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Assessment of genetic variability in finger millet (*Eleusine coracana* L. Gaertn.)

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Abstract
Finger millet, a nutri-cereal is grown for both food and fodder. Knowledge on genetic variability and heritability of yield contributing traits is important for efficient planning of crop improvement programme. In this endeavour, 18 finger millet lines were studied to assess the amount of genetic variability. Analysis of variance for 18 finger millet breeding lines revealed significant variation for all the yield contributing and yield devastating traits indicating presence of variability for selection to operate. High broad sense heritability and GAM were recorded for disease parameters while days to 50% flowering, days to maturity and grain yield recorded high heritability with moderate GAM. This clearly indicated that disease reaction is highly heritable with additive gene action which can be used as selection criterion for attaining disease resistant lines. Grain yield was observed to have moderate heritability with moderate GAM indicating preponderance of both additive and non additive gene action. This trait can be selected by selecting against finger blast, neck blast and banded blight which are highly heritable and strongly negatively associated with grain yield.

Keywords: Finger millet, variability, correlation

Introduction
Finger millet (*Eleusine coracana* L. Gaertn.) is one of the small millets valued for food, fodder and nutritional security. It is an allotetraploid with $2n = 4x = 36$ chromosomes. It is highly self-pollinated annual crop which is cultivated in arid and semi-arid regions of Central Africa and India. It belongs to the family poaceae, sub-family, chloridoideae. In India, it occupies sixth position after wheat, rice, maize, sorghum and bajra. India is the largest producer with an area, production and productivity of 1.19 million hectares, 1.98 million ton and 1661 kg per ha, respectively (Sood *et al.*, 2019) [16]. Finger millet is highly nutritious as its grains contain 65-75% Carbohydrates, 5-8% protein, 15 -20% dietary fiber and 2.5-3.5% minerals. It also contains 5-8% *eleusinin,* a quality protein, which our body can easily absorb. The beauty of the crop is that it can be grown even undulated lands with little soil formation.

Though finger millet is a hardy crop, it is also affected by many diseases like blast, banded blight, blast, brown leaf spot, foot rot and viral diseases. The major constraint in the profitable production of finger millet in all the millet growing areas of the world is blast and banded blight. The blast pathogen attacks all aerial parts of finger millet plant causing leaf, neck and finger blast and often resulting in >50% yield losses (Patro *et al.,* 2017) [14]. Hence, development of a high yielding variety with resistance to blast is the major concern in finger millet breeding.

Breeding effort in finger millet is little because of self pollination and very small size of flower which impedes hand emasculation. However, efforts are made to create variability through use of hot water emasculation and contact method of pollination. The Variability so developed can be utilised for developing high yielding varieties resistant to blast for the benefit of farmers. Hence, the present investigation was carried out to assess the genetic variability of finger millet for yield, blast and other important traits.

Material and Methods
The experimental was conducted with 8 finger millet lines including two check varieties (VR 847 and VL 352) developed by crossing high yielding varieties with blast resistant lines. All genotypes were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2018. Genotypes were planted in a randomized complete block design (RCBD) with three replications and a spacing of 30×10 cm. per each entry. Every genotype was grown in 10 lines each of 3 m length. Fertilizers, DAP (87 kg/ha), MOP (42 kg/ha) and Urea (22 kg/ha) were applied basally at the time of land preparation and remaining 22 kg/ha Urea was applied three weeks after sowing.

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Standard management practices were followed to maintain a healthy crop. Observations were recorded on five plants for plant height (cm), number of productive tillers per plant, main ear length (cm) and number of fingers per main ear, flag leaf length (cm), flag leaf width (cm), No. of leaves/main tiller, peduncle length (cm), length from the top node to leaf sheath junction (cm). Days to 50% flowering, days was recorded by visualizing the entire plot. Fodder yield and grain yield were recorded on per plot basis and then converted into per hectare. Leaf blast (Table 1) was recorded by using 0 - 5 scale and Percent Disease Index (PDI) was calculated by using the following formula:

PDI = Sum of all disease ratings / Total no. of ratings × 100

Neck blast (%) = No. of infected panicles / Total no. of panicles × 100

Finger blast (%) = No. of infected fingers / Average no. of fingers × 100

Banded blight (%) = No. of infected plants / Total No. of plants × 100

Table 1: Standard evaluation system (SES) scale for leaf blast disease.

