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# Genetic variability studies in finger millet under terminal moisture stress

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## Abstract

Finger millet is an important staple food crop of Karnataka. Terminal Drought is one of the major constrain under current climate change scenario which affects productivity of Ragi. Evaluation of genotypes based on variability parameters enables to identify drought tolerant lines. Maximum phenotypic and genotypic coefficient variation was found in number of productive tillers, finger length, number of roots under terminal moisture stress environment and dry matter, seed yield per plant in both moisture stress free and terminal moisture stress environments. Whereas, the character like plant height, 1000 seed weight, exhibited minimum phenotypic and genotypic coefficient of variation in both environments. The use of heritability values coupled with genetic advance would be more reliable than heritability alone.

Keywords: Moisture stress free condition (MSF), terminal moisture stress (TMS)

# Introduction

Finger millet belongs to family *Poaceae*, subfamily *Chloridoideae* and genus *Eleusine*. It originated in East Africa and came to India around 2000 BC. It is widely grown in arid and semiarid areas of Africa and Asia. In India, it ranks sixth in production after wheat, rice, maize, sorghum and bajra. It occupies an area of 1.016 million hectares, with a production of 13.85 million tons and productivity of about 1363 kg per hectare. The major finger millet growing states are Karnataka, Maharastra, Uttarakhand, Tamil Nadu, Simandra, Orissa, Jharkhand, Chhattisgarh. It is mainly grown and consumed in Karnataka, Andhra Pradesh, Tamil Nadu, Odisha, Maharashtra, Uttarakhand and Goa. In Karnataka, it is popularly known as "Ragi" grown in an area of 0.598 million hectares with a Production of 0.86 million tones. Finger millet is considered one of the most nutritious cereals which contains about 65–75% carbohydrates, 5–8% protein, 15–20% dietary fiber and 2.5–3.5% minerals, 1–2% ether extractives. Of all the cereals and millets, finger millet has the highest amount of calcium (344 mg) and potassium (408 mg). (Devi *et al*, 2014) <sup>[5]</sup>.

The shifts in rainfall pattern driven by climate change, the crop frequently under drought stress (DS) at flowering and grain filling stages. If plant experiences water stress at the terminal stage (mostly critical phases like grain filling) of life cycle then it is called "Terminal moisture stress (TMS)". Either due to limited water supply to the roots. This condition often coincides under arid and semiarid climates and cause severe threat for productivity by limiting the rate and duration of grain filling growth. The present study was undertaken during *Rabi 2018* at Agricultural Research Station, Hagari, Ballari, Karnataka to know genetic variability and to identify superior genotypes for yield and its components under Terminal Moisture Stress (TMS) among finger millet accessions.

# Materials and Method

The experimental material consists of sixty six genotypes of Ragi along with four checks *i.e.* GPU 28, GPU67, GPU 45, ML365 provided by All India Co-ordinated Small Millets Improvement Project, GKVK, Bengaluru. Two experiments were under taken in the augmented design, the Finger millet genotypes were raised in Moisture Stress Free (MSF) & Terminal Moisture Stress (TMS) environmental conditions. Each genotype was grown in 2 m long single row plot. Observations were recorded for nine quantitative characters *viz.*, days to fifty per cent flowering, plant height (cm), number of fingers, finger length, number of roots, root length, dry matter, 1000 seed weight and seed yield on five competitive plants selected at random for each genotypes. The mean values on these observations were subjected for

statistical analysis to compute analysis of variance, PCV and GCV (Burton and De Vane, 1953: Federer, 1977)<sup>[4, 6]</sup>, Heritability (Robinson (1949)<sup>[24]</sup> in broad sense for all the characters (Lush, 1949)<sup>[21]</sup> and genetic advance for each character (Johnson *et al.*, 1995)<sup>[14]</sup>.

# **Results and Discussion**

Analysis of Variance revealed that presence of significant amount of variation in blocks, entries, germplasm accessions and accession versus check varieties under both MSF and TMS environments, except for number of productive tillers for the checks. Since all the traits exhibited highly significant difference among treatments which is prerequisite for further statistical analysis was carried (Table 1).

