



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(12): 2190-2196
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www.thepharmajournal.com
Received: 19-09-2023
Accepted: 23-11-2023

DarjiTanvi
Department of Genetics and
Plant Breeding, N. M. College of
Agriculture, Navsari
Agricultural University, Navsari,
Gujarat, India

Patil HE
Associate Research Scientist
(PB), Hill Millet Research
Station, Navsari Agricultural
University, Waghi (The Dangs),
Gujarat, India

Genetic variability study in barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] for yield and yield attributes

DarjiTanvi and Patil HE

Abstract

Assessments of genetic variability was carried out in a set of forty-one genotypes of Barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] grown in a Randomized Block Design with three replications during the Kharif, 2019 at Hill Millet Research Station, Navsari Agricultural University, Waghai, The Dangs. The basic objective of the experiment was to assess the extent of morphological variation as well as genetic divergence in the available barnyard millet germplasm, which will serve as base for future barnyard millet crop improvement programmes. Fourteen different characters related to seed yield were recorded and subjected to estimation of genetic variability of the genotypes. The analysis of variance revealed significant differences between genotypes indicating presence of sufficient amount of variability in all the characters studied. Wide range of variability was observed for different traits indicating the scope for selection of suitable breeding material for further improvement. The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation for most of the characters indicating the influence of environmental factors. Moderate genotypic and phenotypic coefficient of variation found for the traits viz., plant height at maturity, productive tillers per plant, branches per panicle, panicle (finger) length, straw yield per plant, 1000 seed weight, protein content, fat content, Fe content and Zn content. The results indicated the presence of wide variation for these characters under study to allow further improvement by selection of these individual traits. High heritability coupled with high genetic advance was observed for the traits viz., plant height at maturity, branches per panicle, panicle (finger) length, straw yield per plant, 1000 seed weight, protein content, fat content, Fe content and Zn content. Moderate genotypic coefficient of variation coupled with high heritability as well as genetic advance were observed for the same traits indicating that these traits were governed by additive genes and phenotypic selection would be effective for genetic improvement in these traits.

Keywords: Genetic variability, heritability, genetic advance, coefficient of variation, barnyard millet

Introduction

Millets are some of the oldest important nutria cereal crop and cultivated under dry land agriculture. Small millet crops have a long history of cultivation of more than 5000 years and grown in many states (Gowda *et al.*, 2006) ^[16] due to their unique adaptation properties for poor degraded lands and ability to tolerate abiotic stress. Millets refers to a group of annual grasses mainly found in the arid and semi-arid regions of the world and belongs to the grass family Poaceae with small edible seeds which do not shatter readily at maturity (Thurston, 1989) ^[51] and include seven genera; *Pennisetum*, *Panicum*, *Setaria*, *Paspalum* and *Echinochloa*, all in the tribe *Paniceae*, genus *Eleusine* in the tribe *Chlorideae* and genus *Eragrostis* in the tribe *Festuceae*.

Barnyard millet is considered to be a direct domesticate of the wild species *E. colona* (L.), jungle rice, which is also a hexaploid with $2n = 54$ (Yabuno 1966) ^[56]. The genus *Echinochloa* includes some 20 species those are distributed widely in the warmer parts of the world. Two of the main species, *E. crusgalli* and *E. frumentacea* are grown as cereals. In addition to these two domesticated species, the genus includes about 30 annual and biennial wild species distributed worldwide (Clayton and Renvoize, 1986) ^[9]. These millet species are morphologically very dissimilar.

Barnyard millet is tall, robust, annual and grows up to 220 cm high. It has a short generation time, fastest growth among all small millets and completes the life cycle in 60–90 days (depending upon accession and growth environment) (Padulosi *et al.*, 2009) ^[35]. It is mostly grown in kharif season. Barnyard millet has a wide adaptation capacity and can grow up to an altitude of 2000 m above mean sea level during summer season (Gupta *et al.*, 2009) ^[17].

