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ASSESSMENT OF GENETIC VARIABILITY IN FINGER MILLET (*ELEUSINE CORACANA* (L.) GAERTN) GENOTYPES FOR AGRO-MORPHOLOGICAL AND BIOCHEMICAL TRAITS

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ABSTRACT

The investigation was carried out to know the genetic variability, heritability and genetic advance analysis of 55 finger millet genotypes. The experiment was carried out at four locations *viz*., Hill Millet Research Station, NAU, Waghai, The Dangs; Niger Research station, NAU, Vanarasi, Gujarat; Agronomy Farm, N. M. College of Agriculture, NAU, Navsari and Krishi Vigyan Kendra, Dediyapada, Gujarat during *Kharif* – 2022 essentially for creating four environments. All the 55 genotypes were screened under field conditions by adopting Randomized Block Design with three replications. The results revealed that the values of phenotypic coefficients of variability were greater than genotypic coefficients of variability for all the traits studied. Moderate genotypic and phenotypic coefficient of variation found for the traits *viz.*, days to 50% flower, fingers per panicle, Ear head weight (g), 1000 grain weight (g), harvest index (%), calcium content (mg/100g) and protein content (%). The analysis of variance revealed that highly significant differences were recorded among the genotypes for all the studied characters, which indicate the presence of wide range of variability among genotypes and scope of selection for improvement. The high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz*., days to 50% flowering, ear head length (cm), 1000 seed weight (g), protein content (%), calcium content (mg/100g) and iron content (mg/100g). It forces to conclude that these characters are governed by additive gene action and phenotypic selection based on these traits in the segregating generations would likely to be more effective. In addition to the genetic variability, knowledge on heritability and expected genetic advance helps the breeder to employ the suitable breeding strategy.

Key words **:** Finger millet, genetic variability, heritability, genetic advance, breeding

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn) is an annual *kharif* crop and knows as African millet and Ragi. It is self-pollinated tetraploid species (2n=4x=36, AABB), belong to family poaceae and the genus *Eleusine* and plant mainly grown in two major continents, Africa and Asia for both grain and forage purpose (Sood *et al.*, 2017; Sood *et al*., 2019). The name finger millet was coined from its morphological appearance of fingers/spikes, which look like human fingers. From the cultivation point of view, it is the sixth largest cropafter wheat,rice, maize, sorghum and bajra mainly among the rural populations of Africa and India and fourth important crop among millets globally (Ceasar *et al*., 2018). In India, it is mainly grown in the

states of Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Orissa, Gujarat, Jharkhand, Uttar Pradesh, Madhya Pradesh and Uttarakhand.Among the various millets, finger millet ranks fourth on a global scale of production next tosorghum pearl and foxtail millet (Maharajan *et al.*, 2019). It serves as a food-security crop because ofits high nutritional value and excellent storage qualities (Ramashia *et al*., 2018). It is being Used as food (grains) in developing countries and as animal Feed (straw) in developed countries indicating that it is considered as a poor man's food (Ceasar *et al*., 2018; Wambi *et al*., 2020).

Finger millet is highly nutritious crop as its grain contains 65–75% carbohydrates, 2.5–3.5% minerals, 5–8% protein, 15–20% dietary fiber (Chetan and Malleshi, 2007). The grains of finger millet are rich in fiber, protein, minerals has low glycemic index which helps to manage diabetes and blood pressure. Its calcium (Ca) content (344 mg 100 g-1) is tenfold higher than wheat (*Triticum aestivum*), maize (*Zea mays*), and rice (*Oryza sativa*) and three times higher than milk (Shobana *et al*., 2013; Kumar *et al*., 2016). Millets are suitable staples when focusing on the food and nutritional security of the common people (Tiwari *et al*., 2022, Yadav *et al*., 2023, Swapnil *et al*. 2024).

Exploitation of genetic variability existing in the working germplasm is the first principle in the improvement of any crop. Knowledge on the magnitude of variability present in a crop species for different traits is of utmost importance as it provides the basis for effective selection (Singh *et al*. 2020). The utilization of any species in a breeding program depends upon its genetic diversity and adaptability in different environments (Rai and Jat, 2022). Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and presence of enormous genetic variability. The characterization and evaluation are the important pre-requisites for effective utilization of germplasm and also to identify sources of useful genes and superior genotypes. The phenotype of a character is the result of interaction between genotype and environment. Partitioning of phenotypic variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. Heritability measures the relative amount of the heritable portion of variability. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to phenotypic variation. Basic information on heritability is a pre-requisite for planning any breeding program. Genetic advance indicates the amount of progress that could beexpected with selection for a particular character. Estimates of heritability along with estimates of geneticadvance are more useful in selection method ratherthan heritability or genetic advance alone.