The salient features of mean values (Table 2) for each character are described in ensuing paragraphs. Under moisture stress free condition (MSF) the days to fifty percent flowering ranged from 45 to 89 days, with mean of 68.16 under moisture stress free environment. The estimates phenotypic and genotypic coefficients of variability were 13.56 and 10.74 per cent respectively, which indicates the moderate PCV and GCV.These findings were concurring with the results of Kadam *et al.* (2009) <sup>[16]</sup>. Whereas under terminal moisture stress environment the days to fifty per cent flowering ranged from 43 to 88 days with mean value of 63.08. The observed phenotypic and genotypic coefficients of variability were 14.31 and 13.740 per cent, respectively. Observations are in line with findings of Reddy *et al.* (2013) <sup>[23]</sup> and Singamsetti *et al.* (2018) <sup>[26]</sup>.

Under moisture stress free condition (MSF) the plant height ranged from 55.2 to 88.6 with mean of 71.88 under moisture stress free environment. The observed phenotypic and genotypic coefficients of variability were 9.42 and 9.34 per cent respectively. Whereas Plant height ranged from 49.38 to 80.6 with mean of 65.27 under terminal moisture stress environment. The recorded phenotypic and genotypic coefficients of variability were 7.71 and 6.79 per cent, respectively. Similar results are in line with findings of by Keerthana *et al.* (2019) <sup>[18]</sup>.

Under moisture stress free condition (MSF) the number of productive tillers under moisture free stress environment ranged from 1 to 2 with mean 1.7. The observed phenotypic and genotypic coefficients of variability were 27.55 and 25.69 per cent, respectively. Whereas Under moisture stress, the number of productive tillers ranged from 1 to 2 with mean of 1.79, and phenotypic and genotypic coefficients of variability were 23.19 and 16.18 per cent, respectively. The results are in line with John (2006) <sup>[13]</sup>.

Under moisture stress free condition (MSF) the number of fingers ranged from 4 to 13 with mean of 7.85. The observed phenotypic and genotypic coefficients of variability were 18.37 and 15.19 per cent, respectively. Whereas under terminal stress the number of fingers ranged from 4 to 9 with mean value 6.73. The phenotypic and genotypic coefficients of variability were 14.44 and 10.92 per cent, respectively The PCV and GCV values are moderate. The results were in accordance with the findings of Gowda *et al.* (2008) <sup>[9]</sup>.

Under moisture stress free condition (MSF) the finger length ranged from 4.8 to 14.6 with mean of 8.75. The phenotypic and genotypic coefficients of variability were 22.68 and 22.05 per cent, respectively. However, under moisture stress Finger length ranged from 5 to 12.8 with mean of 8.49. The phenotypic and genotypic coefficients of variability were 15.26 and 14.61 per cent, respectively. The less difference between the values of GCV and PCV revealed that environmental influence on the phenotypic expression of this character. The selection for improvement of such character may be useful. These results are in conformity with the findings by Keerthana *et al.* (2019) <sup>[18]</sup>.

Under moisture stress free condition (MSF) the root number ranged from 8 to 35 with mean of 19.67. The phenotypic and genotypic coefficients of variability were 27.03 and 26.36 per cent. Under terminal moisture stress (TMS) the root number ranged from 10 to 28 with mean of 17.95. The phenotypic and genotypic coefficients of variability were 20.373 and 17.06 per cent respectively. The least difference of GCV and PCV indicates that this trait had less influence of environmental factors. The selection for improvement of such character may be useful respectively. The result was proclaimed by Salini *et al.* (2010) <sup>[25]</sup>.