Corresponding Author:
DarjiTanvi
Department of Genetics and
Plant Breeding, N. M. College of
Agriculture, Navsari
Agricultural University, Navsari,
Gujarat, India

It is variable in flowering time, inflorescence shape, morphological features and pigmentation of spikelets, plant type and other plant traits. For proper growth of *E. frumentacea*, the optimum temperature range is 27–33 °C and 15–22 °C day and night, respectively (Muldoon *et al.*, 1982). Barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] (2n=4x=36) also called as Jhangora, Sawan or Madira is largely a self-pollinated crop, tall erect upto 60 to 120 cm in height, the stem as well as leaves being green in colour. Its leaves are flat, glabrous or slightly hairs without ligules. The racemes are few to numerous, densely crowded at the apex with spikelets arranged in 4 irregular rows on the triquetrous rachis. The spikelets are two-flowered, 2-3 mm long, ovate to elliptical, lower lemma awnless but sharp pointed, sub-sessile and placed on short rough pedicels subtended by two glumes (De Wet *et al.*, 1983) [10]. The second lemma bears hermaphrodite flowers with three stamens ovary superior contains two distinct styles with plumose stigma (Sundararaj and Thulasidas, 1976) [49]. The grain is caryopsis and white or yellow in colour (Prasad, 2005) [39]. The flower opens in the upper raceme first and flowering is from the top of inflorescence to downwards. The panicle takes 10-14 days for emergence and takes 10-15 for completion of flowering under the hill conditions. Flowers open from 5-10 a.m. with maximum number of flower opens between 6-7 a.m. (Jayaraman *et al.*, 1997; Sundararaj and Thulasidas, 1976) [19, 49]. Within the individual raceme, flowering starts first at both the marginal ends first and then proceed to the middle of the raceme. Before the anthers dehiscence, the stigmatic branches spread and flower opens (Seetharam *et al.*, 2003) [45]. The flower closes within half an hour.

In order to achieve the goal of increased production by increasing the yield potential of genotypes, knowledge of variability, inheritance, direction and magnitude of association between various traits and their stable performance is essential for plant breeder.

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. 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. An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme, because the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type.

Grain yield is a complex polygenic quantitative trait, greatly affected by environment. Hence, selection of superior genotypes directly based on the performance of yield may not be very effective but selection based on its component characters would prove more effective as reported in other plants (Fisher, 1918) [13]. Correlation studies would provide estimates of degree of association between yield and its various components and also among the components.

Heritability estimates along with genetic advance are fairly helpful in predicting the important traits under selection and in formulating suitable selection procedures.

Hence, the present study conducted on forty-one genotypes of Barnyard millet to harness the information related to genetic

variability, heritability and genetic advance for different traits.

Materials and Methods

The experiment was conducted at Hill Millet Research Station, Navsari Agricultural University, Waghai (The Dangs) using 41 genotypes of barnyard millets in randomized block design with three replications. The gross plot is divided into three blocks which were taken as a replications while the blocks are further divided into equal 41 plots. Five randomly selected plants from each genotypes in each replications were used to record observations for morphological characters. Data were recorded on total 14 morphological and biochemical traits *viz.*, Days to 50% flowering, Days to maturity, Plant height at maturity (cm), Productive tillers per plant, Branches per plant, Panicle (Finger) length (cm), Grain yield per plant (g), Straw yield per plant (g), 1000 Seed weight (g). Protein content (%). Fat content (%). Ca content (mg/100g), Fe content (mg/100g) and Zn content (mg/100g). The mean of five plants was subjected to statistical analysis, to estimate analysis of variance as suggested by Panse and Sukhatme (1967) [37]. Genotypic and phenotypic coefficient of variability were computed according to the method suggested by Burton (1952) [5]. Heritability in broad sense was calculated as per the formula given by Allard (1960) [2]. Range of heritability was categorized as suggested by Robinson *et al.*, (1949) [42]. Genetic advance was expressed as percent of mean by using the formula expounded by Johnson *et al.*, (1955) [23]. Traits were classified as having high, moderate or low genetic advance as per the method suggested by Johnson *et al.*, (1955) [23].

Results and Discussion

Analysis of variance

The genotypic differences were highly significant for all the fourteen characters indicating considerable amount of genetic variability among the genotypes tested in the present study, suggesting ample scope for improvement of yield and various yield attributing characters. The analysis of variance indicating the mean sum of squares for all the fourteen characters studied, are summarized in Table 1.

