Genetic studies on variability, heritability and genetic gain of yield and yield related traits

ABSTRACT

The present work comprised of 40 foxtail millet advanced breeding lines obtained from small millet scheme, MARS, Dharwad. These lines with checks viz., DHFT-109-3 and HMT-100-1 were evaluated in replicated yield trial at millet scheme, MARS, Dharwad, during *rabi* 2020-21 for assessing genetic variability, heritability, and genetic gain among 17 traits. Wide range of variation provides an ample scope for selection of superior and desired advanced breeding lines by the plant breeders for further improvement of these characters. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits under study. In the present study foxtail millet advanced breeding lines exhibited moderate PCV and GCV for the most important economic traits viz., panicle length (15.85% and18.01 %), panicle girth (15.25% and 15.45%), productive tiller per plant (18.44% and 19.40%) and straw yield per hectare ~~and~~ (19.92% and 21.39%). The high phenotypic coefficient of variation and genotypic coefficient of variation were observed for characters viz., specific leaf area (21.08% and 22.44%), specific leaf weight (20.52% and 26.72%), grain yield per plant (9.32% and 10.99 %), grain yield per plot (8.85 % and 10.49%) and straw yield per ha (19.92 and 21.39)~~.,~~ ~~Moderate to high heritability coupled with higher magnitude of expected genetic advance for a particular trait indicates the additive gene action. On the contrary higher heritability coupled with low genetic advance is observed for any given trait, indicates the presence of non additive gene action.~~ Most of the traits viz., plant height(79 %), flag leaf length(98%), flag leaf width (80%), number of productive tillers per plant (90%), panicle length(98%), panicle girth (97 %), SPAD at 50 per cent flowering (92%), test weight (63%), specific leaf area (88%), specific leaf weight (87%), grain yield per plant(71%) and straw yield per hectare (87%) showed the high estimates of broad sense heritability (h2 b) indicating the reliability of the estimates for variation between advanced breeding lines and effectiveness of selection.

Comment [L1]: Mention the order of values for GCV and PCV. Improve the sentence accordingly.

Keywords: *Variability, Heritability, Grain Yield, Foxtail Millet, Breeding Lines*

Introduction:

Millets are one of the oldest foods known to man & possibly the first cereal grain to be used for domestic purposes. Millets are small-seeded grasses grown in diverse soils, varying rainfall regimes and in areas widely differing in thermo and photoperiods. The resilience exhibited by these crops helps adjust themselves to different kinds of ecological niches. Being eco-friendly nature these crops are included under organic agriculture. All these have made them quite indispensable to rainfed, tribal and hill agriculture where crop substitution is difficult. Foxtail millet (*Setaria italica* L.) is an annual, diploid (2n=2x=18) and self-pollinated crop. It is an important ancient crop of dryland agriculture and the potential climate-resilient crop for food and nutritional security in the current climate change scenario.

It is one of the most economically important millet crops grown for grain, which is used mainly for human consumption, animal, poultry, cage birds feeding and as straw. The grain of foxtail millet is ovoid, 2 mm long, yellow enclosed by husk varying from pale yellow to orange, red, brown or black colour. Hence, it should undergo de husking before being used as food. The grain can be cooked in the same manner as rice and has many food applications (porridge, pudding, bread, cakes, flour, chips, rolls, noodles, etc.). It is an important staple food in India and northern China.

Foxtail millet ranks second in the world's total production of millets. China has the highest area under foxtail millet and leads first in production of foxtail millet in world. In India, it is cultivated in an area of 5 lakh hectares with a production of 2.9 million tons, the productivity of 600 kg per hectare. At present, foxtail millet is cultivated on a limited area in Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and north eastern states (1). Foxtail millet has an important place in the world agriculture providing approximately six million tons of food to millions of people, mainly on poor or marginal soils in southern Europe and in temperate, subtropical and tropical Asia. It will grow in altitudes from sea level to 2000 m. Foxtail millet is fairly tolerant to drought; it cannot tolerate water-logging.

Foxtail millet grains are rich in Protein (10-12%), Fat (4.7%), carbohydrates (60.6%), Lysine (2.29 - 2.7%) and Thiamin (0.59 mg). The grains with husk intact have long shelf life which is a preferable attribute (Ravi *et al.*, 2010). Grains with dietary fiber, improves glycemic index and lowers plasma lipid concentrations in patients with type 2 diabetes (6).

