Mysore J. Agric. Sci., 58 (4) : 136-143 (2024)

Deciphering Genetic Variability Parameters in Partial Male Sterile and Virescence Lines of Finger Millet [*Eleusine coracana* (L.) Gaertn.]

J. Meenakshi[1], T. E. Nagaraja[2], M. V. C. Gowda[3], Sujatha Bhat[4], S. Gazala Parveen[5],
Chetana[6] and D. N. Vinutha[7]
[1&6]Department of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bengaluru - 560 065
[2,3,4,5&7]ICAR-AICRP on Small Millets, UAS, GKVK, Bengaluru - 560 065
e-Mail : meena05kshi@gmail.com

Authors Contribution

J. Meenakshi :
Conceptualization, curation data analysis and draft writing;

T. E. Nagaraja &
M. V. C. Gowda :
Conceptualization, design and draft editing;

Sujatha Bhat :
Experimental design and conceptualization;

S. Gazala Parveen;
Chetana &
D. N. Vinutha :
Data analysis, manuscript editing and curation

Corresponding Author :
J. Meenakshi

Received : May 2024
Accepted : July 2024

Abstract

Finger millet is an important cereal owing to its nutritive qualities. It is highly self-pollinated, allotetraploid crop with extremely small-sized flower makes hybridization a bottleneck to exploit the variability. Partial male sterile and virescence lines are of greater importance in finger millet breeding since, it facilitates easy identification of true F_1s in seedling stage with the help of virescence maker. Selection of appropriate parents is key to success of hybridization and crop improvement. In this back drop the present study was conducted during *kharif*, 2021 and *kharif*, 2022 utilizing twenty-three finger millet lines comprising 11 partial male sterile, six partial male sterile with virescence marker and six virescent lines to unravel the genetic variability parameters. Analysis of variance indicated the selection of experimental material was appropriate. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for number of productive tillers, grain yield per plant, ear head weight and threshing percentage in both seasons. The line 20-12 was earliest flowering, 3-3-1 had long finger length and highest productive tillers and the virescent line vir early had highest yield per plant. Days to fifty per cent flowering showed low PCV and GCV in both the seasons. High heritability and high GAM were observed for traits like peduncle length, ear length, finger length, finger width, finger number, productive tillers, test weight, grain yield per plant and ear head weight in *kharif,* 2021 and traits *viz.,* finger number, grain yield per plant and threshing percentage in *kharif*, 2022. These results suggest that the trait expression is less influenced by the environment and selection would be effective. Partial male sterile and virescence lines have substantial amount of variability and most of the traits under study exhibit high heritability and genetic advance and could be exploited in crop improvement program.

Keywords : Finger millet, Partial male sterility, PCV, GCV, Heritability, Genetic advance

Finger millet, colloquially known as ragi in South India is consumed by habitants of arid and semi-arid countries of Asia and Africa. It is scientifically termed as *Eleusine coracana*, belongs to order poales, family *poaceae*, sub family *Chloridoideae*. *Eleusine africana* is said to be the wild progenitor of the crop (Chennaveeraiah and Hiremath, 1974 and Hilu & De Wet, 1976) and East Africa is considered as the primary centre of origin (De wet, 1995). It is allotetraploid species with chromosome number 2n=4x=36, highly self-pollinated crop. A very large number of cereal crops *viz.*, quinoa, millets, teff, sorghum, bajra, wheat, rice and maize etc. have been cultivated since ancient times, however, due to consumer preferences, selection and domestication process crop diversity has drastically reduced in recent decades where more than 50 per cent of world dietary intake is dominated by major cereals *i.e.,* rice, maize and wheat. Continued consumption of these cereals leads to health issues like weight gain, diabetes and other coronary diseases. It is high time to bring in the other underutilized millet crops into lime light. However, finger millet has gained its importance owing to its nutritive value. The varieties in finger millet have reached yield stagnation, in order to increase yield potential release of variability is essential. The size of flowers is extremely small and polyploidy nature of finger millet turns out to be bottleneck for hybridization. However, male sterile lines could be utilized to create genetic variability and exploit heterosis in finger millet. But, studies on partial male sterility (PS lines) in finger millet are scarce, which attracts the researchers to investigate the variability present in PS lines. The usage of PS lines in hybridization had advantage since the hybrid recovery percentage is very high ranging from 29-80 per cent (Manjappa, 2017) when compared to emasculation and pollination which results in only 2-3 per cent (Gupta, 2006) of crossed seeds. The sterility in partial male sterility is due failure of pollen tube growth after pollination (Manjappa, 2017). This property of low seed set per cent makes them worthy genetic resources to be used in finger millet hybridization program. Usage of partial sterile lines helps in identification of true F_1s during seed set stage which also requires more time and space. While, usage of partial sterile line with virescence marker helps in identification of true F_1s in the seedling stage in the nursery which saves time, resources and labour. In this regard, the present research was framed to study the extent of genetic variability in partial male sterile (PS lines) and virescence lines of finger millet to assess their utility in crop improvement programmes.