Therefore, study of genetic variability of grain yield and its component characters among different varieties provides a strong basis for selection of desirable genotypes for augmentation of yield and other agronomic characters. The objective of the current study was to identify the best genotypes as parents for further breeding program based on the genetic variability of various finger millet genotypes based on their agro-morphological characteristics.

Materials and Methods

The investigation was carried out to know the genetic variability, heritability and genetic advance analysis of 55 finger millet genotypes (Table 1).The expriment was carried out at four location *viz*., Hill Millet Research Station, NAU, Waghai, The Dangs; Niger Research station, NAU, Vanarasi, Gujarat; Agronomy Farm, N.M. College of Agriculture, NAU, Navsari and Krishi Vigyan Kendra, Dediyapada, Gujarat during *Kharif* – 2022 essentially for creating four environments. All the 55 genotypes were screened under field conditions by adopting Randomized Block Design with three replications. Each entry was planted in a plot size of 51.5 × 8.75 m^2accommodating 4 row each entry with 2.25 m row length), keeping row-to-row and plant-to-plant distance of 22.5 cm × 7.5 cm, respectively. All recommended practices were followed and timely plant protection measures were taken to avoid damage through insect-pests and diseases. Both sowing and transplanting at all four locations was done. Various observations were recorded on five competitive plants selected randomly from each single row plot in each replication excluding border except for days to 50 % flowering and days to maturity, where it was recorded on population basis. Observations were recorded for morphological and biochemical observations is given as follows: Days to 50 % flowering, Days to maturity, Plant height (cm), Productive tillers per plant, Fingers per ear head, Main ear head length (cm), Finger width (cm), 1000 seed weight (g), Grain yield per plant (g), Fodder yield per plant (g), Weight of matured panicle per plant (g), Protein Content (%), Calcium content (mg/100g) and Iron content (mg/100g). The data were subjected to analysis of variance according to the method recommended by Panse and Sukhatme (1985). Phenotypic and genotypic coefficients of variation were computed according to the method suggested by Burton (1952). Heritability on broad sense was

calculated as per formula given by Allard (1960). Genetic advance was expressed by using the formula suggested by Johnson *et al*. (1955).

Table 1 : List of genotypes

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	FM-3009	**19.**	FM-3003	**37.**	FM-4002
2.	FM-3015	**20.**	FM-3011	**38.**	FM-4011
3.	FM-3012	**21.**	FM-3006	**39.**	FM-4007
4.	FM-3013	**22.**	FM-3014	**40.**	FM-4010
5.	FM-3023	**23.**	FM-3028	**41.**	WN-494
6.	FM-3010	**24.**	FM-3005	**42.**	WN-544
7.	FM-3024	**25.**	FM-3016	**43.**	WN-548
8.	FM-3018	**26.**	FM-3021	**44.**	WN-550
9.	FM-3019	**27.**	FM-3004	**45.**	WN-560
10.	FM-3020	**28.**	FM-3025	**46.**	WN-569
11.	FM-3022	**29.**	FM-4008	**47.**	WN-581
12.	FM-3001	**30.**	FM-4012	**48.**	WN-591
13.	FM-3027	**31.**	FM-4006	**49.**	WN-561
14.	FM-3017	**32.**	FM-4004	**50.**	WN-562
15.	FM-3008	**33.**	FM-4001	**51.**	WN-566
16.	FM-3002	**34.**	FM-4009	**52.**	WN-572
17.	FM-3007	**35.**	FM-4003	**53.**	WN-575
18.	FM-3026	**36.**	FM-4005	**54.**	WN-577
				55.	WN-592