In spite of the health benefits provided by foxtail millet, it has remained as a neglected crop from the mainstream of crop improvement research compared to other cereals such as maize (*Zea mays)*, rice (*Oryza sativa*), wheat (*Triticum aestivum*), sorghum (*Sorghum bicolor*) and pearl millet (*Pennisetum glaucum*). The minor millets were neglected in the era of Green Revolution. Dehusking is difficult and designed machines are not available in millet growing areas. In addition, distribution of fine grains through public distribution system made the consumers to shift entirely to fine grains. All these have contributed to less demand and low production and availability.

Any crop improvement method requires an understanding of the available variability. Yield is a complex character and is the product of the contribution of various yield components. Presence of a wider spectrum of variability will enhance the chances of selecting a desired genotype. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby helps the breeder to employ a suitable breeding strategy to achieve the desired goals. To study the extent of genetic variability, heritability and genetic advance for yield and its attributes.

Material and method

Experimental material for the present study was comprised of 40 advanced breeding lines of foxtail millet. These were obtained from the Small millet scheme, Main agricultural research station, University of agricultural sciences, Dharwad, Karnataka. These advanced breeding lines are listed in Table 1. The variety Dhft-109-3 was used as national check, HMT-100-1 as local check. ~~The details of experimental techniques followed and materials used during course of investigation are presented under following headings and carried out to elicit the information on magnitude of genetic and variability for yield and yield attributes.~~ The field experiment was conducted during *rabi* 2020-21 at Main agricultural research station, University of A~~a~~gricultural S~~s~~ciences, Dharwad to ~~and~~ study the extent of genetic variability, heritability and genetic advance for yield and its attributes.

Comment [L2]: 38 advanced breeding lines along with two checks is clear. Change everywhere.

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Comment [L3]: Mention the experimental design used in the study in this paragraph

The details of the material used and techniques adopted for analysis and interpretation are described as follows.

~~Experimental material for the present study was comprised of 40 advanced breeding lines of foxtail millet. These were obtained from the Small millet scheme, Main agricultural research station, University of agricultural sciences, Dharwad, Karnataka. These advanced breeding lines are listed in Table 1. The variety Dhft-109-3 was used as national check, HMT-100-1 as local check.~~

Table 1: List of advanced breeding lines employed in the research program with their pedigree/source

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Sl. No.	Advanced breeding lines	Pedigree
1.	DHFt-20-1-1	Co-5 X DHFt-333
2.	DHFt-20-1-2	Co-6 X DHFt-333
3.	DHFt-20-1-3	Co-5 X DHFt-109-3
4.	DHFt-20-1-4	Co-5 X DHFt-333
5.	DHFt-20-1-5.	Co-6 X DHFT-109-3
6.	DHFt-20-1-6.	GPUS-30 X DHFt-109-3
7.	DHFt-20-1-7.	GPUS-30 X GS-145
8.	DHFt-20-1-8.	Co-5 X DHFt-333
9.	DHFt-20-1-9.	PS-4 X DHFt-109-3
10.	DHFt-20-1-10.	DHFt-333 X DHFt-109-3
11.	DHFt-20-1-11.	DHFt-333 X PS-4
12.	DHFt-20-1-12.	DHFt-333 X GPUS-33
13.	DHFt-20-1-13.	DHFt-333 X Co-5
14.	DHFt-20-1-14.	DHFt-2-5 X DHFt-333
15.	DHFt-20-1-15.	PS-4 X Co-5
16.	DHFt-20-1-16.	PS-4 X DHFt-109-3
17.	DHFt-20-1-17.	DHFt-77 X DHFt-333