MATERIAL AND METHODS

The PS lines (Fig. 1a) were developed by inducing mutations in a well-known finger millet variety GPU 28 by treating it with Ethyl methyl sulfonate (EMS), a chemical mutagen and virescence lines (Fig.1b) were developed by treating the finger millet variety Indaf-8 with the same chemical mutagen (Manjappa *et al.,* 2019).


Fig. 1 : (a) Panicle view of partial sterile line 28-1-2, b) Field view of virescence line

The resultant lines were utilized to study the genetic parameters *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability h^2 (bs) and genetic advance as per cent mean (GAM). The current study was conducted at Zonal Agricultural Research Station (ZARS), ICAR-AICRP (Small millets), University of Agricultural Sciences (UAS), Bangalore located at altitude of 937m above mean sea level, latitude of 13.04 ^{0}N and longitude of 77.34^0 E. The experimental material consisted of 23 lines that included 11 partial male sterile, six partial male sterile lines with virescence marker and six virescent lines (Table 1)

TABLE 1

Finger millet partial sterile and virescence lines used in the present study

Partial sterile lines	Partial sterile lines with virescence marker	Virescence lines
PS1	19-5-2 (Vir PS)	Vir early
14-5 (PS1×PR202)	1-16-5 (Vir PS2)	Vir 32b
20-12 (PS1×TRV - 1)	E-13-2 (Vir PS3)	Vir 33b
23-4-1 (PS1×GE 4693)	14-5-1 (Vir PS4)	Vir 33
32-1 (PS1×Indaf 7)	21-8-4 (Vir PS5)	GE 1
34-3 (PS1×GPU 66)	21-8-4	28-1
44-3-1 (PS1× Indaf 8)		
44-1 (PS1×GE-1)		
29-8-1 (PS1×PR202)		
28-1-2 (PS1×GE4972)		
3-3-1 (VL149)		

TABLE 2

Mean performance of partial sterile and virescence lines evaluated for quantitative traits in *kharif*, 2021