In moisture stress free condition (MSF) the root length ranged from 12.34 to 28.25 with mean of 19.82. The phenotypic and genotypic coefficients of variability were 16.64 and 15.25 per cent respectively. In terminal moisture stress the root length ranged from 13.6 to 38, with mean of 23.01.The phenotypic and genotypic coefficients of variability were 14.65 and 14.52 per cent, respectively Narrow difference of GCV and PCV indicates that this trait had less influence of environmental factors. The selection for improvement of such character may be useful. These results are in conformity with the findings Anantharaju and Meenakshiganesan (2006) <sup>[2]</sup>.

Moisture stress free condition (MSF) the dry matter ranged from 20 to 65g with mean of 37.62g. The moderate phenotypic and genotypic coefficients of variability were 25.28 and 23.42 per cent, respectively. However, under terminal moisture stress (TMS) the dry matter ranged from 10 to 55g with mean 30.38g. The phenotypic and genotypic coefficients of variability were 30.04 and 27.34 per cent, respectively. Dry matter ranged from 10 to 55 g with mean 30.38g. The phenotypic and genotypic coefficients of variability were 30.04 and 27.34 per cent, respectively. Conforming results were earlier proclaimed by Keerthana *et al.* (2019) <sup>[18]</sup>.

Under moisture stress free condition (MSF) the 1000 seed weight, the range is from 1.7 to 2.6g with mean value 2.00g. The phenotypic and genotypic coefficients of variability were 5.17 and 5.11 per cent, respectively. Whereas Under terminal moisture stress (TMS) 1000 seed weight the range from 1.7 to 2.3g with mean of 1.91g. The phenotypic and genotypic coefficients of variability were 4.17 and 4.11 per cent, respectively. Lower values of PCV and GCV indicating presence of non additive genes, similar observations were also made by Krishnappa *et al.* (2009) <sup>[19]</sup>.

Under moisture stress free condition (MSF) the Seed yield per plant ranged from 1 to 15.2 g/plant with mean 7.08 g/plant. The phenotypic and genotypic coefficients of variability were 53.31 and 49.61 per cent, respectively. Under terminal moisture stress (TMS), the seed yield ranged from 0.34 to 11.98 g/plant with mean of 2.26 g/plant. The phenotypic and genotypic coefficients of variability were 85.63 and 77.88 per cent, respectively. High magnitude of PCV and GCV shows that there is a higher variability of that trait. The results are in line with Rao *et al.* (2013) <sup>[22]</sup>.

Under moisture stress free condition (MSF) the Days to fifty per cent, heritability estimates of 62.71 per cent with an moderate gentic advance mean 17.52 were observed for this trait indicating the operation of both additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effect rather than simple selection. Conforming results were earlier proclaimed by Gowda *et al.* (2008) <sup>[9]</sup>. Whereas High heritability estimates of 92 per cent with an expected genetic advance of mean 27.17 were observed for this trait under terminal moisture stress (TMS). For this trait direct phenotypic selection may be effective due to preponderance of additive gene action. Similar results were in line with Krishnappa (2009) <sup>[19]</sup> and Keerthana *et al.* (2019) <sup>[18]</sup>.

Under moisture stress free condition (MSF) the Plant height high heritability of 98.7 percent with a genetic advance mean 19.06 was observed. In same way High heritability coupled with high genetic advance over mean indicating that trait is under the control of additive gene effects. Direct phenotypic selection may be effective due to preponderance of additive gene action. Same results are in line with findings of by Ganapathy *et al.* (2011) <sup>[7]</sup>. Similar way High heritability of 77.65 percent with an genetic advance mean 12.33 was observed for plant height under TMS environment clearly revealed that the presence of non-additive gene action, thus simple selection procedure in early segregating generations will respectively. Plant height showed low genetic advance. These results were in agreement with the findings of Joshi and Mehra (1989) <sup>[15]</sup>.

Under moisture stress free condition (MSF) the number of productive tillers High heritability estimates of 86.96 percent and gentic advance mean 49.36 were observed for this trait, revealed that the trait is mainly additive gene actions and that they can be scored by their phenotypic performance. The results are in line with John (2006) <sup>[13]</sup>. However under TMS Medium Heritability estimates of 48.66 per cent with an high expected genetic advance mean 23.25 were observed for this trait. Conforming results were earlier proclaimed by Gowda *et al.* (2008) <sup>[9]</sup>.