18.	DHFt-20-1-18.	DHFt-2-5-3 X DHFt-333
19.	DHFt-20-1-19.	DHFt-2-5-3 X DHFt-2-5
20.	DHFt-20-1-20.	DHFt-333 X DHFt-109-3
21.	DHFt-20-1-21.	DHFt-109-3 X DHFt-2-3
22.	DHFt-20-1-22.	DHFt-109-3 X DHFt-333
23.	DHFt-20-1-23.	DHFt-5-6 X GPUS-30
24.	DHFt-20-2-1.	DHFt-109-3 X DHFt-2-5
25.	DHFt-20-2-2	Co-6 X GS-1919
26.	DHFt-20-2-3	Co-5 X PS-4
27.	DHFt-20-2-4	Co-6 X GS-145
28.	DHFt-20-2-5	Co-5 X PS-4
29.	DHFt-20-2-6	Co-5 X GPUS-30
30.	DHFt-20-2-7	Co-6 X GS-1919
31.	DHFt-20-2-8	Co-5 X PS-4
32.	DHFt-20-2-9	GPUS-26 X Co-7
33.	DHFt-20-2-10	GPUS-26 X Co-7
34.	DHFt-20-2-11	GPUS-26 X Co-7
35.	DHFt-20-2-12	Co-6 X PS-4
36.	DHFt-20-9-30	Co-5 X Co-6
37.	DHFt-2-3	Co-6 X PS-4
38	DHFt-2-5	Co-5 X GS-1919
39	DHFt-109-3	National check
40	HMT-100-1	Local check

The data obtained from n evaluation of foxtail millet advanced breeding lines were subjected to the following analyses which are detailed here.

Analysis of Variance (ANOVA)

The mean values of the advanced breeding lines were subjected to analysis of variance.

Analysis of variance of RCBD

Sources of Variance	Degrees of Freedom	Sum of squares	Mean square	Computed F
Replication	r-1	RSS	RMS	RMS/EMS
Genotypes	g-1	GSS	GMS	GMS/EMS
Error	(g-1) (r-1)	ESS	EMS	
Total	rg-1	TSS		

Estimation of genetic parameters

In order to identify and ascertain the genetic variability among the advanced breeding lines and to confirm the presence of environmental influence on various characteristics of advanced breeding lines, different genetic parameters were estimated by adopting following formulae.

Estimation of variance component

Genotypic and phenotypic components of variance were calculated using following formulae

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{MSS (Genotype)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \text{MSS (Genotype)} + \text{MSS (error)}$$

Coefficient of variability

The genotypic and phenotypic coefficient of variability was computed for each character using methodology suggested by Burton and Devane (1953).

$$\text{Genotypic coefficient of variability (GCA)} = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCA)} = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic Variance.

$\sigma^2 p$ = Phenotypic Variance.

$\overline{X}$ = Grand mean of the characters.

The GCV and PCV values were classified as suggested by

0-10 %: Low, 10-20 %: Moderate, > 20 %: High

Comment [L4]: By who? Reference is missing here.

Heritability

Heritability measures the proportion of phenotypic variance due to genotype. Heritability Broad Sense was (h^2_{BS}) computed for each character as the ratio of genetic variance to total variance as suggested by (5).

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2_g}{\sigma^2_p}$$

Where, $\sigma^2 g$ and $\sigma^2 p$ are genotypic and phenotypic variance respectively.

The heritability values were classified into low, medium and high as suggested by (11)

0-30 per cent : Low,
30-60 per cent : Moderate
>60 per cent : High

Genetic Advance over mean

Genetic advance for each character was computed using formula given by (7) indicating the rate of improvement achieved by the character.

$$GA = i \times h^2 \times \sqrt{\sigma^2_p}$$

Where, i = Intensity of selection, which is equal to 2.06 when top 5% of the plants are selected, $\sigma 2$ p = Phenotypic variance and h^2 = Heritability broad sense.

Using genetic advance, genetic advance as per cent of mean was estimated to compare genetic advance across characters. It is estimated and classified according to (7).

$$\text{Genetics advance as per cent of mean} = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

The classification is detailed below.

0-10 per cent : Low,
10-20 per cent : Moderate and
-> 20 per cent : High

~~Advanced breeding lines vary significantly with respect to selected 17 characters.~~

Results and Discussion

The result of ANOVA with advanced breeding lines as a source of variation for all the characters was found statistically significant which reflected the existence of sufficient variability among the advanced breeding lines. The source of variation was found statistically significant for p~~P~~lant height (cm), flag leaf length (cm), flag leaf width (cm), panicle length (cm), panicle girth (cm), peduncle length (cm), SPAD at 50% flowering, days to maturity, days to 50% flowering, test weight (g), productive tillers/plant, specific leaf weight (g/dm^2), specific leaf area (dm^2/g), grain yield per plant (g), growing degree days (^{o}C), Grain yield per hectare (q/ha), Straw yield per hectare (q/ha).

Comment [L5]: Reframe the sentence.