Partial sterile / virescence line	DTFF	FLL	PL	EL	FL	FW	FN	PT	PH	TW	YLD	EW	TP
28-1	71.00	26.03	20.33	7.29	6.05	0.85	7.57	1.76	83.67	3.68	4.43	7.54	58.78
Vir early	74.00	29.50	24.92	9.14	6.35	0.90	8.65	1.07	92.70	3.38	7.09	12.91	55.70
Vir32b	76.50	29.50	26.25	9.29	6.58	0.84	8.75	1.05	93.68	3.67	6.64	8.96	74.06
Vir 33B	73.50	31.10	23.22	9.06	6.56	0.94	10.14	1.00	90.60	3.25	6.75	11.25	59.87
Vir 33	72.00	27.15	21.73	9.80	6.95	0.79	9.24	1.14	89.55	2.91	5.25	7.95	66.13
GE 1	72.00	27.05	20.44	10.03	6.83	0.81	8.27	1.26	82.59	2.81	4.74	7.34	64.97
19-5-2	71.50	24.72	15.67	6.11	4.25	0.58	7.50	1.44	70.06	3.61	1.89	2.61	76.75
1-16-5	69.00	27.73	20.36	8.03	5.63	0.62	7.19	1.44	77.53	3.46	3.83	5.75	69.51
E-13-2	72.00	27.94	18.83	6.13	4.73	0.52	8.21	1.26	71.86	3.44	1.11	3.56	30.38
14-5-1	74.50	27.47	22.17	7.81	5.72	0.67	7.86	1.40	74.49	3.10	1.69	3.62	49.44
21-8-4	75.50	27.25	25.08	9.78	6.79	0.69	8.70	1.00	82.85	3.22	2.08	4.50	46.21
21-8-4(gn)	75.50	29.78	26.57	10.01	6.91	0.74	8.14	1.00	86.28	3.08	2.66	4.94	53.49
3-3-1	63.00	30.12	25.53	12.39	8.67	0.50	6.80	1.47	96.31	3.85	2.59	5.05	51.32
14-5	69.00	32.02	25.74	9.21	6.36	0.48	6.95	1.26	108.21	4.06	1.48	5.17	31.88
20-12	57.50	31.74	22.69	9.55	6.48	0.57	6.06	1.64	94.50	4.08	2.00	3.61	57.43
23-4-1	71.50	36.22	30.13	10.35	8.52	0.60	5.09	1.13	106.47	4.15	2.24	4.70	48.07
32-1	70.00	33.26	24.32	8.18	6.13	0.49	7.48	1.78	98.91	5.38	2.27	5.53	42.67
34-3	71.00	31.72	22.86	8.47	6.11	0.50	7.11	1.17	86.89	4.42	1.98	4.31	45.92
44-3-1	75.50	29.94	20.58	10.23	7.02	0.63	9.19	1.39	96.28	2.89	3.45	6.94	48.52
44-1	75.50	29.93	23.31	9.33	6.68	0.66	7.99	1.06	92.61	3.47	2.88	4.51	65.18
29-8-1	68.00	32.63	22.10	10.36	8.30	0.66	6.15	1.15	89.45	3.99	2.35	4.95	47.50
28-1-2	66.00	33.00	26.08	9.65	7.00	0.57	6.20	2.10	101.50	3.94	2.05	3.85	53.25
PS-1	67.00	32.33	23.25	9.08	6.28	0.46	7.33	2.89	99.33	3.67	1.92	6.63	28.97
Mean	70.91	29.91	23.13	9.09	6.55	0.65	7.67	1.38	89.83	3.63	3.19	5.92	53.3
Max	76.50	36.22	30.13	12.39	8.67	0.94	10.14	2.89	108.21	5.38	7.09	12.91	76.75
Min	57.50	24.72	15.67	6.11	4.25	0.46	5.09	1.00	70.06	2.81	1.11	2.61	28.97
Sem	1.57	1.46	1.28	0.41	0.28	0.03	0.45	0.2	4.48	0.29	0.49	0.87	7.92
CD @5%	4.62	4.28	3.76	1.2	0.82	0.12	1.34	0.6	13.14	0.87	1.45	2.55	23.23

DTFF- days to fifty percent flowering, FLL- flag leaf length, PL- peduncle length, EL- ear length, FL- Finger length, FW- finger width, FN- finger number, PT- number of productive tillers, PH- plant height, TW- test weight, YLD- grain yield per plant, EHW- ear head weight, TP- threshing percentage that were evaluated in randomized complete block design with two replications in two seasons *i.e., kharif,* 2021 and *kharif,* 2022. Each plot consisted of 10 rows of 3m length with a spacing of 30×10cm. The observations were recorded on five random plants in each replication in both the season and their mean values were used for the statistical analysis. The data was recorded on thirteen quantitative traits *viz.,* days to 50 per cent flowering, flag leaf length (cm), peduncle length (cm), ear length (cm), finger length (cm), finger width (cm), finger number, productive tiller, plant height (cm), test weight (g), grain yield (g), ear head weight (g) and threshing percentage.

