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Heritability and trait association in finger millet *[Eleusine coracana (L.)*

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Abstract

Finger millet, is a drought hardy cereal grown for both food and fodder in dry regions of Africa and Asia. Understanding the amount and nature of genetic variation is imperative for any crop improvement. Hence, the present study was aimed to assess the heritability and association of different traits in finger millet. The results revealed significant differences among the genotypes studied for all traits except number of productive tillers per plant which was more influenced by the environment. It is a known fact that grain yield is governed by many genes with small effects and selection for grain yield per se is difficult though it is of additive in nature. The same applies for the grain yield in this study which recorded high heritability along with high GAM. Hence, indirect selection *via* easily heritable traits like finger blast, neck blast and banded blight which are likely to be governed by one or two genes will help in solving the issue. Selection of high yielding and disease resistant genotypes like VR 1112 and VR 1118 offer better possibility to be released as a variety for cultivation in farmers fields.

Keywords: Finger millet, variability

Introduction

Small millets are small grained cereals which are components of traditional food basket. Finger millet (*Eleusine coracana* L. Gaertn.) is one among them, which is an annual herb belonging to the family poaceae, sub-family, chloridoideae. It is cultivated in more than 25 countries of Asian African sub-continent for human consumption. The grain is highly nutritious and contains 65-75% carbohydrates, 5-8% protein, 15-20% dietary fibre (Chetan and Malleshi, 2007) [6]. It is a hardy crop for both abiotic and biotic stresses and hence can be grown in wide range of soils and climate. It is highly nutritive and is a rich source of Calcium, minerals, essential amino acids and fiber and is low in fat content. Unsaturated fat is the main component of finger millet fat. It does not contain gluten and hence is a good alternative for gluten sensitive people.

In recent years, finger millet is also affected by few diseases out which blast and banded blight are likely cause severe damage (Patro *et al.*, 2017) [14]. Though the ultimate aim of a breeder is to develop a high yielding variety, the sustainability of a variety for longer time in farmer's fields depends on its disease resistance to major diseases. Development of a high yielding variety with resistance to major diseases is very important in breeding for new varieties of finger millet. Hence, the present study was taken up to estimate the heritability and association of grain yield with other traits.

Material and Methods

The experimental was conducted with nine finger millet lines including two check varieties (VR 847 and Vakula) 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. 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 (Table1) was recorded by using 0 - 5 scale and Percent Disease Index (PDI) was calculated by using the following formula:

$PDI = \text{Sum of all disease ratings} / \text{Total no. of ratings} \times 100$

$\text{Neck blast (\%)} = \text{No. of infected panicles} / \text{Total no. of panicles} \times 100$

$\text{Finger blast (\%)} = \text{No. of infected fingers} / \text{Average no. of fingers} \times 100$

$\text{Banded blight (\%)} = \text{No. of infected plants} / \text{Total No. of plants} \times 100$

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

Table 2: Standard Evaluation System (SES) scale for sheath blight disease

Score	Description	Reaction
0	No incidence	No disease/HR
1	Vertical spread of the lesions up to 20% of plant height	HR
2	Vertical spread of the lesions up to 21-30% of plant height	R
3	Vertical spread of the lesions up to 31-45% of plant height	MR/MS
4	Vertical spread of the lesions up to 46-65% of plant height	S
5	Vertical spread of the lesions up to 66-100% of plant height	HS

Analysis of variance and summary statistics was calculated as per Panse and Sukathme (1967) [13]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953) [5]. Heritability in broad sense was computed as per Allard (1960) [11]. 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

Analysis of Variance components (Table 3) revealed significant differences for all the traits studied except for No. of productive tillers/plant indicating presence of adequate amount of variability among different genotypes for all those traits.