Table 2: Analysis of variance for 17 quantitative characters in different foxtail millet advanced breeding lines

Source of variation	df	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Panicle length (cm)	Panicle girth (cm)	Peduncle length (cm)	SPAD at 50% flowering	Days to maturity
Replication	2	50.78	0.044	0.02	1.19	0.0077	1.58	3.96	4.41
Treatments	40	339.59**	29.36**	0.13**	29.85**	0.321**	16.00**	90.9**	5.11**
Error	78	28.07	0.17	0.01	2.65	0.003	5.46	2.43	1.54
Mean		116.144	27.61	2.23	19.00	2.13	13.0497	48.5242	84.20
CD @ 5 %		8.6125	0.6741	0.1642	2.6454	0.0863	3.7969	2.5301	2.015
CV (%)		4.5618	1.50	4.5157	8.5639	2.4865	17.8992	3.2077	1.4720

Source of variation	df	Days to 50% flowering	Test weight (g)	Productive tillers/plant	Specific leaf weight (g/dm^2)	Specific leaf area (dm^2/g)	Grain yield per plant (g)	Growing degree days (^{o}C)	Grain yield per hectare (q/ha)	Straw yield per hectare (q/ha)
Replicate	2	12.00	0.0013	0.06	0.073	3.83	8.74	173.61	4.105	12.30
Treatments	40	2.87**	0.40**	1.10**	1.48**	135.70**	50.27**	423.72**	27.36**	174.10**
Error	78	0.68	0.066	0.04	0.06	5.77	5.97	140.64	2.99	8.50
Mean		55.7333	4.8663	3.22	3.35	31.22	43.423	443.42	30.3349	37.3128
CD @ 5 %		1.3414	0.418	0.32	0.4008	3.91	3.9732	19.2773	2.8119	4.7317
CV (%)		1.4807	5.2901	6.1607	7.353	7.6955	5.629	2.6745	5.7024	7.8013

* Significant at 0.05 probability level and ** Significant at 0.01 probability level

Table 3: Mean values of foxtail millet advanced breeding lines for 17 yield and yield attributes

S. N	Advanced breeding lines	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}
1	DHFt-20-1-1	114.50	27.00	2.10	20.10	1.90	11.10	46.80	85.00	55.30	4.70	2.30	3.60	28.20	44.90	438.50	31.40	33.70
2	DHFt-20-1-2	97.20	31.50	2.40	14.50	2.20	14.40	48.20	85.00	56.70	4.70	4.10	2.90	35.20	46.70	455.10	32.70	37.60
3	DHFt-20-1-3	124.20	34.40	2.50	21.30	2.70	12.10	49.70	82.70	56.30	4.90	3.10	2.80	35.50	43.80	446.80	30.70	33.00
4	DHFt-20-1-4	123.30	30.50	2.50	19.70	2.50	13.90	50.20	82.70	55.30	4.90	3.00	3.40	29.40	39.70	438.50	27.80	32.90
5	DHFt-20-1-5.	118.40	27.30	2.10	18.40	2.00	13.80	45.20	82.30	55.70	4.70	3.00	3.70	27.40	50.20	442.70	35.10	29.60
6	DHFt-20-1-6.	119.80	25.00	2.50	20.30	2.40	12.80	51.50	83.00	55.30	4.80	3.50	3.50	28.40	41.00	434.40	28.70	33.50
7	DHFt-20-1-7.	117.90	26.80	2.20	15.90	1.70	10.30	55.00	84.70	54.70	4.70	3.60	3.00	32.90	44.60	430.20	31.20	42.40
8	DHFt-20-1-8.	113.70	28.30	2.10	18.50	2.20	6.90	43.60	86.00	57.30	5.50	4.00	3.60	27.80	43.10	463.90	30.10	43.90
9	DHFt-20-1-9.	113.00	25.70	2.30	17.10	2.10	10.20	45.90	85.30	54.00	4.70	3.10	3.80	26.70	38.60	430.30	27.00	38.30
10	DHFt-20-1-10.	130.60	25.80	2.10	19.70	2.20	12.10	47.40	82.30	57.70	4.60	4.00	3.80	26.40	39.40	468.60	27.60	31.70
11	DHFt-20-1-11.	124.40	26.50	1.80	16.60	1.60	10.30	51.30	82.00	57.70	4.80	4.00	3.20	31.60	41.80	468.60	29.30	34.10
12	DHFt-20-1-12.	112.10	26.30	2.30	15.80	1.90	16.10	53.60	83.00	56.00	5.00	3.10	3.70	27.40	41.30	446.80	28.90	32.20
13	DHFt-20-1-13.	106.50	28.20	2.10	18.50	1.80	11.70	49.30	83.70	56.00	5.30	3.40	3.80	26.20	39.10	446.80	27.40	29.90
14	DHFt-20-1-14.	91.30	25.40	2.50	19.50	2.30	9.30	51.00	85.70	56.70	5.30	3.30	2.90	34.80	41.10	455.10	28.80	39.00
15	DHFt-20-1-15.	87.30	22.80	1.90	13.00	1.90	14.50	38.60	83.70	55.70	4.50	4.00	5.70	17.70	38.40	442.70	26.80	20.50
16	DHFt-20-1-16.	111.40	28.50	2.20	15.60	2.20	16.80	45.40	84.00	56.30	4.70	2.20	2.10	48.70	41.40	450.90	29.00	28.70
17	DHFt-20-1-17.	113.20	26.40	2.30	16.10	2.10	16.30	51.30	83.30	56.00	4.60	2.30	3.00	33.20	39.80	446.80	27.90	27.40
18	DHFt-20-1-18.	111.10	23.50	2.00	16.60	2.10	15.20	50.90	84.00	56.00	5.10	3.30	4.40	22.60	42.70	446.80	29.90	31.20
19	DHFt-20-1-19.	106.40	26.50	2.10	14.60	1.40	16.50	45.90	86.00	57.00	4.70	3.60	4.10	24.50	44.10	451.50	30.80	33.00
20	DHFt-20-1-20.	115.20	28.40	2.30	17.60	2.00	11.70	63.30	86.70	54.00	4.80	3.50	3.00	33.50	37.50	422.00	26.20	46.80
21	DHFt-20-1-21.	110.90	25.40	2.50	24.80	2.60	13.70	50.00	85.00	55.70	5.40	3.70	3.50	28.80	50.40	442.60	35.30	43.90