Analysis of variance (ANOVA) was done as per the procedure given by Panse and Sukhatme (1967). The method outlined by Burton and Devane (1952) was used to estimate PCV and GCV. Heritability in broad sense (h^2(bs)) as suggested by Lush (1940) and Robinson *et al.* (1949) was estimated. Genetic advance as percent of mean (GAM) was estimated as described by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the partial male sterile lines, with virescence marker and virescent lines for all the traits studied *i.e.,* days to fifty per cent flowering, flag leaf length, peduncle length, ear length, finger length, finger width, finger number, productive tiller, plant height, test weight, grain yield, ear head weight, threshing percentage in both the seasons except for ear length and test weight in *kharif,* 2022. The significant differences justify the substantial variability in the experimental material and their utilization in finger millet breeding programs. Similar results were reported by Nagaraja *et al.* (2023) in germplasm lines of finger millet, Mulualem (2022), Hema *et al.* (2022), Udamala *et al.* (2020) and Ulaganathan & Nirmalakumari, (2015) in finger millet germplasm lines.

The mean, minimum and maximum values for all the traits among the 23 lines is presented in the Table 2 and 3. The estimates of GCV, PCV, h^2 (bs) and GAM for all the traits is summarized in Table 4, Fig. 2a and 2b. All the partial sterile lines used in the study flowered from 57.50 days (20-12) to 76.50 days (Vir 32b) with mean of 70.91 days, their finger length varied from 4.25 cm (19-5-2) to 8.67cm (3-3-1) with a mean of 6.55 cm, number of productive tillers ranged from 1 (21-8-4) to 2.89 (PS-1) with a mean of 1.38 and the grain yield per plant ranged from 1.11g (E-13-2) to 7.09g (vir early) with a mean of 3.19g in *kharif,* 2021 (Table 2). Similarly, days to 50 per cent flowering varied from 61.25 (20-12) to 75.75 (Vir 33) with a mean of 70.32 days, finger length varied from 5.6 cm (19-5-2) to 10.13cm (vir 33b) with a mean of 7.74cm, number of productive tillers ranged from 1.2 (28-1) to 3.70 (3-3-1) with a mean of 2.57 and the grain yield per plant ranged from 1.41g (PS1) to 15.71g (vir early) with a mean of 5.99g in *kharif*, 2022 (Table 3). Since PS1 was first partial sterile line developed (Manjappa *et al.,* 2019), the performance of all the sterile lines were compared with PS1. Lines that had better performance than PS1 with respect to various traits like, days to fifty per cent flowering (20-12, 3-3-1), flag leaf length (23-4-1, 32-1), ear length (3-3-1, 23-4-1), finger length (3-3-1, 23-4-1), finger number (21-8-4, 21-8-4gn), test weight (32-1, 20-12) and grain yield (4-3-1, 20-12) were identified and these lines can be used as parental lines for hybridization.

The GCV for all the traits was lesser than PCV, signifying that environmental effect is associated with the expression of the traits studied but, the difference between estimates of GCV and PCV was low for most of the traits which suggests that even though the environmental effect is present, it is negligible (Table 4). Similar results were reported by Udamala *et al.* (2020) in finger millet. High PCV and GCV was observed for number of productive tillers, grain yield per plant, ear head weight and threshing per cent in both the seasons, while days to 50 per cent flowering showed low PCV and GCV in both the seasons (Table 4).

High magnitude of PCV and GCV indicated sufficient amount of variation present for these characters and offers ample scope for selection and crop improvement. The results were in consonance with

TABLE 3

Mean performance of partial sterile and virescence lines evaluated for quantitative traits in *kharif*, 2022