Similar results for most of the characters were also reported by Goswami and Asthana (1984) [15], Chunilal *et al.* (1996) [8], Kebera *et al.* (2006) [29], John (2007) [22], Ganapathy *et al.* (2011) [14], Priyadarshini *et al.* (2011) [40], Ulaganathan and Nirmalakumari (2011) [52], Lule *et al.* (2012) [31], Chaudhari (2013) [7], Dhanalakshmi *et al.* (2013) [12], Karad and Patil (2013) [28], Reddy *et al.* (2013) [41], Suryanarayana *et al.* (2014) [50], Malambane and Jaisil (2015) [32], Saundaryakumari and Singh (2015) [44], Ulaganathan and Nirmalakumari (2015) [53], Sapkal *et al.* (2018) [43] in finger millet while Selvi *et al.* (2014) [46] and Patel *et al.* (2018) [38] in little millet while Lakshmana and Guagari (2001) [30], Brunda *et al.* (2014) [6] and Jyothsna *et al.* (2016) [25] in foxtail millet while Subramanian *et al.* (2010) [48] and Nirubana *et al.* (2017) [34] in kodo millet while Jyothsna *et al.* (2016) [25] in barnyard millet.

Variability studies

Success of any crop improvement programme depends upon the variability in the material. A large amount of variation is necessary in a breeding population to enable the breeder to carry out effective selection.

The range, mean, genotypic, phenotypic and environmental variance, phenotypic and genotypic coefficients of variation,

heritability and expected genetic advance as percentage of mean for fourteen characters are presented in Table 2 and 3. High to moderate estimates of genotypic and phenotypic variance were observed for the traits viz., days to 50% flowering, days to maturity, plant height at maturity, straw yield per plant and grain yield per plant. Similar results for these traits were also reported by John (2006)^[21] for days to 50% flowering, days to maturity, plant height at maturity, straw yield per plant; Kebere *et al.* (2006)^[29] for plant height, days to 50% flowering, days to maturity and grain yield per plant; John (2007)^[22] for days to 50% flowering, plant height at maturity, straw yield per plant; Dhanalakshmi *et al.* (2013)^[12] for days to 50% flowering, plant height; Reddy *et al.* (2013)^[41] for days to 50% flowering, plant height at maturity, straw yield; Wolie *et al.* (2013)^[55] for grain yield per plant, plant height at maturity and days to maturity; Suryanarayana *et al.* (2014)^[50] for days to maturity, plant height at maturity; Saundaryakumari and Singh (2015)^[44] for plant height at maturity, grain yield per plant, days to maturity and days to 50% flowering; Devaliya *et al.* (2018)^[11] for plant height at maturity, days to 50% flowering, straw yield per plant and days to maturity in finger millet. while in little millet similar results were reported by Vasadia (2015)^[54] for days to 50% flowering, straw yield, plant height at maturity and Patel *et al.* (2018)^[38] for days to 50% flowering, days to maturity, plant height at maturity, straw yield per plant while in foxtail millet similar results were reported by Lakshmana and Guagari (2001)^[30] for grain yield per plant, straw yield per plant, plant height at maturity and days to maturity. Low estimates of genotypic and phenotypic variance were observed for the traits viz., productive tillers per plant, branches per plant, panicle length, 1000 seed weight, protein content, fat content, Ca content, Fe content and Zn content. Similar results in finger millet were also obtained by Kebere *et al.* (2006)^[29] for productive tillers per plant, panicle length, 1000 seed weight; John (2007)^[22] for productive tillers per plant, 1000 seed weight; Suryanarayana *et al.* (2014)^[50] for productive tillers per plant; Devaliya *et al.* (2018)^[11] for productive tillers per plant, panicle length, 1000 seed weight while in little millet similar results were reported by Patel *et*