Results and Discussion

Genetic parameters of variability

Genetic variability studies provide basic information regarding the genetic parameters of the genotypes based on which breeding methods are constituted for further crop improvement. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitivity of crop to environment, heritability of the character, genetic advance and genetic divergence. The analyses of variance for all the fifteen traits in individual environments are presented in the Table 2. Mean sum of squares for replication under each environment was found non-significant for all traits except for finger width (cm) in the environment E3 (Navsari) and E4 (Dediyapada) which means that experimental sites were homogenous at all the locations. Mean sum of squares for genotypes was found highly significant all the characters across all the environments under study. This suggested that large amount of variability and diversity is present among all the genotypes in all the environments which can be further utilized by the plant breeders for selecting desired genotypes having all favourable traits in order to improve yield and its component traits.The analysis of variance showed a wide range of variation and significant differences for all the characters under study, indicating the presence of adequate variability for further improvement. The estimates of mean, range, phenotypic variance, and genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean are presented in Table 4. Mean performance of genotypes in respect of fifteen characters under study have been presented in Table 3.Considering *per se* performance for all traits it can be suggested that most promising genotypes in respect of grain yield per plant (g) were FM-3022, FM-3001, FM-3008, FM-3026, FM-4012, FM-4007, WN-544, WN-548, WN-550, WN-581, WN-591, WN-561, WN-562, WN-566, WN-575, WN-577 and WN-592 as they recorded higher grain yield per plant. Most promising genotypes in respect of fodder yield per plant (g) were FM-3013, FM-3024, FM-3008, FM-3026, FM-3016, FM-4003, FM-4005, WN-494, WN-550, WN-569, WN-591, WN-561, WN-562, WN-566, WN-572, WN-575 and WN-577.The earliest genotype FM-3021 flowered at 55.00 days whereas the late genotype FM-3010 flowered at 93.00 days. The highest productive tillers per plant was observed in WN-592 (6.16) and lowest for FM-3013 (4.59).The highest spikes per panicle were observed in WN-592 (9.23) and lowest for FM-3025 (4.77). Genotype FM-3019 (0.69 cm) had lowest finger width while genotype WN-577 and WN-592 (1.04 cm) had highest finger width among all the genotypes under study across all

environments. Value for 1000 grain weight (g) ranged from 2.11 g (FM-4010) to 3.30 g (FM-3026). The general mean for this trait was 2.68 g. Hence, these genotypes had highest value of above-mentioned desirable characters. These genotypes may be used as donor parent for transferring these characters in recipient parent in combination breeding program.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV):

Moderate genotypic and phenotypic coefficient of variation found for the traits *viz.*, days to 50% flower, fingers per panicle, Ear head weight (g), 1000 grain weight (g), harvest index (%), calcium content (mg/100g) and protein content (%). Similar findings were also reported by Singamsetti *et al*. (2018), Keerthana *et al*. (2019). Low to moderate genotypic and phenotypic coefficient of variation found for the traits *viz.*, plant height (cm). Low genotypic and phenotypic coefficient of variation found for the traits *viz.*, days to maturity, productive tillers per plant and finger width. Thus, there is little or no scope for improvement for such characters. On top of that their heritability and genetic advance estimates were also low to moderate so there is absence of any room for improvement for such characters utilizing current population.

Table 2 : Analysis of variance (environment wise) for all fifteen traits under study

Source of Variation	D. F.	Plant height (cm)				Days to 50 % flowering				Days to maturity			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Replications	2	6.17	5.65	5.39	4.80	1.73	3.65	8.82	2.35	4.50	5.87	1.92	5.43
Genotypes	54	4.51**	3.86**	3.44**	3.19**	3.01**	3.15**	3.00**	3.02**	3.12**	3.39**	2.84**	3.46**
Error	108	1.03	9.75	8.82	9.14	7.33	9.61	1.10	6.65	10.00	6.74	5.92	5.22
Total	164	2.91	2.60	2.37	2.24	1.04	1.10	1.06	1.04	1.09	1.16	9.74	1.17

Source of Variation	D. F.	Productive tillers per plant				Fingers per panicle				Finger width (cm)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Replications	2	1.65	6.52	5.72	1.52	6.67	6.68	1.02	5.29	1.13	3.87	1.96	1.69
Genotypes	54	3.32**	3.10**	4.03**	4.43**	5.72**	3.63**	3.97**	2.74**	1.67**	1.81**	1.87**	1.93**
Error	108	5.04	6.31	4.16	3.01	4.07	4.67	4.92	4.07	3.17	3.25	3.16	3.72
Total	164	1.44	1.42	1.61	1.66	1.91	1.23	1.34	9.30	5.70	6.18	6.38	6.60