In MSF (moisture stress free) number of fingers per ear Heritability of 68.41 per cent with an expected genetic advance mean of 25.88 was observed for number of fingers per ear. However High heritability (90.93%) and high GAM (28.04) was observed for this trait, The results obtained was on par with Anantharaju and Meenakshiganesan (2006)<sup>[2]</sup> and John (2006)<sup>[13]</sup>. However Moderate Heritability of 57.26 per cent with genetic advance mean of 17.03 was recorded for number of fingers per ear under TMS environment. This trait governed by both additive and non additive gene action.

In MSF(moisture stress free) finger length (cm) A high heritability of 94.53 percent with an expected an genetic advance mean 44.17 was observed for this trait making selection effective due to additive gene action. These results are in conformity with the findings by Appadurai *et al.* (1977), Goswami and Asthana (1984) <sup>[8]</sup>. Under TMS also High heritability of 91.63 percent with an genetic advance mean 28.82 was recorded for finger length indicating individual plant selection effective due to additive gene action These results are in conformity with the findings by Haradari *et al.* (2012) <sup>[12]</sup>.

In MSF (moisture stress free) root number Heritability of per cent 95.14 with an expected genetic advance of 52.98 mean of was observed for this trait making selection effective due to additive gene action. These results are in conformity with the findings by for root number under moisture free stress. Under TMS, Heritability of 70.16 per cent with an genetic advance mean of 29.44 was observed for root number under stress environment. The result was in conformity with the finding by Rasel *et al.* (2018).

In MSF(moisture stress free) root length (cm) was Heritability of 84 per cent with an genetic advance of mean of 28.79 for root length was observed for this trait making selection effective due to additive gene action. These results are in conformity with the findings by Pushpam *et al.* (2017). Mean while under TMS high Heritability of 98.16 per cent with an expected genetic advance mean of 29.63 was recorded for root length under stress. High values of heritability, with high genetic advance make the selection effective due to additive gene action.

In MSF (moisture stress free) dry matter (g) High heritability estimates of 85.88 per cent with high genetic advance mean 44.72 were observed for this making selection effective due to additive gene action. Whereas TMS the high heritability of 82.84 percent with an very high expected genetic advance mean 51.27 was recorded for seed yield per plant under TMS. The selection is effective due to additive gene action. The results are in line with Aditya *et al.* (2011).

In MSF (moisture stress free) 1000 seed weight under MSF Heritability of 97.53 per cent with an expected genetic advance of mean of 10.40 was observed for 1000 seed weight. High heritability with low genetic advance indicates non additive gene action. So selection process at early segregating generation will not be effective. Similar observations were also made by Agalodai, *et al.* (1979) <sup>[1]</sup>, Under TMS, Heritability of 92.53 per cent with an expected genetic advance mean of 8.40 was recorded for 1000 seed weight under stress. High heritability with low genetic advance indicates non additive gene action. Hence selection process at early segregating generation will not be effective. Yogeesh *et al.* (2016) <sup>[28]</sup>.

In MSF (moisture stress free) condition seed yield per plant, Heritability of 86.61 with a very high expected genetic advance mean 95.11 was recorded for seed yield per plant under non stress. High heritability coupled with high genetic advance indicated heritability was mainly due to additive gene effects thus selection for this trait may be effective for development of superior genotypes in future breeding programme by applying appropriate selection procedure and breeding method. These findings were in confirmative with pervious results of Agalodai (1979)<sup>[1]</sup>. A high heritability of with 82.71 an very high expected genetic advance mean 145.90 was recorded for seed yield per plant under TMS environment. The results revealed that the trait is mainly additive gene actions and that they can be scored by their phenotypic performance and the results were in accordance with the findings of Sumathi et al. (2007)<sup>[27]</sup>.