In the present study, VR 1112 (41.6 q/ha) and VR 1118 (41.1 q/ha) had significantly out yielded the local check, Sri Chaitanya (32.5 q/ha) for grain yield among medium duration group while among early duration group, VR 1115 (39.2 q/ha) and VR 1117 (35.5 q/ha) recorded significant higher grain yields compared to early check, Vakula (24.3 q/ha) (Table 4). GPU 45 was the earliest with 99 days to maturity followed by VR 1117 with 100 days to maturity. These two genotypes can be utilized for breeding earliness in finger millet. Vakula can be used for breeding non-lodging genotypes since it was observed to be the shortest (100.6 cm) among all nine genotypes studied. Longer ears were noticed in Vakula (10.5cm) followed by VR 1112 (10.0cm). Long ear length is indicative of getting higher grain yield. It was proved for VR 1112 while it was not realized in Vakula. It may be because of its shorter duration and higher incidence of neck blast, finger blast and banded blight diseases compared to other genotypes. No. of leaves/main tiller were more in VR 1110 (15) while longest leaf (42.7 cm) was observed in VR 1120 indicating more photosynthetic ability of these genotypes. Less leaf blast score was recorded in VR 1117, VR 1120 and Vakula with 1.4 grade. VR 1112 (2.7%) and VR 1110 (3.1%) had very less neck blast incidence while VR 1112 (4.5%) followed by VR 1118(6.5%) recoded less finger blast incidence. Incidence of banded blight was very low in VR 1110 (5%) followed by VR

1118 (5.9%). All genotypes were resistant all the diseases studied, however VR 1112, VR 1118, VR 1110 were highly resistant genotypes.

Narrow range of variations PCV and GCV were observed for days to 50% flowering, days to maturity, plant height, leaf width, neck blast and finger blast indicating less variation among genotypes for these traits (Table 5). It may be because the material used for the study were advanced breeding lines which even passed the preliminary station trial. However, high variations were noticed in No. of productive tillers/plant, finger length, finger width while moderate variations were recorded for No. of finger/ear, ear length, peduncle length, grain yield, fodder yield, leaf blast and banded blight. These results are in consonance with earlier studies of Bezawetaw *et al.* (2006) [4] and Lule *et al.* (2012) [11]. Presence of variability implies possibility of selections. For reliable selection on has to depend on heritability studies. Highly heritable traits are governed by genotypic variances rather than with environmental variance. Hence, there is more chance for success in selection of genotypes based on heritability. However, heritability informs whether the variation is genetic or non genetic while Genetic Advance as Percent Mean (GAM) enlightens the aspect of gene action. Hence heritability along with GAM studies are meaningful. In the present investigation, low heritability with low GAM were observed for No. of productive tillers/plant, ear length and length from node to leaf sheath junction indicating the main role of environment in determining the phenotype. These traits cannot be improved upon selection in the present population.

High heritability and high GAM were recorded for days to 50% flowering, grain yield and all disease parameters. Similar results were reported by Shinde *et al.* (2014) [15], Jyothsna *et al.* (2016) [10], Mahanthesha (2017) [12] and Devaliya *et al.* (2018) [7]. Though these traits recorded narrow to medium variation, whatever variation is existing could be efficiently selected since high heritability and high GAM indicates preponderance of additive gene action and additive gene action is very much selection responsive. In this study grain yield can be selected as such because of presence of additive gene action but since grain yield is controlled by many genes

with small effects, it is better to find associated traits with additive gene action but governed by less number of genes. Days to 50% flowering and days to maturity were highly associated in positive direction while fodder yield was observed to be significantly and positively associated with peduncle length and grain yield (Table 6). The results were similar with the earlier reports of Wolie *et al.* (2011) [16] and Anuradha *et al.* (2017a&b) [1, 2]. Though, fodder yield and peduncle recorded moderate heritability with moderate GAM indicating both additive and non-additive gene action, to some extent it can be indirectly selected through peduncle length as the latter is governed by few genes while the former is governed by many genes. The highly desired trait, grain yield

was positively and significantly associated with No. of productive tillers per plant and fodder yield among agronomic traits. In this study, grain yield cannot be selected indirectly via No. of productive tillers as it is supposed to possess only environmental variation. It cannot even be selected through fodder yield since both of them are governed by many genes and moreover grain yield was predicted to be of additive gene action while fodder yield to be of non additive and additive gene action. The only option left for indirect selection is through disease incidence for which it is significantly negatively correlated. Disease resistance is mostly governed by one or two genes and moreover the preponderance of additive gene action will hasten up the selection process.