Contd...

S. N	Advanced breeding lines	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}
22	DHFt-20-1-22.	124.50	26.40	2.30	19.70	2.20	9.20	49.80	86.00	54.00	5.20	3.10	3.70	26.90	41.10	422.00	28.70	38.20
23	DHFt-20-1-23.	132.80	34.50	2.40	22.60	2.30	14.00	46.00	87.00	56.00	5.50	3.90	3.20	31.90	40.60	446.80	28.40	43.90
24	DHFt-20-2-1.	126.00	35.00	2.50	20.70	2.20	12.50	55.60	83.30	55.00	5.20	2.80	2.80	36.50	48.70	434.40	34.10	47.40
25	DHFt-20-2-2	132.90	24.50	2.10	19.60	1.90	10.60	49.50	83.70	54.70	5.40	2.30	4.00	25.10	51.00	430.20	35.70	54.70
26	DHFt-20-2-3	111.00	28.60	2.50	24.80	2.10	12.60	48.80	84.00	54.70	4.30	3.00	3.60	27.70	46.80	430.20	32.80	41.60
27	DHFt-20-2-4	122.30	28.40	2.40	21.10	2.40	14.20	61.30	83.70	56.30	5.60	3.50	5.00	20.00	44.50	451.50	31.10	44.00
28	DHFt-20-2-5	123.30	32.40	2.40	24.00	2.60	13.60	55.20	84.70	56.30	5.10	3.70	2.80	35.40	49.00	450.90	34.30	46.90
29	DHFt-20-2-6	122.60	25.10	2.30	22.50	2.90	12.80	45.40	83.70	57.70	5.20	4.60	1.80	54.20	47.10	468.60	33.00	40.10
30	DHFt-20-2-7	124.30	26.20	2.50	21.90	2.40	12.50	47.80	86.00	56.00	4.90	2.60	2.70	37.20	46.50	446.80	32.50	50.90
31	DHFt-20-2-8	121.10	28.80	2.40	20.00	2.40	14.80	44.10	83.70	55.70	4.70	3.60	2.80	36.20	43.40	442.70	30.40	30.60
32	DHFt-20-2-9	99.20	22.60	1.80	16.60	1.80	14.50	33.30	82.30	55.70	4.50	2.40	3.40	29.50	41.30	442.70	28.90	24.70
33	DHFt-20-2-10	120.30	28.60	2.10	19.30	1.70	13.80	47.20	84.70	54.70	4.60	3.40	2.70	37.40	46.70	430.20	32.70	42.30
34	DHFt-20-2-11	126.50	31.20	2.20	20.80	2.40	16.90	51.30	84.00	55.30	4.80	3.80	2.90	35.30	45.80	438.50	32.10	41.80
35	DHFt-20-2-12	114.60	27.70	2.10	20.10	1.90	11.10	46.80	85.00	55.30	4.70	2.30	3.60	28.20	45.30	438.50	31.70	41.10
36	DHFt-20-9-30	123.50	29.50	2.10	23.70	2.20	13.90	43.80	85.70	55.70	4.70	2.30	3.60	28.80	44.80	442.70	31.30	37.80
37	DHFt 2-3	126.10	28.30	1.90	18.70	2.50	11.00	46.30	85.00	54.70	5.00	3.00	2.70	37.60	52.30	430.20	36.60	47.00
38	DHFt 2-5	99.20	22.60	2.00	13.30	1.80	12.80	38.80	83.70	55.70	3.80	2.50	2.80	35.40	37.50	442.70	22.40	29.90
39	HMT 100-1	111.30	23.70	2.20	13.70	1.60	15.90	51.60	84.00	56.30	4.90	3.10	3.40	29.20	37.00	451.50	26.80	27.80
40	DHFt-109-3	122.00	30.50	2.40	23.00	2.20	15.50	44.50	82.30	54.30	4.30	3.10	3.40	29.80	38.20	426.10	27.20	38.30