Selecting the traits of genotypes based on least difference between PCV and GCV as well as high heritability coupled with genetic advance. It is fairly advisable that one more crop cycles under field environment for further confirmation of results in future. Evaluation of germplasm for based on this variability parameters enables to identify drought tolerant lines that can be utilized for finger millet improvement programme. Table 1: Analysis of variance (mean sum of squares) for 10 quantitative characters studied in finger millet genotypes under MSF and TMS environments.

Source of variation	D f	Days to fifty per cent flowering Plant height (cm)			Numbe productiv		Number of finger		Finger length (cm)		
Source of variation		NS	S	NS	S	NS	S	NS	S	NS	S
Blocks (b)	10	91.95*	19.16*	0.377	2.76	0.02	0.08	1.70**	0.36	0.45*	0.54**
Entries (e) (Germplasm accessions + check entries)	69	119.57**	133.97**	122.23**	63.42**	0.32**	0.20**	7.56**	1.98**	9.12**	2.79**
Check entries (c)	3	240.87**	52.20**	1312.94**	469.08**	0.02	0.14	43.11**	13.17**	85.79**	10.98**
Germplasm accessions (g)	65	115.21**	123.86**	68.61**	36.25**	0.25**	0.20**	1.99**	1.08**	5.51**	2.45**
Accessions v/s Check varieties	1	39.27	1036.25**	35.48**	612.09**	5.63**	0.78**	262.96**	26.80**	13.76**	0.77*
Non genetic Error	30	32.35	6.53	0.82	5.76	0.02	0.08	0.46	0.35	0.2	0.13
* & ** Significant at 5% and 1%											

NS: Non stress, S: Terminal Stress

D f	Root number		Root length (cm)		Dry matter	1000 seed weight (g)		Seed yield (g/plant)		
	NS	S	NS	S	NS	S	NS	S	NS	S
10	1.75	1.568	2.2	0.15	6.82	6.51	0	0	0.35	1.31
69	60.44**	30.63**	21.24**	28.11**	193.55**	136.32**	0.020**	3.74**	19.49**	5.38**
3	389.65**	273.36**	147.34**	276.38**	1644.51**	647.60**	0.03**	0.17**	55.45**	2.36
65	33.16**	15.79**	15.74**	16.93**	114.94**	103.20**	0.01**	3.90**	16.99**	5.59**
1	845.46**	267.27**	0.3	10.63**	950.40**	755.20**	0.17**	4.24**	73.93**	0.39
30	1.07	3.44	1.75	0.2	11.19	12.35	0	0	1.56	0.67
	10 69 3 65 1	D f NS 10 1.75 69 60.44** 3 389.65** 65 33.16** 1 845.46**	NS S   10 1.75 1.568   69 60.44** 30.63**   3 389.65** 273.36**   65 33.16** 15.79**   1 845.46** 267.27**	NS NS   10 1.75 1.568 2.2   69 60.44** 30.63** 21.24**   3 389.65** 273.36** 147.34**   65 33.16** 15.79** 15.74**   1 845.46** 267.27** 0.3	NS NS S   10 1.75 1.568 2.2 0.15   69 60.44** 30.63** 21.24** 28.11**   3 389.65** 273.36** 147.34** 276.38**   65 33.16** 15.79** 15.74** 16.93**   1 845.46** 267.27** 0.3 10.63**	NS NS S NS   10 1.75 1.568 2.2 0.15 6.82   69 60.44** 30.63** 21.24** 28.11** 193.55**   3 389.65** 273.36** 147.34** 276.38** 1644.51**   65 33.16** 15.79** 15.74** 16.93** 114.94**   1 845.46** 267.27** 0.3 10.63** 950.40**	NS S NS S NS S   10 1.75 1.568 2.2 0.15 6.82 6.51   69 60.44** 30.63** 21.24** 28.11** 193.55** 136.32**   3 389.65** 273.36** 147.34** 276.38** 1644.51** 647.60**   65 33.16** 15.79** 15.74** 16.93** 114.94** 103.20**   1 845.46** 267.27** 0.3 10.63** 950.40** 755.20**	D f Root number Root length (cm) Dry matter (g/plant) weigh weigh   NS S NS S NS S NS   10 1.75 1.568 2.2 0.15 6.82 6.51 0   69 60.44** 30.63** 21.24** 28.11** 193.55** 136.32** 0.020**   3 389.65** 273.36** 147.34** 276.38** 1644.51** 647.60** 0.03**   65 33.16** 15.79** 15.74** 16.93** 114.94** 103.20** 0.01**   1 845.46** 267.27** 0.3 10.63** 950.40** 755.20** 0.17**	Bot Root number Root length (cm) Dry matter (g/plant) weight (g)   NS S NS S NS S NS S   10 1.75 1.568 2.2 0.15 6.82 6.51 0 0   69 60.44** 30.63** 21.24** 28.11** 193.55** 136.32** 0.020** 3.74**   3 389.65** 273.36** 147.34** 276.38** 1644.51** 647.60** 0.03** 0.17**   65 33.16** 15.79** 15.74** 16.93** 114.94** 103.20** 0.01** 3.90**   1 845.46** 267.27** 0.3 10.63** 950.40** 755.20** 0.17** 4.24**	D f Root number Root length (cm) Dry matter (g/plant) weight (g) Seed yield   NS S NS S NS S NS S NS   10 1.75 1.568 2.2 0.15 6.82 6.51 0 0 0.35   69 60.44** 30.63** 21.24** 28.11** 193.55** 136.32** 0.020** 3.74** 19.49**   3 389.65** 273.36** 147.34** 276.38** 1644.51** 647.60** 0.03** 0.17** 55.45**   65 33.16** 15.79** 15.74** 16.93** 114.94** 103.20** 0.01** 3.90** 16.99**   1 845.46** 267.27** 0.3 10.63** 950.40** 755.20** 0.17** 4.24** 73.93**