Partial sterile / virescence line	DTFF	FLL	PL	EL	FL	FW	FN	PT	PH	TW	YLD	EW	TP
28-1	73.50	25.45	19.65	7.35	6.30	0.82	7.60	1.20	85.40	3.77	4.50	7.20	62.28
Vir early	75.50	28.80	19.50	7.20	6.25	1.12	8.60	2.20	99.30	3.41	15.72	19.78	77.97
Vir 32b	74.00	33.70	23.90	8.00	6.90	1.07	9.80	1.50	98.00	3.53	12.78	16.96	75.42
Vir 33B	75.00	27.70	20.00	7.80	6.73	1.00	10.13	1.70	95.78	3.64	11.61	15.11	76.94
Vir 33	75.75	31.60	25.00	7.35	6.50	1.09	9.90	1.70	95.00	3.76	11.38	14.68	77.82
GE 1	75.50	22.20	18.50	8.85	7.70	1.16	9.20	2.20	88.60	3.74	13.89	17.29	80.36
19-5-2	63.00	24.40	17.30	6.50	5.40	0.87	5.60	3.30	75.00	3.59	1.63	4.15	40.01
1-16-5	67.25	29.50	19.40	7.40	5.90	0.93	6.70	3.50	84.60	3.57	3.74	7.04	52.50
E-13-2	71.50	24.60	19.00	7.45	6.50	0.98	7.10	2.00	85.20	3.54	3.94	7.76	49.22
14-5-1	75.50	22.90	16.90	7.20	5.95	0.94	7.20	2.70	72.00	3.94	2.99	5.80	48.30
21-8-4	75.50	26.10	18.20	9.15	7.31	0.96	8.40	2.20	93.50	3.17	4.74	8.63	52.17
21-8-4(gn)	75.50	26.20	18.80	8.05	7.25	0.94	8.60	2.10	82.60	3.26	3.75	7.46	48.05
3-3-1	64.75	28.60	19.30	8.30	7.30	1.02	6.80	3.70	96.20	3.61	3.95	7.55	52.41
14-5	69.00	30.30	24.30	8.40	6.85	1.00	7.20	3.00	102.00	4.18	3.18	7.36	41.12
20-12	61.25	27.40	21.90	8.85	7.35	0.93	6.90	3.10	99.70	4.20	7.43	10.72	68.45
23-4-1	63.00	34.40	27.00	10.05	8.97	0.93	6.50	3.00	114.80	4.06	4.88	8.23	59.46
32-1	66.50	30.80	22.20	7.15	6.25	1.00	7.30	2.70	96.90	3.89	4.23	6.96	57.44
34-3	67.25	28.50	21.30	7.30	6.30	1.00	7.30	2.50	98.10	3.68	4.84	8.27	58.72
44-3-1	75.75	27.20	18.50	9.10	7.95	0.93	9.50	2.50	87.40	3.89	3.82	8.13	47.07
44-1	75.25	26.80	20.00	8.15	6.75	0.94	7.40	3.20	93.60	4.07	4.67	9.30	49.94
29-8-1	63.50	31.30	20.90	9.70	8.04	0.98	7.10	3.20	97.50	4.06	4.37	6.95	64.56
28-1-2	66.00	23.90	18.00	8.10	6.45	0.96	6.60	3.30	95.20	4.06	4.48	7.74	55.11
PS-1	67.50	29.80	23.40	6.92	6.00	0.98	6.40	2.70	99.30	3.85	1.42	5.44	26.57
Mean	70.32	27.91	20.56	8.01	6.82	0.98	7.74	2.57	92.85	3.76	5.99	9.5	57.47
Max	75.75	34.4	27	10.05	8.97	1.16	10.13	3.70	114.8	4.2	15.72	19.77	80.36
Min	61.25	22.20	16.90	6.50	5.40	0.82	5.6	1.20	72.00	3.17	1.42	4.14	26.57
Sem	1.11	1.47	1.64	0.5	0.46	0.04	0.56	0.42	5.56	0.23	1.97	2.46	6.51
CD @5%	3.27	5.88	4.82	1.47	1.36	0.12	1.64	1.35	16.31	0.69	5.79	7.21	19.11

DTFF- days to fifty percent flowering, FLL- flag leaf length, PL- peduncle length, EL- ear length, FL- Finger length, FW- finger width, FN- finger number, PT- number of productive tillers, PH- plant height, TW- test weight, YLD- grain yield per plant, EHW- ear head weight, TP- threshing percentage

TABLE 4

Estimates of genetic variability parameters for quantitative traits evaluated in partial sterile and virescence lines of finger millet