Score	Description	Reaction
0	No lesions/symptoms on leaves	No disease/HR
1	Small brown specks of pinhead to slightly elongate, necrotic grey spots with a brown margin, less than 1% area affected	R
2	A typical blast lesion elliptical, 5-10 mm long, 1-5% of leaf area affected	MR
3	A typical blast region elliptical, 1-2 cm long, 6-25% of leaf area affected	MS
4	26-50% leaf area affected	S
5	More than 50% of leaf area affected with coalescing lesions	HS

Analysis of variance and summary statistics was calculated as per Panse and Sukathme (1967) [12]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953) [7]. Heritability in broad sense was computed as per Allard (1960) [1]. Genotypic and phenotypic correlations were calculated according to Falconer (1981) [8]. Heritability and genetic advancement were categorized into low, medium and high as per Johnson et al., (1955) [9].

Results and Discussion
The results from ANOVA (Table 2) revealed existence of ample amount of variability among different genotypes under study. Significant differences were observed for all the characters studied among 18 different genotypes. Similar variations were reported by Nandini et al (2010) [11], Anuradha et al., (2017b&c) [5, 6].
In the present study, early flowering (69 days) and maturity (97 days) were recorded in VR 1151which was almost similar to that of the early check, VL 352 which flowered in 71 and matured in 99 days (Table 3). Plant height ranged from 108cm to 126 cm where shortest height was observed in VR 1156 followed by VR 1153 (109.9 cm). No. of fingers per ear had a narrow range from 6.9 (VR 1151) to 8.5 (VR 1149) whereas ear length and finger length had grater variations ranging from 7.4 to 10.3cm and 5.3 to 8.0cm respectively. Longest fingers were detected in VR 1145 and VR 1149. Greater variation for leaf length from 25.7 cm (VL 352) to 40.0 cm (VR 1145) indicate more choice for selection. Similar variations were reported by Anuradha et al. (2017c, 2019a&b) [6, 2, 3]
An important factor for which the whole experiment was conducted, grain yield ranged from 27.4q/ha (VR 1145) to 45.5q/ha (VR 1149). Highest and lowest yields were recorded by medium duration genotypes. Though VR 1145 had some good features like longer flag leaf length and longest fingers among all genotypes the yield could not be realized instead it was the lowest grain yielder. It may be because, it was more effected by neck blast, finger blast and banded blight compared to other well performing genotypes. All the diseases might have heavily laid penalty on yield. This genotype can be further improved by crossing with blast and banded blight resistant cultivars or this genotype can be

utilized for improving other genotypes with respect to ear and flag leaf length. VR 1149 was endowed with good traits like it was the next highest for finger length and recorded least score for all diseases. Along with VR 1149, VR 1152 (44.8 q/ha), VR 1159 (42.6q/ha), VR 1147 (41.5q/ha) recorded significant increase in yield over the check, Sri Chaitanya (34.4q/ha). Among early duration group, VR 1151 though in 12th position was an extreme good yielder (36.7 q/ha) compared to early check, VL 352 (28.0 q/ha). These genotypes upon multi location testing if proves good can be released for cultivation in farmers fields. Fodder yield was higher in VR 1154 (94.6q/ha) followed by VR 1155 (93.8q/ha). Highly resistant reaction for finger blast, neck blast and banded blight was noticed in VR 1149, VR 1152, VR 1159 and VR 1147 while all genotypes had almost resistant to moderately resistant reaction.
Phenotypic coefficient of variation (PCV) values were higher than genotypic coefficient of variation values (GCV) indicating the role of environment in expression of characters (Table 4). GCV varied from low (3.2 for plant height) to high (49.9 for finger blast). Environment coefficient of variation (ECV) was more than 10% for No. of productive tillers/plant, finger width, flag leaf width, grain yield, fodder yield, leaf blast, finger blast, banded blight indicating the role of environment in attaining the phenotype for these traits. GCV and PCV helps in knowing the amount of variation while heritability and genetic advance as percent mean (GAM) provides a clue for selection of genotypes. High broad sense heritability and GAM were observed for all disease parameters like leaf blast, neck blast, finger blast and banded blight indicating ample additive gene action for these traits which can be relied upon for simple selection. Traits like days to 50% flowering, days to maturity and finger length recorded high heritability with moderate GAM while GY and other traits like Ear length (cm), finger width, flag leaf length and fodder yield recorded moderate heritability and moderate GAM indicating the role of both additive and non additive gene action. Similar results for days to 50% flowering and days to maturity by Nandini et al (2010) [11], Patil and Mane (2013) [13] in second environment, Anuradha et al., (2017a) [4], Anuradha and Patro (2019a&b) [2, 3] while Singamsetti et al., (2018) [15] recorded both as high.