\* & \*\* Significant at 5% and 1%

NS: Non stress, S: Terminal Stress

Table 2: Genetic variability parameters for 10 different characters in finger millet genotypes under MSF and TMS environments.

Characters	Mean		Range					•		Genetic advance as pe cent of mean		
	NS	S	N S	S	Р	G	Р	G	N S	S	N S	S
Days to fifty percent flowering	68.16	63.04	45-89	43-88	13.56	10.74	4.31	13.74	62	92	17.52	27.17
Plant height (cm)	71.88	65.27	55.2-88.6	49.38-80.6	9.42	9.34	7.71	6.79	98	077	19.06	12.33
Number of productive tillers	.7	1.79	1-2	1-2	27.55	25.69	23.19	16.18	86	048	49.36	23.25
Number of fingers	7.85	6.73	4-13	4-9	18.37	15.19	14.44	10.92	68	057	25.88	17.03
Finger length (cm)	8.75	8.49	4.8-14.6	5-12.8	22.68	22.06	15.26	14.61	94	091	44.17	28.82
	Days to fifty percent flowering Plant height (cm) Number of productive tillers Number of fingers	Characters N S   Days to fifty percent flowering 68.16   Plant height (cm) 71.88   Number of productive tillers .7   Number of fingers 7.85	NS S   Days to fifty percent flowering 68.16 63.04   Plant height (cm) 71.88 65.27   Number of productive tillers .7 1.79   Number of fingers 7.85 6.73	NS S NS   Days to fifty percent flowering 68.16 63.04 45-89   Plant height (cm) 71.88 65.27 55.2-88.6   Number of productive tillers .7 1.79 1-2   Number of fingers 7.85 6.73 4-13	NS S NS S   Days to fifty percent flowering 68.16 63.04 45-89 43-88   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6   Number of productive tillers .7 1.79 1-2 1-2   Number of fingers 7.85 6.73 4-13 4-9	Mean Range under m   NS S NS S P   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42   Number of productive tillers .7 1.79 1-2 1-2 27.55   Number of fingers 7.85 6.73 4-13 4-9 18.37	NS S NS S P G   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19	Mean Range under non stress Variance   NS S NS S P G P   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74 4.31   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34 7.71   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69 23.19   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19 14.44	Mean Range under non stress Variance under stress   NS S NS S NS S P G P G   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74 4.31 13.74   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34 7.71 6.79   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69 23.19 16.18   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19 14.44 10.92	Mean Range under non stress Variance under stress ()   NS S NS S P G P K NS NS   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74 4.31 13.74 62   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34 7.71 6.79 98   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69 23.19 16.18 86   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19 14.44 10.92 68	Mean Range under non stress Variance under stress (%)   NS S NS S P G P G NS S   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74 4.31 13.74 62 92   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34 7.71 6.79 98 077   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69 23.19 16.18 86 048   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19 14.44 10.92 68 057	Mean Range under non stress Variance under stress (%) cent of   NS S NS S NS S P G P G NS S NS   Days to fifty percent flowering 68.16 63.04 45-89 43-88 13.56 10.74 4.31 13.74 62 92 17.52   Plant height (cm) 71.88 65.27 55.2-88.6 49.38-80.6 9.42 9.34 7.71 6.79 98 077 19.06   Number of productive tillers .7 1.79 1-2 1-2 27.55 25.69 23.19 16.18 86 048 49.36   Number of fingers 7.85 6.73 4-13 4-9 18.37 15.19 14.44 10.92 68 057 25.88