al. (2018)^[38] for productive tillers per plant, branches per plant, 1000 seed weight, protein content, fat content, iron content and zinc content. Moderate genotypic and phenotypic coefficient of variation found for the traits viz., plant height at maturity, productive tillers per plant, branches per panicle, panicle length, straw yield per plant, 1000 seed weight, protein content, fat content, Fe content and Zn content. Moderate genotypic and phenotypic coefficient of variation for such traits were also observed by Ganapathy *et al.* (2011)^[14] for panicle length; Priyadharshini *et al.* (2011)^[40] for panicle length, protein content; Ulaganathan and Nirmalakumari (2011)^[52] for 1000 seed weight, plant height at maturity and panicle length; Lule *et al.* (2012)^[31] for 1000 seed weight, productive tillers number; Reddy *et al.* (2013)^[41] for straw yield per plant; Suryanarayana *et al.* (2014)^[50] for plant height at maturity; Saundaryakumari and Singh (2015)^[44] for plant height at maturity and Devaliya *et al.* (2018)^[11] for productive tillers per plant and straw yield per plant in finger millet while Patel *et al.* (2018)^[38] for 1000 seed weight, protein content, fat content and Fe content in little millet. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the interaction of genotypes with environment. The result indicated large extent of genetic variability among the genotypes. From the variability studies, it could be concluded that phenotypic selection would be effective for plant height at maturity, productive tillers per plant, branches per panicle, panicle length, straw yield per plant, 1000 seed weight, protein content, fat content, Fe content and Zn content. The lower value of genotypic coefficient of variation and phenotypic coefficient of variation observed for the traits viz., days to 50% flowering, days to maturity, grain yield per plant and Ca content. Similar results were also obtained by Kebere *et al.* (2006)^[29] for days to maturity; Shet *et al.* (2010)^[47] for days to 50% flowering; Ganapathy *et al.* (2011)^[14] for days to maturity; Haradari *et al.* (2011)^[18] for days to 50% flowering and days to maturity; Priyadharshini *et al.* (2011)^[40] for days to 50% flowering; Ulaganathan and Nirmalakumari (2011)^[52] for days to 50% flowering and days

Table 1: Analysis of variance for fourteen traits in forty-one genotypes of Barnyard millet

Source of variation	Degree of freedom	Mean sum of square						
		Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	Productive tillers per plant	Branches per plant	Panicle (Finger) length (cm)	Grain yield per plant (g)
Genotypes	40	107.85**	125.77**	1266.11**	0.46**	1.70**	23.53**	1044.08**
Replication	2	4.54	7.34	2.78	0.07	0.13	1.58	222.45
Error	80	1.853	2.65	43.216	0.067	0.061	0.768	424.605
S. Em.±		0.79	0.94	3.8	0.15	0.14	0.51	11.9
CD at 5%		2.21	2.65	10.68	0.42	0.42	1.42	33.48
CV (%)		2.23	1.76	4.26	7.85	3.52	5.02	13.16

Source of variation	Degree of freedom	Mean sum of square						
		Straw yield per plant (g)	1000 seed weight (g)	Protein content (%)	Fat content (%)	Ca content (mg/100g)	Fe content (mg/100g)	Zn content (mg/100g)
Genotypes	40	13035.02**	1.07**	5.82**	1.45**	2.15**	2.28**	1.81**
Replication	2	4143.59	0.36	0.32	0.08	0.11	0.05	0.04
Error	80	2271.852	0.137	0.188	0.047	0.054	0.02	0.019
S. Em.±		27.52	0.21	0.25	0.12	0.13	0.08	0.08
CD at 5%		77.45	0.60	0.70	0.35	0.38	0.23	0.22
CV (%)		10.48	8.37	4.92	4.92	2.34	2.01	2.48

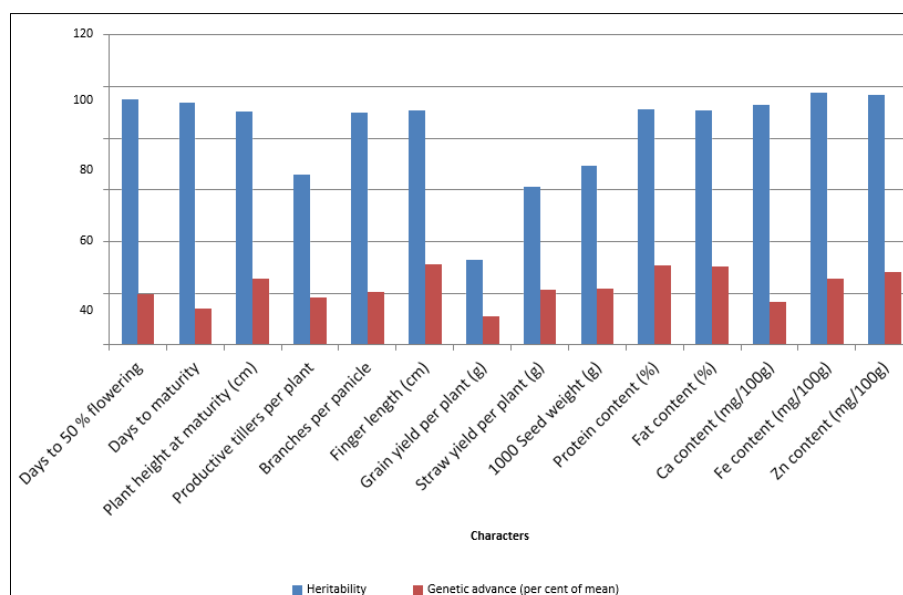
** Significant at 1% level * Significant at 5% level