Few traits which were observed to have more ECV like No. of finger per ear, peduncle length, node to leaf junction length, leaf number and flag leaf width recorded moderate heritability with low GAM indicating excess role of non additive gene action rather than additive gene action which is difficult for simple selection. The variation observed for plant height and No. of productive tillers per plant were purely due to changes in environment and will not respond for selection. Similar results were reported earlier by Lule *et al.*, (2012) [10] Patil and Mane (2013) [13] in third environment.

Since important traits like grain yield were having both additive and non additive gene action, these traits can be improved through indirect selection of associated traits which respond well to simple selection. Correlation studies (Table 5) revealed significant negative association of grain yield with all disease traits except leaf blast while fodder yield recorded significant positive association with days to 50% flowering and maturity. Neck blast, finger blast and banded blight were associated strongly in positive direction. Since all disease traits were assessed to have additive nature of gene action as observed from high heritability and high GAM, all these three traits can be easily selected against. Indirect selection of grain yield which is supposed to contain both additive and non additive gene action can be achieved by selection against all disease traits which it was negatively correlated.

Table 2: ANOVA of 18 finger millet genotypes

Source of Variations	df	Mean Squares																		
		DFF	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
Treatments	17	80.5	0.5	0.6	1.8	1.6	0.1	2.5	3.5	2.6	34.9	0.1	80.2	339.5	0.7	41.5	55.5	45.4	80.5	0.5
Replications	2	205.1	2.0	1.6	1.6	0.1	0.0	6.2	2.2	4.9	25.4	0.1	65.4	153.3	1.0	19.8	19.0	10.6	205.1	2.0
Error	34	37.7	0.3	0.3	0.6	0.3	0.0	0.9	1.3	0.6	12.1	0.0	23.9	132.5	0.1	0.7	1.4	1.9	37.7	0.3
p (Trt)		0.00	0.00	0.03	0.03	0.02	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00
P (Rep)		0.55	0.17	0.01	0.00	0.01	0.07	0.67	0.30	0.00	0.20	0.00	0.14	0.01	0.08	0.33	0.00	0.00	0.00	0.01

Note: DFF: Days to 50% flowering; DM: Days to maturity; Plant height (cm); NPT: No. of productive tillers per plant; NFE: No. of finger per ear; EL: Ear length (cm); FL: Finger length (cm); Finger width (cm); PDL: peduncle length (cm); NLJ: length from the top node to leaf sheath junction (cm); NL: No. of leaves/main tiller ; FLL: Flag leaf length (cm); FLW: Flag leaf width (cm); GY: Grain yield (q/ha); FY: Fodder yield (q/ha), LB: Leaf blast (Grade); FB: Finger blast (%), Neck blast (%) and BB: Banded blight (%)