\* & \*\* Significant at 5% and 1% NS: Non stress, S: Terminal Stress

Sl. No.	Characters	Mean		Range		Coefficient o under no		Coeffi Variance u			Genetic advance per cent of mea		
		N S	S	N S	S	Р	G	Р	G	N S	S	N S	S
6	Root number	19.67	17.95	8-35	10-28	27.03	26.36	20.37	17.06	95	70	52.98	29.44
7	Root length (cm)	19.82	23.01	12.3-28.25	13.6-38	16.64	15.25	14.65	14.52	84	98	28.79	29.63
8	Dry matter (g/plant)	37.62	30.38	20-65	10-55	25.28	23.42	30.04	27.34	85	82	44.72	51.27
9	1000 seed weight (g)	2.00	1.91	1.7-2.6	1.7-2.3	5.17	5.11	4.17	4.11	97	92	10.40	8.4
10	Seed yield (g/plant)	7.08	2.26	1-15.2	0.34-11.8	53.31	49.61	85.63	77.88	86	82	95.11	145.9

NS: Non stress, S: Terminal Stress, P: Phenotype, G: Genotype

# References

- 1. Agalodai AV, Desai KB, Tikka SBS. Analysis of parameters of variability and interrelationship of yield attributes in finger millet. Indian J Agril. Sci. 1979; 49:924-928.
- 2. Anantharaju P, Meenakshiganesan N. Genetic variability in finger millet (*Eleusine coracana* L.). Int. J Trop. Agric. 2006; 24(1-2):269-274.
- 3. Anonymous, 2017, http://agricoop.nic.in/agristatistics
- 4. Burton GW, Devane EH. Estimating heritability in talli Feschue (*Festuca arundinacea*) from replicated clones' material. Agron. J. 1953; 45(10):478-481.
- 5. Devi VG, Roobon BN, Sasikala V, Sahasranamam V, Abraham A. Isorhamnetin-3-glucoside alleviates oxidative stress and opacification in selenite cataract *in vitro*. Toxicol. Invitro. 2010; 24(6):1662-1669.
- 6. Federer WT. Experimental Design: Theory and Application. McMillan, New York, 1977.
- Ganapathy S, Kumari NA, Muthiah AR. Genetic variability and interrealtionship analyses for economic traits in finger millet germplasm. World J Agril. Sci. 2011; 7(2):185-188.
- Goswami P, Asthana AN. Genetic variability in indigenous varieties of finger millet in Sikkim. Indian J Agril. Sci. 1984; 54:959-961.