Trait	Mean		GCV		PCV		h^2 (bs)		GAM	
	K-21	K-22	K-21	K-22	K-21	K-22	K-21	K-22	K-21	K-22
DTFF	70.91	70.32	5.95	7.21	6.73	7.55	78.17	91.17	10.84	14.14
FLL	29.91	27.91	7.77	10.41	10.40	12.82	55.89	65.96	11.97	17.42
PL	23.13	20.56	12.07	10.14	14.40	15.15	70.24	44.54	20.83	13.94
EL	9.09	8.01	14.79	9.68	16.10	13.13	84.32	54.32	27.98	14.69
FL	6.55	6.82	15.05	9.98	16.23	13.86	85.99	51.80	28.76	14.79
FW	0.65	0.98	21.05	6.53	22.70	8.83	85.97	54.67	40.21	9.94
FN	7.67	7.74	14.19	10.28	16.53	17.97	73.74	67.29	25.11	24.92
PT	1.38	2.57	27.77	19.44	34.89	31.97	63.35	36.96	45.53	24.34
PH	89.83	92.85	10.28	8.04	12.47	11.67	68.00	47.39	17.47	11.40
TW	3.63	3.76	13.74	4.11	17.99	9.76	58.36	17.72	21.63	3.56
YLD	3.19	5.99	53.62	59.07	57.98	75.21	85.54	61.69	102.17	95.58
EHW	5.92	9.50	39.95	35.91	45.05	51.29	78.64	49.04	72.98	51.81
TP	53.30	57.47	19.17	21.44	28.45	26.77	45.42	64.14	26.62	35.37

DTFF- days to fifty percent flowering, FLL- flag leaf length, PL- peduncle length, EL- ear length, FL- Finger length, FW- finger width, FN- finger number, PT- number of productive tillers, PH- plant height, TW- test weight, YLD- grain yield per plant, EHW- ear head weight, TP- threshing percentage, GCV-genotypic co-efficient of variation, PCV- Phenotypic co-efficient of variation, h_2 (bs)-heritability broad sense, GAM- genetic advance as percent mean, K- *kharif.*

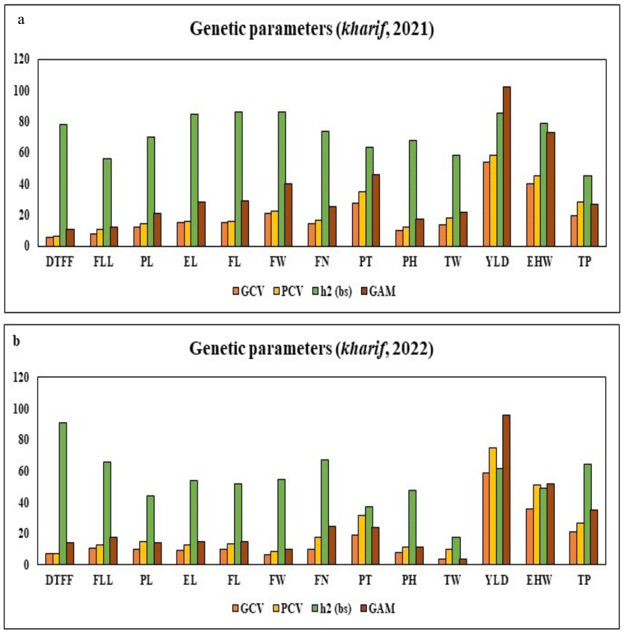

Fig. 2 : Histogram representation of mean, GCV-genotypic co-efficient of variation, PCV-Phenotypic co-efficient of variation, h_2-heritability broad sense, GAM-genetic advance as percent mean of 13 quantitative traits: a) *kharif,* 2021, b) *kharif,* 2022

that of Hema *et al.* (2022), Shashibhushan *et al.* (2022) and Bhavsar *et al.* (2020) in finger millet. Contrastingly, the traits like ear length, finger length, finger width and plant height depicted low GCV with moderate PCV in *kharif,* 2022 suggesting selection would not be effective. Rest of the traits recorded moderate PCV and GCV in *kharif*, 2021 and *kharif,* 2022. High PCV and moderate GCV was noticed for number of productive tillers (Table 4), narrow difference between PCV and GCV was observed for all the traits except number of productive tillers and ear head weight that implies a significant portion of the variability in these traits is attributed to genetic factors, as the influence of the environment is minimal. Similar results were reported by Jyothsna *et al.* (2016) and Anuradha *et al.* (2017) in finger millet. Similar studies have been carried by Singh *et al.* (2013) in rice male sterile lines for flower morphological traits.