X_1= Plant height (cm)
X_2= Flag leaf length (cm)
X_3= Flag leaf width (cm)
X_4= Panicle length (cm)
X_5= Panicle girth (cm)
X_6= Peduncle length (cm)
X_7= SPAD at 50% flowering
X_8= Days to maturity
X_9= Days to 50% flowering
X_{10}=Test weight (g)
X_{11}= Productive tillers/plant
X_{12}=Specific leaf weight (g/dm^2)
X_{13}= Specific leaf area (dm^2/g)
X_{14}= Grain yield per plant (g)
X_{15}= Growing degree days (^{o}C)
X_{16}= Grain yield per hectare (q/ha)
X_{17}=Straw yield per hectare (q/ha)

Table 4: Estimation of genetic parameters in respect of 17 yield and yield attributes in foxtail millet advanced breeding lines

Character	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GAM (%)
		Minimum	Maximum				
Plant height (cm)	116.14	87.33	132.93	8.774	9.88	79	16.04
Flag leaf length (cm)	27.62	22.57	35.03	11.30	11.40	98	23.07
Flag leaf width (cm)	2.24	1.80	2.54	8.95	10.02	80	16.46
Panicle length (cm)	19.00	12.97	24.83	15.85	18.01	77	28.72
Panicle girth (cm)	2.135	1.41	2.85	15.25	15.45	97	31.00
Peduncle length (cm)	13.05	6.90	16.90	14.37	22.96	40	18.53
SPAD at 50% flowering	48.52	33.27	63.30	11.19	11.64	92	22.16
Days to maturity	84.21	82.00	87.00	1.30	1.96	44	1.76
Days to 50% flowering	55.73	54.00	57.67	1.53	2.13	52	2.28
Test weight (g)	4.87	3.80	5.63	6.89	8.69	63	11.27
Productive tillers/plant	3.23	2.20	4.63	18.44	19.40	90	35.94
Specific leaf weight (g/dm2)	3.35	1.85	5.65	20.52	21.79	87	39.79
Specific leaf area (dm2/g)	31.22	17.73	54.17	21.08	22.44	88	40.79
Grain yield per plant (g)	43.42	37.03	52.29	8.85	10.49	71	15.38
Growing degree days (°C)	443.42	422.02	468.63	2.19	3.46	40	2.86
Grain yield per hectare (q/ha)	30.33	22.43	36.60	9.39	10.99	73	16.55
Straw yield per hectare (q/ha)	37.31	20.53	54.75	19.92	21.39	87	38.20

Analysis of variance

The analysis of variance done using a total of 40 advanced breeding lines revealed that significant differences were observed all the traits studied including yield and yield components and non significant differences existed between the replications. This indicates the presence of considerable amount of variability in the material under study for yield and yield component traits. The genotypes with top performance for the traits were presented in table 5.