- Gowda J, Ratnakar S, Suvarna, Somu G. Genetic variability and correlation studies in interspecific crosses of finger millet (*Eleusine coracana* L.). Crop Res. 2008; 36(1, 2&3):239-243.
- Gowda J, Ratnakar S, Suvarna Somu G. Genetic variability and correlation studies in interspecific crosses of finger millet (*Eleusine coracana* L.). Crop Res. 2008; 36(1, 2&3):239-243.
- Hanson GH, Robinson HF, Comstack RE. Biometrical studies of yield in segregating populations of Korian Lespedeza. Agron. J. 1953; 48(6):267-282.
- Haradari C, Ugalat J, Nagabhushan. A study on character association genetic variability and yield components of finger millet (*Eleusine* coracana L.). J Crop Weed. 2012; 8(2):32-35.
- John K. Variability and correlation studies in quantitative traits of Finger millet (*Eleusine coracana* L.). Agric. Sci. Digest. 2006; 26(3):166-169.
- Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybeans. Agron. J. 1955; 47(7):314-318.
- 15. Joshi K, Mehra HS. Investigations on variation, heritability and genetic advance in ragi germplasm from Uttar Pradesh hills. In Finger millet genetics and breeding

in India. Proceedings of National Seminar, Univ. Agric. Sci., Bangalore (India), 1989, 73-75.

- Kadam DD, Kulkarni SR, Jadhav BS. Genetic variability correlation and path analysis in finger millet (*Eleusine coracana*). J Res. Maharashtra Agricultural Univ. 2009; 34(2):131-134.
- 17. Kebere B, Prapa S, Wasana W, Vipa H. Genetic variation, heritability and path -analysis in Ethiopian finger millet landraces. Nat. Sci. 2006; 40:322-334.
- Keerthana K, Chitra S, Subramanian A, Nithila S, Elangovan M. Studies on genetic variability in finger millet (*Eleusine coracana* L.) genotypes under sodic conditions. Electron. J. Plant Sci. 2019; 10(2):566-569.
- 19. Krishnappa M, Ramesh S, Chandraprakash J, Gowda J, Bharathi Doss DD. Genetic analysis of economic traits in finger millet. Uni. Agric. Sci., Bangalore (India), 2009.
- 20. Krishnappa M, Ramesh S, Chandraprakash J, Gowda J, Bharathi Doss DD. Genetic analysis of economic traits in finger millet. Uni. Agric. Sci., Bangalore (India), 2009.
- 21. Lush JL. Heritability, genetic advance and character association on rabi sorghum. Hereditas, 1949, 356-375.
- Rao PJM, Upender M, Vijay BA. Variability and genetic diversity studies in redgram [*Cajanus cajan* (L.) Millsp.]. Int. J App. Bio. Phar. Tech. 2013; 4(4):48-51.
- 23. Reddy CVCM, Reddy PVRM, Munirathnam P, Gowda J. Studies of genetic variability in yield and yield attributing traits of finger millet (*Eleusine coracana* L.). Indian J Agric. Res. 2013; 47(6):549-552.
- 24. Robinson HF, Compstock RE, Harey PH. Estimates of heritability and degrees of dominance in corn. Agron. J. 1949; 43:353-359.
- Salini K, Nirmalakumari A, Muthiah AR, Senthil N. Evaluation of proso-millet (*Panicum miliaceum* L.) germplasm collections. Electron. J Plant Sci. 2010; 1(4):489-499.
- 26. Singamsetti A, Patro TSSK, Anuradha N, Divya M. Studies on genetic variability for yield and yield attributing traits in Finger millet (*Eluesine coracana* L.). Int. J Curr. Microbiol. Appl. Sci. 2018; 7:90-95.
- 27. Sumathi P, John J, Muralidharan V. genetic variability in the hybrids of finger millet (*Eleusine coracana*). Crop res. 2007; 33(1, 2& 3):192-194.
- Yogeesh LN, Naryanareddy AB, Nanjareddy YA, Gowda, High temperature tolerant genotypes of Finger Millet (*Eleusine coracana* L.) J Nature. Environ & Pollution. Techno. 2016; 4(15):1293-1296.