Source of Variation	D. F.	Ear head length (cm)				Ear head Weight (g)				1000 grain weight (g)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Replications	2	8.04	5.12	1.18	8.00	1.95	2.20	1.66**	1.68**	5.34	4.82	4.59	4.32
Genotypes	54	1.07**	1.04**	1.05**	1.04**	9.31**	8.30**	7.46**	7.98**	3.46**	3.12**	2.94**	2.82**
Error	108	2.91	3.66	4.24	3.18	1.20	1.23	1.29	1.12	3.48	3.14	2.97	2.82
Total	164	3.55	3.46	3.49	3.46	4.09	3.81	3.51	3.56	1.43	1.29	1.22	1.17

Source of Variation	D. F.	Grain yield per plant (g)				Fodder yield per plant (g)				Harvest Index (%)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Replications	2	2.83	2.38	1.94	1.50	1.91	1.55	1.31	1.21	2.95	3.03	2.97	5.12
Genotypes	54	8.64**	6.41**	4.37**	3.19**	5.75**	4.65**	4.52**	4.66**	5.78**	3.89**	7.26**	8.25**
Error	108	5.70	4.71	3.70	2.78	3.45	2.97	2.47	2.25	5.02	4.87	4.69	3.78
Total	164	3.57	2.71	1.92	1.42	2.35	1.92	1.81	1.83	2.59	1.97	3.06	3.03

Source of Variation	D. F.	Iron content (mg/100g)				Calcium content (mg/100g)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Replications	2	5.75	2.81	1.23	6.61	5.13	9.60	4.25	1.13
Genotypes	54	1.21**	1.24**	1.24**	1.25**	2.48**	3.19**	2.36**	2.74**
Error	108	4.11	3.89	4.25	4.01	3.72	3.58	2.56	3.00
Total	164	4.01	4.12	4.11	4.13	8.43	1.07	7.96	9.22

Source of Variation	D. F.	Protein (%)			
		E_1	E_2	E_3	E_4
Replications	2	7.40	1.16	4.70	8.19
Genotypes	54	2.79**	2.73**	2.90**	2.73**
Error	108	2.50	2.39	2.19	2.56
Total	164	9.36	9.16	9.69	9.17

* and ** significant at 5 and 1 per cent levels, respectively.

Table 3: Mean, minimum and maximum values for all fifteen characters along with respective phenotypic, genotypic and environmental

Sr. No.	Characters	Range		Mean	Variance		
		Minimum	Maximum		Phenotypic	Genotypic	Environmental
1	Plant height (cm)	88.34	137.41	120.06	188.26	112.37	75.89
2	Days to 50 % flowering	54.94	93.30	76.61	107.30	99.56	7.74
3	Days to maturity	91.75	129.40	115.00	111.41	100.89	10.53
4	Productive tillers per plant	4.59	6.16	5.22	0.16	0.08	0.08
5	Fingers per panicle	4.77	9.23	6.71	1.37	0.82	0.55
6	Finger width (cm)	0.69	1.04	0.86	0.01	0.01	0.0007
7	Ear head length (cm)	4.53	13.29	7.88	3.53	3.50	0.04
8	Ear head weight (g)	12.80	19.05	15.95	3.56	2.65	0.91
9	1000 Seed weight (g)	2.11	3.30	2.68	0.12	0.10	0.02
10	Grain yield per plant (g)	4.95	10.13	7.06	2.17	1.71	0.45
11	Fodder yield per plant (g)	11.98	25.48	18.50	18.18	13.06	5.11
12	Harvest index (%)	19.23	38.38	28.00	24.04	14.07	9.97
13	Iron content (mg/100g)	2.03	4.88	3.12	0.42	0.41	0.003
14	Calcium content (mg/100g)	205.05	336.30	277.13	919.15	818.75	100.40
15	Protein content (%)	6.03	9.59	7.40	0.95	0.92	0.03

Table 4 : Genotypic and Phenotypic Coefficient of Variation (GCV and PCV) for all fifteen characters along with respective heritability, genetic advance and genetic advance (% of mean)