Variability, heritability and genetic advance

Analysis of variance may not reveal the absolute variability and this could be accessed through standardizing the phenotypic and genotypic variances by obtaining the coefficients of variability. Hence, the components of variation such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were computed. Further it is essential for selection to separate out the environmental influence from the total variability. This indicates the accuracy with which a genotype can be identified by its phenotypic performance. The estimates of heritability alone fail to indicate the response to selection. Therefore, the heritability estimates appeared to be more meaningful when accompanied by estimates of genetic advance. Hence, the genetic advances as per cent mean (GAM) was also estimated.

One of the ways in which variability is assessed through a simple approach of examining range values. Wide range of variation provides an ample scope for selection of superior and desired advanced breeding lines by the plant breeders for further improvement of these characters. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits under study.

In the present study foxtail millet advanced breeding lines exhibited moderate PCV and GCV for the most important economic traits *viz*., panicle length (15.85% and18.01 %), panicle girth(15.25% and 15.45%), productive tiller per plant (18.44% and 19.40%) and straw yield per hectare and (19.92% and 21.39 %). These results are in accordance with earlier reports where moderate GCV and PCV for characters *viz*., number of tillers, panicle length, straw yield and test weight (10), (9), (4), (8) and (13).

Table 5: Top performing genotypes for traits economically important traits:

Comment [L6]: Give the mean values also.

Panicle girth	Productive tillers per plant	Flag leaf length	Grain yield per plant	Grain yield per hectare
DHFt-20-1-21.	DHFt-20-2-6	DHFt-20-2-1.	DHFt-2-3	DHFt-20-2-2
DHFt-20-2-3	DHFt-20-1-2	DHFt-20-1-23.	DHFt-20-2-2	DHFt-20-2-7
DHFt-20-2-5	DHFt-20-1-8.	DHFt-20-1-3	DHFt-20-1-21.	DHFt-20-2-1.
DHFt-20-9-30	DHFt-20-1-10.	DHFt-20-2-5	DHFt-20-1-5.	DHFt-2-3
DHFt-109-3	DHFt-20-1-11.	DHFt-20-1-2	DHFt-20-2-5	DHFt-20-2-5
DHFt-20-1-23.	DHFt-20-1-15.	DHFt-20-2-11	DHFt-20-2-1.	DHFt-20-1-20.
DHFt-20-2-6	DHFt-20-1-23.	DHFt-20-1-4	DHFt-20-2-6	DHFt-20-2-4
DHFt-20-2-7	DHFt-20-2-11	DHFt-109-3	DHFt-20-2-3	DHFt-20-1-8.
DHFt-20-1-3	DHFt-20-1-21.	DHFt-20-9-30	DHFt-20-1-2	DHFt-20-1-21.

DHFt-20-2-4	DHFt-20-2-5	DHFt-20-2-8	DHFt-20-2-10	DHFt-20-1-23.

The high phenotypic coefficient of variation and genotypic coefficient of variation were observed for characters *viz*., specific leaf area (21.08% and 22.44%), specific leaf weight (20.52% and 26.72%), grain yield per plant (9.32% and 10.99 %), grain yield per plot (8.85 % and 10.49%), and straw yield per ha (19.92 and 21.39). Similar results were reported by (3). GCV describes inheritance of genetic variation. It also indicates the lower environmental influence on the expression of these characters and Hence, these characters can be relied upon for selection. The data showed close PCV and GCV values for almost all the traits. This shows that major portion of PCV was contributed by GCV this suggests that observed variation due to the genetic factors, provides the higher scope for improvement.

On the whole, coefficient of variation indicated moderate amount of variability for most of the traits expect days to maturity, plant height and panicle girth which had the low values The close correspondence between the estimates of GCV and PCV for most of the traits indicated the lesser environmental influence on the expression of these traits, which is also reflected by their high heritability values.

5.3.1 Heritability and Genetic advance

Heritability is a quantitative measure which provides information about the correspondence between genotypic variance and phenotypic variance, *i.e.*, the ratio of variance due to heritable differences (σ^2 g) to the total phenotypic variance (σ^2 p) and expressed as per cent. Genetic coefficient of variation alone would not indicate proportion of total heritable variation. However, the heritability estimates are better indicators of heritable portion of the variation. The broad sense heritability percentage includes the contribution of additive gene effects, allelic interactions due to dominance and non allelic due to epistasis. Genetic advance provides knowledge about expected genetic gain for particular trait after selection.