Table 3: ANOVA of nine finger millet genotypes

Source of Variations	df	Mean Squares																		
		DFE	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
Treatments	8	230.6	235.5	194.3	0.4	0.6	0.9	0.9	0.1	3.1	1.7	5.2	29.2	0.1	107.0	247.9	0.6	28.5	37.3	34.7
Replications	2	3.1	2.4	28.1	0.4	0.1	1.5	2.0	0.0	0.5	0.6	0.8	52.7	0.1	2.5	52.5	0.7	9.2	1.7	32.3
Error	16	1.5	2.6	29.4	0.2	0.2	0.5	0.4	0.0	1.0	1.1	1.5	6.2	0.0	16.7	81.0	0.1	0.2	2.2	1.0
p (Trt)		0.00	0.00	0.00	0.16	0.02	0.15	0.06	0.05	0.02	0.21	0.02	0.00	0.01	0.00	0.03	0.00	0.00	0.00	0.00
p (Rep)		0.16	0.42	0.41	0.19	0.66	0.06	0.02	0.53	0.64	0.60	0.62	0.00	0.02	0.86	0.54	0.01	0.00	0.48	0.00

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); NJL: 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 4: Performance of nine finger millet genotypes

S. No.	Entry	DFE	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
1	VR 1110	85.3	117.3	115.9	3.4	7.9	9.3	6.6	1.2	11.2	12.2	15.2	34.4	1.2	39.1	67.1	2.1	3.1	6.9	5.0
2	VR 1112	93.0	120.0	124.6	3.3	7.8	10.0	6.5	1.6	12.4	12.9	13.6	35.8	1.2	41.6*	81.1	1.7	2.7	4.5	6.4
3	VR 1115	74.3	101.0	114.6	2.6	8.1	9.7	6.8	1.2	12.5	10.9	14.4	35.5	1.1	31.8*	68.4	1.7	5.5	11.4	9.0
4	VR 1117	72.0	100.3	125.0	3.1	8.6	9.6	6.8	1.3	12.9	11.3	14.8	33.4	1.3	35.1*	69.5	1.4	4.6	10.5	7.5
5	VR 1118	81.0	111.0	122.5	3.1	7.5	9.6	6.9	1.2	13.3	11.8	13.8	39.6	1.6	41.1*	89.9	2.7	3.8	6.5	5.9
6	VR 1120	91.0	119.0	125.1	2.9	7.2	9.9	7.3	1.5	12.5	11.4	13.3	42.7	1.2	27.6	69.1	1.4	6.6	12.7	10.4
7	Vakula	74.0	103.7	100.6	2.5	8.0	10.5	7.2	1.2	10.7	11.7	11.3	39.7	1.3	24.6	59.1	1.4	11.4	15.0	14.3
8	GPU 45	70.3	99.3	118.6	2.5	7.7	9.0	6.0	1.0	10.8	12.6	11.7	37.0	1.1	29.2	67.2	1.7	8.6	13.1	12.2
9	VR 847	89.0	118.0	124.7	2.4	7.3	8.7	5.6	1.3	10.9	10.7	13.5	34.2	1.0	31.7	66.5	2.1	9.7	11.9	13.3
	Mean	81.1	110.0	119.1	2.9	7.8	9.6	6.7	1.3	11.9	11.7	13.5	36.9	1.2	33.5	70.9	1.8	6.2	10.3	9.3
	CD (1%)	2.9	3.9	12.9	1.1	1.0	1.6	1.5	0.4	1.7	1.8	2.1	5.9	0.3	9.8	21.5	0.7	0.9	3.6	2.4
	CD (5%)	2.1	2.8	9.4	0.8	0.7	1.2	1.1	0.3	2.4	2.5	2.9	4.3	0.2	7.1	15.6	0.5	0.7	2.6	1.7
	CV (%)	1.5	1.5	4.6	16.4	5.3	7.1	9.2	14.2	8.3	8.8	9.1	6.7	9.8	12.2	12.7	17.4	6.2	14.5	10.8