Table 2: Range, mean and components of variance for fourteen traits in forty-one genotypes of barnyard millet

Sr. No	Characters	Range		Mean	Variance		
		Minimum	Maximum		Genotypic	Phenotypic	Environmental
1.	Days to 50% flowering	47.70	72.30	60.92	35.33	37.18	1.85
2.	Days to maturity	78.00	105.00	92.66	41.04	43.69	2.65
3.	Plant height at maturity (cm)	107.00	185.40	154.18	407.63	450.85	43.22
4.	Productive tillers per plant	2.50	4.10	3.30	0.13	0.20	0.07
5.	Branches per panicle	5.60	8.40	7.03	0.55	0.61	0.06
6.	Panicle (Finger) length (cm)	9.90	21.70	17.45	7.59	8.36	0.77
7.	Grain yield per plant (g)	118.70	193.80	156.58	206.49	631.10	424.61
8.	Straw yield per plant (g)	276.30	543.30	454.73	3587.72	5859.58	2271.85
9.	1000 seed weight (g)	2.80	5.50	4.42	0.31	0.45	0.14
10.	Protein content (%)	5.00	10.90	8.80	1.88	2.07	0.19
11.	Fat content (%)	2.50	5.40	4.40	0.47	0.52	0.05
12.	Ca content (mg/100g)	8.80	11.40	9.96	0.70	0.75	0.05
13.	Fe content (mg/100g)	5.30	8.40	6.95	0.75	0.77	0.02
14.	Zn content (mg/100g)	4.10	6.60	5.56	0.60	0.62	0.02

Table 3: Genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for fourteen traits in forty-one genotypes of Barnyard millet

Sr. No	Characters	GCV%	PCV%	Heritability Broad sense (%)	Genetic advance	Genetic advance (% of mean)
1.	Days to 50% flowering	9.757	10.010	95.000	11.936	19.593
2.	Days to maturity	6.914	7.134	93.900	12.791	13.804
3.	Plant height at maturity (cm)	13.096	13.794	90.100	39.482	25.611
4.	Productive tiller per plant	10.904	13.437	65.800	0.602	18.228
5.	Branch per panicle	10.521	11.093	89.900	1.444	20.554
6.	Panicle (Finger) length (cm)	15.783	16.563	90.800	5.407	30.982
7.	Grain yield per plant (g)	9.202	16.055	32.800	17.017	10.865
8.	Straw yield per plant (g)	13.172	16.834	61.200	96.550	21.232
9.	1000 seed weight (g)	12.603	15.131	69.400	0.957	21.624
10.	Protein content (%)	15.562	16.322	90.900	2.691	30.565
11.	Fat content (%)	15.415	16.178	90.800	1.339	30.259
12.	Ca content (mg/100g)	8.385	8.705	92.800	1.657	16.637
13.	Fe content (mg/100g)	12.484	12.644	97.500	1.766	25.390
14.	Zn content (mg/100g)	13.882	14.102	96.900	1.566	28.153

**Fig 1:** Heritability (%) and genetic advance (percent of mean) of various characters of barnyard millet

To maturity; Lule *et al.* (2012) [31] for days to 50% flowering and days to maturity; Reddy *et al.* (2013) [41] for days 50% flowering; Suryanarayana *et al.* (2014) [50] for days to 50% flowering and days to maturity and Devaliya *et al.* (2018) [11] for days to 50% flowering, days to maturity in finger millet while Jyotsna *et al.* (2016) [25] for days to maturity in little

millet. Such result also indicated that selection is not effective for those traits because of the narrower genetic variability. GCV were lower for the characters viz., days to 50% flowering, days to maturity, grain yield per plant and Ca content. Suggesting negligible role of environment in the expression of traits, therefore improvement by phenotypic

selection is possible.