Moderate to high heritability coupled with higher magnitude of expected genetic advance for a particular trait indicates the additive gene action. On the contrary higher heritability coupled with low genetic advance is observed for any given trait, indicates the presence of non additive gene action.

In the present study, most of the traits *viz*., plant height(79 %), flag leaf length(98%), flag leaf width (80%), number of productive tillers per plant (90%), panicle length(98%), panicle girth (97 %), SPAD at *50* per cent flowering (92%), test weight (63%), specific leaf area (88%), specific leaf weight (87%), grain yield per plant(71%) and straw yield per hectare (87%) showed the high estimates of broad sense heritability (h^2 b) indicating the reliability of the estimates for variation between advanced breeding lines and effectiveness of selection. In Populations which are genetically more uniform are expected to show lower heritability than the genetically variable population. Also, much variable environmental condition reduces the magnitude of heritability and much uniform environmental condition increases it . Hence, as the study was conducted in the uniform environment, high heritability of these traits in this study may be due to highly variable and genetically diverse advanced breeding lines.

Since, heritability is also influenced by environment, the information on heritability alone may not help in identifying the characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic gain much reliable (7). Heritability provides the information on the magnitude of inheritance of quantitative traits, while genetic advance helps in formulating suitable selection procedures.

The grain yield and its components *viz*., panicle length, panicle girth, productive tillers per plant and straw weight exhibited high genetic advance as per cent of mean coupled with high estimates of h^2b indicating that, the variations are attributable to high level of heritable variation and selection would be effective for improvement of these traits. This indicates that there was low environmental influence on the expression of these characters. Since, these traits are controlled by additive gene action, they can be exploited by pure line selection and mass selection methods. The high estimates of heritability coupled with high genetic advance as per cent of mean are reported in the earlier studies in foxtail millet for number of productive tillers per plant panicle length and panicle girth (2), (13), (9).

High heritability coupled with moderate genetic advance observed for pant height, flag leaf width, peduncle length, test weight, grain yield per plant. This can be exploited by mass selection, progeny selection, hybridization and simple selection for additive gene action and heterosis breeding for non additive gene action. Similarly, (9) reported high heritability with low genetic advance for plant height whereas, test weight (9); (15), grain yield (2), (14), (12), (9), (15).

Days to maturity, days to *50* per cent flowering and growing degree days exhibited low heritability and low genetic advance. This indicates the presence of non additive gene action. Hence, breeding methods like heterosis and population breeding has to be followed to develop early advanced breeding lines.

The present investigation revealed high heritability coupled with high genetic advance as per cent of mean was observed for most of the characters. This indicates the presence of considerable genetic variation and additive gene effects for the characters. Hence, improvement of these characters could be effective through phenotypic selection**.**

Summary and Conclusion

In the present investigation an attempt was made to assess nature and magnitude of genetic variability, genetic advance and heritability for different quantitative characters for yield and yield attributes involving 40 foxtail millet advanced breeding lines, during *rabi* season of 2020-21 at Millet scheme, MARS, UAS, Dharwad. Brief summary of the results obtained are presented below.

Comment [L7]: Recheck.

The analysis of variance revealed the presence of highly significant differences in foxtail millet advanced breeding lines for all the characters under study which indicating presence of genetic variability for most of the traits. High values of PCV and GCV were obtained specific leaf area, specific leaf weight and fodder weight and moderate estimates for panicle length, panicle girth, flag leaf length, peduncle length, SPAD at 50% flowering, productive tillers per plant, grain yield per plant and grain yield per plot and low estimates for plant height, flag leaf width, days to maturity, days to 50% flowering, test weight and growing degree days. This indicates the existence of comparatively high variability for these traits, which could be exploited for improvement of the traits through simple selection methods.

Plant height, flag leaf length, flag leaf width, number of productive tillers per plant, panicle length, panicle girth, SPAD at 50% flowering, test weight, specific leaf area, specific leaf weight, grain yield per plant and straw yield per hectare exhibited higher heritability coupled with high genetic advance as per cent of mean. This indicates the scope of selection in the population, since there is a wide range of variation and additive gene action. Based on above study utilized best lines for further crop improvement programme.

Comment [L8]: I suggest to add future line of work with this breeding material.

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