Table 5: Genetic parameters of nine finger millet lines

S. No	Parameter	DFE	DM	PH	NPT	NFE	EL	FL	FW	PDL	NJL	LN	FLL	FLW	GY	FY	LB	NB	FB	BB
1	Mean	81.1	110.0	119.1	2.9	7.8	9.6	6.7	1.3	11.9	11.7	13.5	36.9	1.2	33.5	70.9	1.8	6.2	10.3	9.3
2	Minimum	70.3	99.3	100.6	2.4	7.2	8.7	5.6	1.0	10.7	10.7	11.3	33.4	1.0	24.6	59.1	1.4	2.7	4.5	70.3
3	Maximum	93.0	120.0	125.1	3.4	8.6	10.5	7.3	1.6	13.3	12.9	15.2	42.7	1.6	39.1	89.9	2.7	11.4	15.0	93.0
4	GCV	10.8	8.0	6.2	8.3	4.7	3.7	6.3	10.3	7.1	3.8	8.2	7.5	10.5	16.4	10.5	22.0	49.4	33.4	35.6
5	PCV	10.9	8.2	7.7	18.4	7.0	8.1	11.1	17.5	10.9	9.6	12.3	10.1	14.4	20.4	16.5	28.1	49.8	36.4	37.2
6	ECV	1.5	1.5	4.6	16.4	5.3	7.1	9.2	14.3	8.3	8.8	9.1	6.7	9.8	12.2	12.7	17.4	6.2	14.5	10.8
7	H ² (B)	98.1	96.7	65.1	20.5	43.7	21.4	32.2	34.4	42.0	15.8	44.7	55.5	53.3	64.3	40.7	61.6	98.5	84.1	91.7
8	Genetic Advance	17.8	17.9	12.3	0.2	0.5	0.3	0.5	0.2	1.1	0.4	1.5	4.3	0.2	9.1	9.8	0.6	6.3	6.5	6.6
9	GAM	22.0	16.2	10.4	7.8	0.3	3.6	7.4	12.4	9.4	3.1	11.3	11.5	15.8	27.1	13.8	35.6	98.0	63.1	70.2

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); NJL: 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 6: Phenotypic correlation among yield and other related traits among nine finger millet genotypes

Trait	DFE	DM	PH	NPT	NFE	EL	FL	PDL	NJL	LN	FW	FLL	FLW	GY	FY	LB	NB	FB
DM	0.9*																	
PH	0.5	0.4																
NPT	0.4	0.4	0.4															
NFE	-0.6	-0.6	-0.3	0.2														
EL	0.0	-0.1	-0.5	0.2	0.3													
FL	-0.1	-0.1	-0.3	0.3	0.2	0.8*												

PDL	0.8*	0.7*	0.5	0.4	-0.2	0.4	0.2											
NLJ	0.1	0.0	0.5	0.5	0.1	0.3	0.5	0.4										
LN	0.1	0.1	0.0	0.5	0.0	0.2	0.0	0.1	-0.1									
FW	0.3	0.3	0.5	0.6	0.3	-0.2	0.0	0.2	0.5	-0.2								
FLL	0.1	0.1	-0.2	-0.1	-0.5	0.5	0.6	0.1	0.1	0.1	-0.5							
FLW	-0.1	-0.1	0.0	0.5	0.1	0.4	0.6	0.0	0.6	0.2	0.1	0.4						
GY	0.4	0.4	0.5	0.8*	0.1	-0.2	-0.1	0.3	0.5	0.4	0.7	-0.4	0.4					
FY	0.3	0.3	0.5	0.5	-0.2	0.0	0.1	0.3	0.7*	0.3	0.3	0.1	0.6	0.8*				
LB	0.2	0.3	0.2	0.2	-0.4	-0.4	-0.3	-0.2	0.2	0.0	0.3	-0.1	0.4	0.6	0.6			
NB	-0.3	-0.3	-0.5	-0.9**	-0.2	0.0	-0.2	-0.4	-0.7*	-0.3	-0.8*	0.3	-0.3	-0.9**	-0.7*	-0.3		
FB	-0.5	-0.5	-0.5	-0.8**	0.0	0.0	0.1	-0.4	-0.5	-0.5	-0.6	0.3	-0.4	-0.9**	-0.8*	-0.5	0.9**	
BB	-0.2	-0.3	-0.4	-0.9**	-0.2	0.0	-0.2	-0.3	-0.6	-0.3	-0.8*	0.3	-0.5	-0.9**	-0.7	-0.4	0.9**	0.9**

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

This study helped in understanding the nature of variability existing for grain yield and other traits including disease parameters. The present study showed that grain yield and fodder yield can be improved indirectly through selection against diseases among genotypes. Resistant genotypes with good yield like VR 1112 and VR 1118 can be selected and relied upon because grain yield and disease parameters were negatively and significantly correlated, moreover all of them were highly heritable indicating additive gene action.

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