Heritability is the heritable portion of phenotypic variance, it is a good index of transmission of characters from parents to offspring (Falconer, 1964). Johnson *et al.* (1955), proffered that heritability and genetic advance together were more valuable for predicting superior individuals compared to relying on information from heritability and genetic advance alone. For selection to be effective, a trait with high heritability should ideally be associated with a considerable genetic advance. High heritability and high GAM were observed for traits like peduncle length, ear length, finger length, finger width, finger number productive tillers, test weight, grain yield per plant and ear head weight in *kharif,* 2021 and traits *viz.,* finger number, grain yield per plant and threshing per cent in *kharif,* 2022. The results are in accordance with studies conducted by Mahanthesha *et al.* (2017). Likewise, Ezeaku *et al.*, 2015 also carried out heritability studies in sterile lines and maintainer lines of pearl millet for agronomic traits.

Further, days to 50 per cent flowering, plant height exhibited high heritability coupled with moderate GAM in *kharif,* 2021 (Table 4, Fig. 2a) and days to 50 per cent flowering, flag leaf length, ear length, finger length, finger width and finger number showed high heritability with moderate GAM in *kharif,* 2022 indicating that selection will be effective for these traits. Test weight showed low heritability coupled with low GAM in *kharif,* 2022 which can be due to influence of environment and selection would not be appropriate (Table 4, Fig. 2b). Since, most of the traits showed high heritability and GAM suggests that the variability in these lines could be exploited in breeding and hybridization program. These PS lines are derived from different genetic backgrounds and possess greater levels of genetic variability for different traits as evident in the study and have potential to be used as parents in crossing program in finger millet.

Acknowledgement : The senior author gratefully acknowledges Council of Scientific and Industrial Research (CSIR), New Delhi, India for providing Junior Research Fellowship (JRF) vide No. 09/0271(15958)/2022-EMR-I dated 07-11-2022 for pursuing Ph.D. degree program at University of Agricultural Sciences, Bangalore, India.

REFERENCES

ANURADHA, N., PATRO, T. S. S. K., DIVYA, M., SANDHYA, Y. R. AND TRIVENI, U., 2017, Genetic variability, heritability and association in advanced breeding lines of finger millet [*Eluesine coracana* (L.) Gaertn.]. *Internl. J. Chemical Studies*, **5** (5) : 1042 - 1044.

ANURADHA, N., PATRO, T. S. S. K., TRIVENI, U. AND RAO, P. J., 2020, Assessment of genetic variability in finger millet (*Eleusine coracana* L. Gaertn.). *J. Pharmacog. Phytochem.*, **9** (4) : 764 - 767.

BHAVSAR, V. V., SAPKAL, S. R., GIRASE, V. S. AND BARHATE, K. K., 2020, Assessment of genetic variability among finger millet local germplasm collected from diverse climate. *Interl. J. Res. Biosci. Agric. Technol.*, pp. : 64 - 73.

BURTON, G. W. AND DE VANE, E. H., 1952, Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 4**5** : 478 - 481.

CHENNAVEERAIAH, M. S. AND HIREMATH, S. C., 1974, Genome analysis of *Eleusine coracana* (L.) Gaertn. *Euphytica*. **23** (3) : 489 - 495.

EL-NAMAKY, R., 2018, The genetic variability of floral and agronomic characteristics of newly-bred cytoplasmic male sterile rice. *Agriculture*, **8** (5) : 68.