Table 3: Performance of 18 finger millet genotypes

S. N	Entry Name	DFF	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
1	VR 1145	87.0	121.0	117.6	3.5	7.0	10.3	8.0	1.2	8.9	10.2	12.6	40.0	1.2	27.4	76.9	2.4	14.3	12.2	15.8
2	VR 1146	78.7	108.3	117.6	3.5	7.5	7.9	5.5	1.1	11.4	10.7	14.0	31.6	1.0	40.3	61.5	1.4	5.9	7.3	6.8
3	VR 1147	76.3	103.7	114.1	3.6	8.0	9.2	6.5	1.2	11.4	11.4	13.1	37.8	1.0	41.5*	73.8	1.1	4.4	4.2	7.3
4	VR 1148	92.3	120.3	122.6	3.1	7.3	8.8	6.1	1.2	10.6	10.9	13.7	35.9	1.2	31.3	68.0	1.7	12.7	12.8	13.8
5	VR 1149	84.7	111.0	125.3	2.9	8.5	9.5	7.1	1.3	11.3	11.8	14.2	34.9	1.1	45.5*	85.4	1.4	1.4	2.3	3.8
6	VR 1150	84.3	117.0	114.8	3.7	8.0	9.3	6.7	1.4	11.5	12.5	14.0	33.4	1.1	39.1	83.8	2.4	5.2	5.3	6.5
7	VR 1151	68.7	97.3	115.9	4.2	7.7	8.7	5.9	1.1	11.1	10.8	12.8	34.2	1.1	36.7*	78.9	2.1	9.4	10.3	12.0
8	VR 1152	86.0	116.3	126.2	3.9	7.1	8.1	5.3	1.2	10.1	10.1	14.9	34.4	1.2	44.8*	85.3	2.1	2.8	2.1	4.1
9	VR 1153	86.0	116.0	109.9	3.1	8.1	8.5	6.7	1.2	11.4	10.0	12.8	30.1	1.3	36.6	95.6	2.1	9.6	11.6	12.7
10	VR 1154	88.7	118.3	123.2	4.4	7.2	8.0	5.3	1.3	11.1	14.7	11.5	30.9	1.2	37.7	94.6	1.1	7.9	5.0	8.5
11	VR 1155	93.3	122.3	120.8	3.8	7.7	8.3	6.6	1.1	11.6	10.5	14.1	35.8	1.5	36.8	93.8	1.4	10.6	9.9	11.4
12	VR 1156	82.0	109.0	108.0	4.0	7.1	7.7	5.8	1.0	10.7	11.0	14.6	28.3	1.0	37.5	81.6	2.1	8.2	8.6	10.7
13	VR 1157	91.7	119.0	120.4	4.1	7.7	7.8	7.0	1.4	13.5	10.8	13.6	33.8	1.1	38.1	86.7	1.4	6.5	6.4	7.9
14	VR 1158	81.0	110.7	122.5	3.9	7.6	7.4	5.6	1.2	11.2	10.8	12.6	30.9	1.1	37.7	84.2	1.1	8.2	8.2	9.1
15	VR 1159	83.0	111.7	120.4	4.0	6.9	8.6	5.6	0.8	11.8	11.1	12.9	33.4	0.9	42.6*	88.0	1.7	3.6	3.3	4.4
16	GPU 45 (C)	78.3	110.0	112.8	3.5	7.0	8.4	6.5	1.1	11.7	12.0	12.5	32.0	1.1	30.2	71.6	2.1	11.8	13.4	14.3
17	VL 352 (C)	71.3	99.0	113.7	3.5	7.5	7.4	5.6	0.8	10.2	11.4	12.9	25.7	1.1	28.0	58.3	1.7	13.6	15.0	15.1
18	VR 847(C)	87.7	117.0	115.0	3.1	7.3	7.6	5.9	1.1	11.2	10.9	14.8	35.6	1.1	34.4	80.7	2.7	8.5	15.3	13.2
	Mean	83.4	112.7	117.8	3.7	7.5	8.4	6.2	1.2	11.2	11.2	13.4	33.3	1.1	37.0	80.5	1.8	8.0	8.5	9.9
	CD (5%)	2.0	2.3	10.2	0.8	0.8	1.2	0.9	0.2	1.6	1.9	1.4	5.8	0.3	8.1	19.1	0.5	1.3	2.0	2.3
	CD (1%)	2.7	3.1	13.7	1.1	1.1	1.7	1.2	0.3	2.1	2.6	1.9	7.8	0.3	10.9	25.6	0.6	1.8	2.6	3.1
	CV (%)	1.5	1.2	5.2	13.8	6.8	8.8	8.8	12.6	8.5	10.3	6.2	10.5	13.3	13.2	14.3	15.7	10.0	13.8	13.9

Table 4: Genetic parameters of 18 finger millet lines

S. N		DFF	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
1	**Mean**	**83.4**	**112.7**	**117.8**	**3.7**	**7.5**	**8.4**	**6.2**	**11.2**	**11.2**	**13.4**	**1.2**	**33.3**	**1.1**	**37.0**	**80.5**	**1.8**	**8.0**	**8.3**	**9.9**
2	Minimum	68.7	97.3	108.0	2.9	6.9	7.4	5.3	8.9	10.0	11.5	0.8	25.7	0.9	27.4	58.3	1.1	1.4	2.1	3.8
3	Maximum	93.3	122.3	126.2	4.4	8.5	10.3	8.0	13.5	14.7	14.9	1.4	40.0	1.5	45.5	95.6	2.7	14.3	15.0	15.8
4	GCV	8.1	6.4	3.2	8.5	4.5	7.7	10.8	12.6	6.6	7.7	5.9	8.3	8.7	11.7	10.3	26.4	45.9	50.0	38.6
5	PCV	8.3	6.6	6.1	16.2	8.2	11.7	13.9	17.9	10.7	12.8	8.5	13.4	15.9	17.7	17.6	30.7	47.0	51.8	41.1
6	ECV	1.5	1.2	5.2	13.8	6.8	8.8	8.8	12.6	8.5	10.3	6.2	10.5	13.3	13.2	14.3	15.7	10.0	13.8	13.9
7	H² (Bs)	96.9	96.5	27.5	27.4	31.0	43.6	60.1	50.1	37.4	35.8	47.5	38.4	29.8	44.0	34.3	73.9	95.5	92.9	88.5
8	GA	13.8	14.7	4.1	0.3	0.4	0.9	1.1	0.2	0.9	1.1	1.1	3.5	0.1	5.9	10.0	0.8	7.4	8.4	7.4
9	GAM	16.5	13.0	3.5	9.2	5.2	10.5	17.2	18.4	8.3	9.5	8.4	10.6	9.8	16.0	12.4	46.8	92.4	99.2	74.9