Sr. No.	Characters	GCV (%)	PCV (%)	ECV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance (% of mean)
1.	Plant height (cm)	8.83	11.43	7.26	59.70	16.87	14.05
2.	Days to 50 % flowering	13.03	13.52	3.63	92.80	19.80	25.84
3.	Days to maturity	8.73	9.18	2.82	90.60	19.69	17.12
4.	Productive tillers per plant	5.32	7.54	5.34	49.80	0.40	7.73
5.	Fingers per panicle	13.50	17.44	11.04	59.90	1.44	21.12
6.	Finger width (cm)	8.76	9.27	3.04	89.30	0.15	17.04
7.	Ear head length (cm)	23.73	23.85	2.38	92.00	3.83	48.64
8.	Ear head weight (g)	10.21	11.83	5.97	74.50	2.89	18.14
9.	1000 Seed weight (g)	11.85	13.13	5.65	81.50	0.59	22.04
10.	Grain yield per plant (g)	18.53	20.83	9.52	69.10	2.40	33.96
11.	Fodder yield per plant (g)	19.53	23.04	12.22	71.50	6.31	34.11
12.	Harvest index (%)	13.40	17.51	11.28	58.50	5.91	21.12
13.	Iron content (mg/100g)	20.55	20.64	1.94	99.10	1.32	42.40
14.	Calcium content (mg/100g)	10.33	10.94	3.62	89.10	55.63	20.08
15.	Protein content (%)	12.96	13.15	2.19	97.20	1.95	26.33

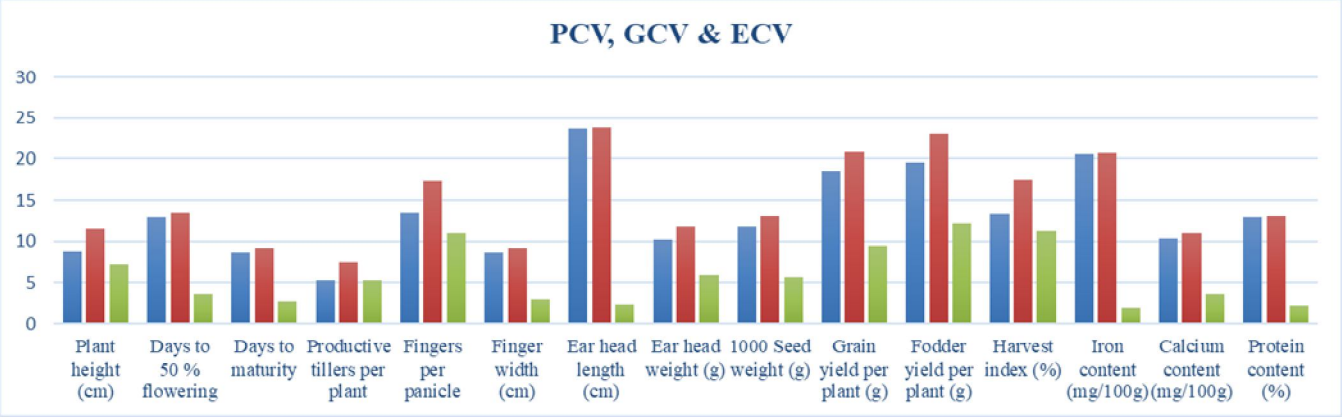

Fig. 1(a) : Bar graph depicting ECV, GCV & PCV for morphological character under study

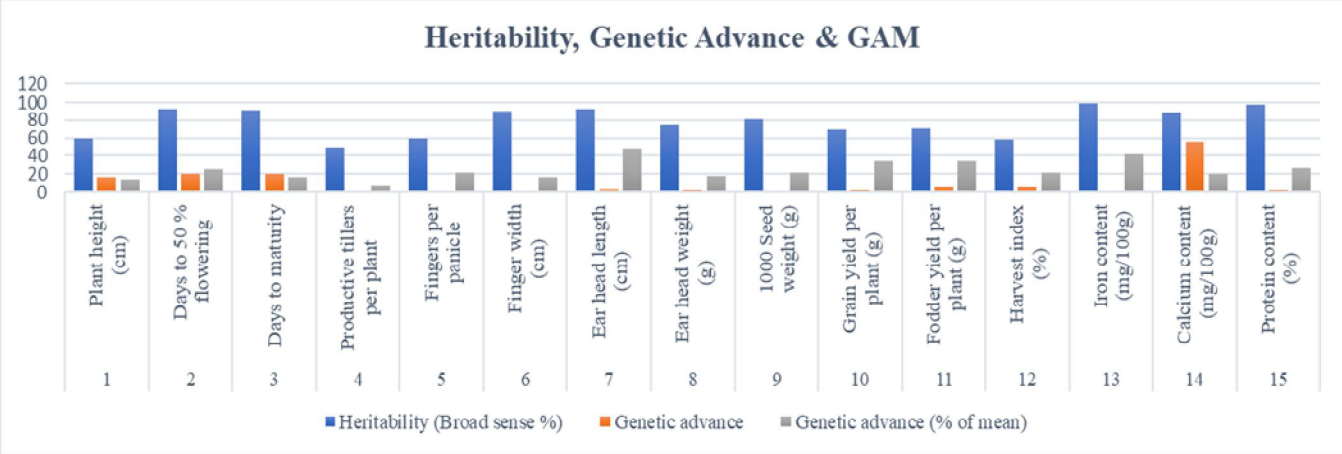

Fig. 1(b) : Bar graph depicting Heritability, Genetic advance & Genetic advance (% of mean) for morphological characters under stud y