It is not possible to determine the amount of variability, which is heritable with the help of genotypic coefficient of variation alone. Burton (1952)^[5] also suggested that GCV together with a heritability estimates would provide better insight for amount of genetic gain expected through phenotypic selection.

The characters *viz.*, days to 50% flowering, days to maturity, plant height at maturity, productive tillers per plant, branches per panicle, panicle length, 1000 seed weight, straw yield per plant, protein content, fat content, Ca content, Fe content and Zn content exhibited high heritability estimates while moderate heritability estimates were observed for grain yield per plant. The result indicated that these characters are governed by additive genes and selection for improvement of such characters could be rewarding. Similar results of high heritability were also obtained by Goswami and Asthana (1984)^[15] for panicle length and days to maturity; Abraham *et al.* (1989)^[1] for 1000 seed weight, days to maturity and days to 50% flowering; John (2006)^[21] for productive tillers per plant, 1000 seed weight, straw yield per plant; Kebere *et al.* (2006)^[29] for productive tillers per plant, panicle length; Shet *et al.* (2010)^[47] for plant height at maturity, panicle length, 1000 seed weight; Ganapathy *et al.* (2011)^[14] for days to 50% flowering, plant height at maturity, productive tillers per plant, panicle length; Haradari *et al.* (2011)^[18] for plant height at maturity, panicle length and days to 50% flowering; Priyadharshini *et al.* (2011)^[40] for days to 50% flowering, plant height at maturity, panicle length, 1000 seed weight and protein content; Ulaganathan and Nirmalakumari (2011)^[52] for days to 50% flowering, days to maturity, plant height at maturity, productive tillers per plant, panicle length, 1000 seed weight; Lule *et al.* (2012)^[31] for days to 50% flowering, plant height at maturity, panicle length and 1000 seed weight; Jayshree and Nagarajasiah (2013)^[20] for days to 50% flowering, plant height at maturity, productive tillers per plant, panicle length; Karad and Patil (2013)^[28] for Fe content, protein content, days to 50% flowering, days to maturity, plant height at maturity, panicle length, 1000 seed weight and straw yield per plant; Wolie and Dessalegn (2013)^[55] for panicle length, days to 50% flowering, productive tillers per plant and 1000 seed weight; Suryanarayana *et al.* (2014)^[50] for plant height at maturity; Saundaryakumari and Singh (2015)^[44] for days to 50% flowering, plant height at maturity, 1000 seed weight, productive tillers per plant and days to maturity; Devaliya *et al.* (2018)^[11] for days to 50% flowering, days to maturity, plant height at maturity, 1000 seed weight, straw yield per plant in finger millet while Selvi *et al.* (2014)^[46] for days to 50% flowering, productive tillers per plant, 1000 seed weight and plant height at maturity; Vasadia (2015)^[54] for days to 50% flowering, productive tillers per plant, plant height at maturity, straw yield per plant and 1000 seed weight; Jyotsna *et al.* (2016)^[25] for days to 50% flowering and days to maturity; Anuradha *et al.* (2017)^[4] for productive tillers per plant, days to 50% flowering, plant height at maturity, days to maturity and straw yield per plant; Patel *et al.*, (2018)^[38] for productive tillers per plant, days to 50% flowering, plant height at maturity, days to maturity, 1000 seed weight, protein content, fat content, Ca content, Fe content, Zn content and straw yield per plant in little millet. Similar results of moderate heritability were also obtained by Kebere *et al.* (2006)^[29] for grain yield per plant; Lule *et al.* (2012)^[31] for grain yield per plant in finger millet. These

results indicated the substantial contribution of additive genetic variance in the expression of these characters and could be improved through individual plant selection.