Note: GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; ECV: Environmental coefficient of variation; H² (Bs): Broad sense Heritability; GA: Genetic Advance and GAM: Genetic Advance per cent Mean

Table 5: Phenotypic correlation among yield and other related traits among 18 finger millet genotypes

Trait	DFF	DM	PH	NPT	NFE	EL	FL	PDL	NJL	LN	FW	FLL	FLW	GY	FY	LB	NB	FB
DM	0.96**																	
PH	0.42	0.36																
NPT	-0.12	-0.11	0.12															
NFE	-0.07	-0.15	0.01	-0.36														
EL	0.09	0.19	0.08	-0.29	0.23													
FL	0.29	0.35	-0.12	-0.38	0.35	0.72**												
PDL	0.15	0.04	0.01	0.19	0.34	-0.30	-0.01											
NLJ	-0.01	-0.01	0.12	0.30	0.01	-0.02	-0.21	0.15										
LN	0.26	0.17	0.04	-0.31	0.12	-0.11	-0.03	0.03	-0.43									
FW	0.46	0.49*	0.31	-0.03	0.46	0.32	0.43	0.25	0.23	0.04								
FLL	0.37	0.41	0.35	-0.19	0.04	0.70**	0.55*	-0.12	-0.22	0.15	0.39							
FLW	0.52*	0.55*	0.20	-0.11	0.17	0.07	0.27	-0.14	-0.14	0.00	0.28	0.18						
GY	0.07	-0.03	0.39	0.18	0.38	0.01	-0.24	0.38	0.05	0.36	0.24	0.08	-0.24					
FY	0.53*	0.51*	0.23	0.30	0.17	0.06	0.13	0.30	0.12	-0.05	0.37	0.13	0.40	0.44				
LB	-0.02	0.12	-0.44	-0.26	-0.27	0.20	0.21	-0.35	-0.29	0.33	-0.10	0.12	0.02	-0.34	-0.05			
NB	-0.03	0.06	-0.36	-0.12	-0.35	-0.04	0.19	-0.39	-0.13	-0.37	-0.25	-0.10	0.40	-0.96**	-0.34	0.26		
FB	-0.14	-0.07	-0.50*	-0.32	-0.23	-0.16	0.14	-0.28	-0.24	-0.20	-0.33	-0.19	0.29	-0.92**	-0.43	0.38	0.93**	
BB	-0.08	-0.01	-0.49*	-0.24	-0.27	-0.04	0.24	-0.37	-0.18	-0.28	-0.25	-0.06	0.35	-0.95**	-0.33	0.39	0.96**	0.97**

Note: DFF: Days to 50% flowering; DM: Days to maturity; Plant height (cm); NPT: No. of productive tillers per plant; NFE: No. of finger per ear; EL: Ear length (cm); FL: Finger length (cm); Finger width (cm); PDL: peduncle length (cm); NLJ: length from the top node to leaf sheath junction (cm); NL: No. of leaves/main tiller ; FLL: Flag leaf length (cm); FLW: Flag leaf width (cm); GY: Grain yield (q/ha); FY: Fodder yield (q/ha), LB: Leaf blast (Grade); FB: Finger blast (%), Neck blast (%) and BB: Banded blight (%)

Conclusion: Significant variation were observed for all 19 traits studied among 18 finger millet genotypes GCV and PCV were low to h for high traits studied indicating low to high variability in the present population. Few traits like No. of productive tillers per plant and plant height (cm) were more influenced by the environment rather by the genotype itself. Grain yield is controlled by both additive and non additive gene action, hence direct selection may not be effective. As this trait is highly associated with NB, FB and BB controlled by additive gene action, selection of grain yield by indirectly selecting against diseases is desirable.

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