Similar result were reported by Ganapathy *et al*. (2011) for days to maturity, Jahnavi and Lal (2023) for days to maturity and peduncle length, Karad and Patil (2013) and Opole *et al*. (2018).The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all characters. This indicates the effect of environmental factors on these characters. This shows presence of largevariation in the genotypes for these characters. Therefore, simple selection can be obtained for the improvement of these characters.

Heritability and genetic advance

High estimates of heritability were found in iron content (99.10 %) followed by protein content (97.20 %), days to 50 % flower (92.80 %), ear head length (92.0 %), days to maturity (90.60 %), finger width (89.30 %), calcium content (89.10 %), 1000 seed weight (81.50 %), ear head weight (74.50 %), fodder yield per plant (69.10 %). Moderate amount of heritability was found in fingers per panicle (59.90 %), plant height (59.70 %), harvest index (58.50 %) and productive tillers per plant (49.80).The high genetic advance expressed as per cent of mean was obtained for ear head length (48.64 %) followed by iron content (42.20 %), fodder yield per plant (34.11 %), protein content (%) (26.33 %), days to 50% flowering (25.84 %), 1000 seed weight (22.04 %) harvest index, fingers per panicle (21.12 %), calcium content (20.08 %). Moderate genetic advance expressed as per cent of mean was obtained for ear head weight (18.14 %) followed by days to maturity (17.12 %), finger width (17.04 %), plant height (14.05 %). Low genetic advance expressed as per cent of mean was obtained for productive tillers per plant (7.73 %).Heritability estimates along with genetic gains were more effective and reliable in predicting the improvement through selection. Estimates of genetic advance in general helped to predict the extent of improvement that could be achieved for improving different characters. In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz*., days to 50% flowering, ear head length (cm), 1000 seed weight (g), protein content (%), calcium content (mg/100g) and iron content (mg/100g). These observations led to conclusions that these characters were governed largely by additive gene action and selection would be rewarding. Similar findings were earlier reported byMahanthesha *et al*. (2017), Devaliya *et al*. (2018), Patel *et al*. (2018), Singamsetti *et al*. (2018), Keerthana *et al*. (2019), Chavan *et al*. (2019), Sindhuja *et al*. (2019), Anuradha *et al*. (2020), Srilatha *et al*. (2020), Karvar *et al*. (2021), Bharathi *et al*. (2022), Madhusri *et al*. (2022),Udamala *et al*. (2022), Chandra *et al*. (2023), Singh *et al*. (2023), Jahnavi *et al*. (2023) and Patel *et al*. (2024) for various traits. High heritability along with moderate genetic advance as per cent of mean was present in days to maturity, finger width and ear head weight indicating that the genotypes under study were diverse with immense genetic potential and further improvement in these traits would possible by practicing simple selection technique. Similar results were also obtained by John *et al*. (2006), Ulaganathan and Nirmala Kumari (2011) and Anuradha *et al*. (2020). Contrasting results were obtained by Mahanthesha *et al*. (2017), Anuradha *et al*. (2019) and Udamala *et al*. (2022).

Conclusion

The genotypes were FM-3022, FM-3001, FM-3008, FM-3026, FM-4012, FM-4007, WN-544, WN-

548, WN-550, WN-581, WN-591, WN-561, WN-562, WN-566, WN-575, WN-577 and WN-592 as they showed better performance for yield components and can be used as parents in future improvement program. The GCV and PCV were both observed to be good for days to 50% flower, fingers per panicle, Ear head weight (g), 1000 grain weight (g), harvest index (%), calcium content (mg/100g) and protein content (%). Thus, these characters provide a good source of variation and hence they are useful in improvement programme for finger millet. High heritability estimates were obtained for almost all the characters, indicating less influence from environmental effects.

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