013).

Priyadharshini, C., A. Nirmalakumari, A.J. Joel and M. Raveendran: Genetic variability and trait relationships in finger millet (*Eleusine coracana* (L.) Gaertn.) hybrids. *Madras Agricul. J.,* **98**, 18-21 (2011).

Ramakrishnan, M., S.A. Ceasar, V. Duraipandiyan, N.A. Al-Dhabi and S. Ignacimuthu: Using molecular markers to assess the genetic diversity and population structure of finger millet (*Eleusine coracana* (L.) Gaertn.) from various geographical regions. *Gene. Resou. Crop Evolu.,* **63**, 361-376 (2016).

Reddy, V.G., H.D. Upadhyaya, C.L.L. Gowda and S. Singh: Characterization of eastern African finger millet germplasm for qualitative and quantitative characters at ICRISAT. *J. SAT Agricul. Res.,* **7**, 9 (2009).

Seethatram, A.: Small millets in Global Agriculture. Oxford and IBH Publishing Co. Pvt. Ltd. New Delhi (1989).

Sharma, D., A. Tiwari, S. Sood, G. Jamra, N.K. Singh, P.K. Meher and A. Kumar: 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**, e0199444 (2018).

Sheoran, O.P., D.S. Tonk, L.S. Kaushik, R.C. Hasija and R.S. Pannu: Statistical software package for agricultural research workers. Recent Advances in Information Theory, Statistics & Computer Applications by D.S. Hooda and R.C. Hasija Department of Mathematics Statistics, CCS HAU, Hisar, pp. 139-143 (1998).

Singh, S., S.K. Gupta, M. Thudi, R.R. Das, V. Anil Kumar, V. Garg, R.K. Varshney, A. Rathore, S.K. Pahuja and D.V. Yadav: Genetic diversity patterns and heterosis prediction based on SSRs and SNPs in hybrid parents of pearl millet. Crop Science (TSI), **58**, 2379-2390 (2018).

Trivedi, A.K., S.K. Verma and R.K.Tyagi. Pheno-physiological evaluation of finger millet germplasm of central himalayan region. *J. Environ. Biol.,* **39**, 31-36 (2018).

Ulaganathan, V. and A. Nirmalakumari. Finger millet germplasm characterization and evaluation using principal component analysis. *Sabrao J. Bree. Gene.,* **47**, 79-88 (2015).

Wolie, A. and T. Dessalegn: Correlation and path coefficient analyses of some yield related traits in finger millet (*Eleusin ecoracana* (L.) Gaertn.) germplasms in northwest Ethiopia. *African J. Agricul. Res.,* **6**, 5099-5105 (2011).

Wright, S.: Correlation and causation. *J. Agric. Res.,* **20**, 557-580 (1921).