In the present study the high heritability coupled with high genetic advance was observed for the traits *viz.*, plant height at maturity, branches per panicle, panicle length, straw yield per plant, 1000 seed weight, protein content, fat content, Fe content and Zn content. It forces to conclude that these characters are governed by additive gene action and selection would be rewarding. Similar findings were earlier reported by Chunilal *et al.* (1996)^[8] for straw yield per plant, panicle length; John (2006)^[21] for straw yield per plant; Kebere *et al.* (2006)^[29] for panicle length; Shet *et al.* (2010)^[47] for panicle length; Ganapathy *et al.* (2011)^[14] for plant height at maturity, panicle length; Priyadharshini *et al.* (2011)^[40] for plant height at maturity, panicle length and protein content; Ulaganathan and Nirmalakumari (2011)^[52] for 1000 seed weight, panicle length and plant height at maturity; Lule *et al.* (2012)^[31] for 1000 seed weight, panicle length and plant height at maturity; Jayshree and Nagarajasiah (2013)^[20] for panicle length; Karad and Patil (2013)^[28] for protein content, Fe content, panicle length, straw yield per plant and 1000 seed weight; Wolie and Dessalegn (2013)^[55] for plant height at maturity and 1000 seed weight; Suryanarayana *et al.* (2014)^[50] for plant height at maturity; Saundaryakumari and Singh (2015)^[44] for 1000 seed weight; Devaliya *et al.* (2018)^[11] for straw yield per plant in finger millet while Ananda *et al.* (2015)^[3] for straw yield per plant; Vasadia (2015)^[54] for straw yield per plant; Patel *et al.* (2018)^[38] for Fe content, fat content, protein content, 1000 seed weight and straw yield per plant in little millet.

The characters *viz.*, days to 50% flowering, days to maturity, productive tillers per plant and Ca content showed high heritability coupled with moderate genetic advance as percent of mean. High heritability accompanied with moderate genetic advance as percent of mean indicated that the genotypes, under study were diverse with immense genetic potential and further improvement in these traits are possible by practicing simple selection technique. Similar results were also obtained by Chunilal *et al.* (1996)^[8] for days to maturity; John (2006)^[21] for days to 50% flowering, Kebere *et al.* (2006)^[29] for days to maturity; Ganapathy *et al.* (2011)^[14] for days to maturity; Priyadharshini *et al.* (2011)^[40] for days to 50% flowering; Ulaganathan and Nirmalakumari (2011)^[52] for days to 50% flowering and days to maturity; Lule *et al.* (2012)^[31] for days to 50% flowering, productive tillers per plant; Karad and Patil (2013)^[28] for days to 50% flowering, days to maturity; Saundaryakumari and Singh (2015)^[44] for days to 50% flowering and days to maturity; Devaliya *et al.* (2018)^[11] for days to 50% flowering in finger millet while Selvi *et al.* (2014)^[46] for days to 50% flowering and Patel *et al.* (2018)^[38] for days to 50% flowering in little millet.

Moderate heritability coupled with moderate genetic advance as percent of mean was observed for the character grain yield per plant. It showed the predominance of additive variance in the expression of this trait. Hence, breeder should use suitable methodology to use additive gene action simultaneously for significant improvement.

In general, present results indicated that high heritability coupled with high genetic advance as percent of mean and moderate GCV and PCV were observed for the traits *viz.*, plant height at maturity, branches per panicle, panicle length, straw yield per plant, 1000 seed weight, protein content, fat

content, Fe content and Zn content indicating these characters are under the control of additive gene effect (Panse, 1957)^[36]. Therefore, for further improvement in these traits using mass selection or progeny selection would be worthwhile. Similar findings were earlier reported by John (2006)^[21] for straw yield per plant; Ganapathy *et al.* (2011)^[14] for plant height at maturity, panicle length; Priyadharshini *et al.* (2011)^[40] plant height at maturity, panicle length and protein content; Ulaganathan and Nirmalakumari (2011)^[52] for plant height at maturity, panicle length and 1000 seed weight; Lule *et al.* (2012)^[31] for plant height at maturity, panicle length and 1000 seed weight; Suryanarayana *et al.* (2014)^[50] for plant height at maturity; Saundaryakumari and Singh (2015)^[44] for 1000 seed weight; Devaliya *et al.* (2018)^[11] for straw yield per plant in finger millet while Patel *et al.* (2018)^[38] for 1000 seed weight, protein content, fat content and Fe content in little millet.

There was a little scope for further improvement in the trait days to 50% flowering, days to maturity, Ca content and grain yield per plant due to low GCV and low PCV.

Results of the present study indicating the role of additive gene action in the inheritance of traits *viz.*, panicle length, plant height at maturity, straw yield per plant, branches per panicle, 1000 seed weight, protein content, fat content, Fe content and Zn content. Hence, further improvement in these characters would be achieved by phenotypic selection.

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