EZEAKU, I. E., ANGARAWAI, I. I., ALADELE, S. E. AND MOHAMMED, S. G., 2015, Correlation, path coefficient analysis and heritability of grain yield components in pearl millet (*Pennisetum glaucum* (L.) R. Br.) parental lines. *J. Plant Breed. Crop Sci.*, **7** (2) : 55 - 60.

FALCONER, D. S., 1964, An Introduction of quantitative genetics-second edition. Oliver and Boyd, Edinburgh. 312 - 324.

GUPTA, A., SRIVASTVA, A. K., BHATT, J. C., 2006, Improvement of millets and pseudo-cereals for rainfed agriculture in hill region in sustainable production from agricultural watersheds in North West Himalaya. *Eds*. (Uttaranchal, India: Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora), pp. : 163 - 174.

Hema, P., Pandey, S. and Yadav, B. N., 2022, Study of genetic variability and character association in elite lines of finger millet [*Eleusine coracana* (L.)] suitable for eastern plain zone of Uttar Pradesh. *Internl. J. Environ. Climate Change*, **12** (12) : 438 - 447.

Hilu, K. W. and De Wet, J. M. J., 1976, Domestication of *Eleusine coracana* (L.) Gaertn. *Econ. Bot.,* **30** : 199 - 208.

Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955, Estimates of genetic and environmental variability in soybean. *Agron. J.*, **7** (7) : 314 - 318.

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

Lush, J. L., 1940, Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *J. Animal Sci.*, **1** : 293 - 301.

Mahanthesha, M., Sujatha, M., Ashok, K. M. and Pandravada, S. R., 2017, Studies on variability, heritability and genetic advance for quantitative characters in finger millet [*Eleusine coracana* (L.) Gaertn] Lines. *Interl. J. Curr. Microbiol. Appl. Sci.*, **6** (6) : 970 - 974.

Manjappa, G., 2017, Heterotic potential of hybrids based on partial male sterile line (PS1) and development of male sterile lines with seedling markers in finger millet (*Eleusine coracana* (L.) Gaertn.) *Ph.D. Thesis* (Unpub.), Univ. Agric. Sci., Bangalore.

Manjappa, G., Rangaiah, S. and Gowda, M. V. C., 2019, Assessment of heterotic potential of hybrids using a novel partial male sterile mutant (PS1) in finger millet (*Eleucine coracana* L. Gaertn). *Mysore J. Agric. Sci.*, **49** (2) : 266 - 269.

Mulualem, T., 2022, Studies on the genetic variability, heritability and genetic advance of finger millet (*Eleusine coracana* L.) genotypes in Northwestern Ethiopia. *J. Curr. Opinion Crop Sci.*, **3** (2) : 55 - 61.

Panse, V. G. and Sukhatme, P. V., 1967, Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi, pp. : 103 - 108.

Robinson, H. F., Comstock, R. E. and Harney, P. H., 1949, Estimates of heritability and degree in corn. *Agron. J.*, **41** : 353 - 359.

Shashibhushan, D., Kumar, C. S. and Kondi, R. K. R., 2022, Genetic parameters and association studies for yield and yield contributing traits in pearl millet cultivars. *In Biol. Forum-Int. J.*, **14** : 416 - 421.

Singh, B. and Singh, R., 2013, Floral variability and correlation studies among selected male sterile lines in rice. *J. Biotechnol. Crop Sci.*, **2** : 34 - 36.

Nagaraja, T. E., Sujatha Bhat and Nandini, C., 2023, Evaluation of genetic diversity in germplasm accessions of finger millet [*Eleusine coracana* (L.) Gaertn.]. *Mysore J. Agric. Sci.,* **57** (2) : 238 - 245.

Udamala, A., Vijayalakshmi, B., Anuradha, N., Patro, T. S. S. K. and Sekhar, V., 2022, Studies on genetic variability for yield and quality traits in finger millet (*Eluesine coracana* L. Gaertn). *IJCMAS*, **9** (9) : 2020.

Ulaganathan, V. and Nirmalakumari, A., 2015, Finger millet germplasm characterization and evaluation using principal component analysis, *SABRAO J. Breed. Genet.,* **47** (2) : 79 - 88.