



Trait Based Adaptation and Yield Stability Parameters in Little Millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.)

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Authors' contributions

This work was carried out in collaboration between both authors. Author VMS carried out the study and drafted the manuscript. Author AN guided the research work and approved the final version of manuscript. Both authors read and approved the final manuscript.

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ABSTRACT

Twelve accessions of little millet genotypes which included 10 germplasm accessions and two released check varieties were studied over five environments of rainy seasons of 2013 for their grain yield and stability. The results have shown that genotypes TNPsu 141 and TNPsu 28 had possessed around unit regression coefficient ($b = 1.24$ to 0.82), thus displaying average stability and are adaptable to all the above five different agro-ecological zones. Also, these genotypes had non-significant S^2_{di} values enabling it to predict the stability. Genotypes TNPsu 17, PM 29, TNPsu 18, and IPmr 886 manifested significantly higher single plant grain yield than the standard check varieties along with regression coefficient values of greater than one expressing above-average stability. These can be performed better in a favourable environment. However, they were classified as unstable due to their significant S^2_{di} values revealing that the performance of the genotypes was unpredictable for the given environment. These genotypes were performed better under optimum conditions. Out of 12 genotypes MS 1826 and MS 4684 had an average response and appeared unpredictable stability. However, among the genotypes studied, TNPsu 141 possessed low yield and perform better in sub-optimum environments which are inferred by less than unit regression.

Keywords: *G x E interaction; linear regression model; littlemillet; phenotypic stability; regression coefficient.*

1. INTRODUCTION

Little millet (*Panicum sumatrense*) a member of the Poaceae (Gramineae) family, is one of the most important food cereals in the tribal people. Indigenous to India, little millet is widely produced in the cool high altitude areas in the region primarily as a source of food and also used for cattle feed [1]. The resilience exhibited by the littlemillet in their adjustment to different ecological situations makes them ideal crops for climate change. In India, the crop is mainly grown in the Southern parts of the country, especially during the main rainy season. It is often valued as nutritious cereal by local people. Similar to other small millets, little millet grain can be stored for several years under local storage conditions without sustaining significant damage by storage pests. This property together with its wider adaptation to resource fragile agro-climatic regions with low rainfall and relatively better nutritional value makes it one of the salient crops among resource -poor communities living in food-insecure areas [2]. In Tamil Nadu it is often grown in poor soils without fertilizers, and thus the average yield rarely exceeds 1 ton/ ha. Lack of high-yielding varieties adapted to diverse agro-ecological conditions is the major reason for low productivity. Evaluation of interaction of genotypes with locations and identifying additional high-yielding varieties that can fit in to a wide range of environments is necessary. This will help in getting information on adaptability and stability of performance of genotypes and lead to increase productivity.

The lack of high -yielding varieties adapted to diverse agro-ecological conditions is the major reason for the low productivity of littlemillet. Morphological characters often do not reliably portray genetic relationships since genotype by environment interaction ($G \times E$) reduces the rate of genetic improvement [3]. Multi-location testing of genotypes provides an opportunity to plant breeders to identify the adaptability of genotype to a particular environment and also stability of the genotype over different environments. The linear regression model of Eberhart and Russell [4] is frequently used for the analysis of genotype X environment interaction, adaptability, and stability performance of genotypes in which the "b" values give information about adaptability and s^2_{di} used as measures of stability of performance. The stable genotype which one

possesses the value of $b = 1$ are stable due to their predictable nature and desirability. They perform better across the environments, i.e., both in poor as well as good environments. The high value of regression ($b > 1$) indicates that the variety is more responsive for the optimum environment, while the low value of regression ($b < 1$), is an indication that they variety may perform better in sub- optimum environment [5].

2. MATERIALS AND METHODS

The study material consisted of 12 genotypes including two checks, ten elite germplasm were selected in the previous study based on single plant grain yield and grain iron content, which were maintained at Departments of Millets, Tamil Nadu Agricultural University, Coimbatore. The check varieties viz., CO(Samai) 4 which is state high yielding and short duration variety, and the other one is national check variety OLM 203 which one is long duration. All the genotypes were evaluated during the rainy (*Kharif*) season 2013 with three replications at five different agro-ecological zones viz., Anchetty, Dharmapuri, Javadhu hill, and Coimbatore early and late *Kharif* seasons. At flowering and maturity stages, observations were recorded on yield and yield component characters such as days to 50 percent flowering, plant height, number of basal tillers per plant, panicle length and single plant grain yield from five randomly selected plants in each entry in each replication. The geographical coordinates and agro-climatic characteristics of the locations are shown in Table 1a and 1b. Five rows of each genotype were planted in a randomized complete block design with 3 replications. The row length was 3 m with row to row spacing of 30 cm. The seeds were manually drilled into each row and later thinned to a spacing of 10 cm between plants. The field was kept free of weeds throughout the testing seasons.

2.1 Statistical Analysis

The mean values for all the characters across the environments were subjected to stability analysis as suggested by Eberhart and Russell [4] for various stability parameters i.e., mean, regression coefficient (b), and deviation from their regression (S^2_{di}) to get the individual genotype response by partitioning the pooled deviation. The significance of the stability

parameter was tested by using appropriate t and F tests. Data were analyzed using the TNAU Stat package. Standard cultural practices were followed throughout the crop season. Analysis of variance of mean values of genotypes over replication was computed for five characters in each environment.

2.1.1 Pooled analysis of variance

The linear model for pooled analysis of variance is,

$$Y_{ijk} = \mu + e_k + (r_{jk} + g_i) + (ge)_{ik} + e_{ijk}$$

Where,

- μ = General mean
- e_k = Effect of k^{th} environment
- r_{jk} = Effect of j^{th} replication within k^{th} environment
- g_i = Effect of i^{th} genotype
- $(ge)_{ik}$ = Effect of interaction of i^{th} genotype in k^{th} environment
- e_{ijk} = Residual effect

Table 1(a). Field locations

S.No	Environment	Place	District	State
1	E1	Anchetty	Krishnagiri	Tamil Nadu
2	E2	Jamunamarathur	Thiruvannamalai	Tamil Nadu
3	E3	Papparapatti	Dharmapuri	Tamil Nadu
4	E4	TNAU (early <i>khari</i>)	Coimbatore	Tamil Nadu
5	E5	TNAU (late <i>khari</i>)	Coimbatore	Tamil Nadu

Table 1(b). Field conditions

Particulars	Environment				
	E1	E2	E3	E4	E5
Latitude	12.35°N	12.64°N	12.07°N	11°N	11°N
Longitude	77.72°E	79.00°E	78.09°E	77°E	77°E
Altitude (MSL)	872 m	1957 m	507m	422 m	422 m
Rainfall	815 mm	1050 mm	853mm	730 mm	730 mm
Source of irrigation	Rainfed	Rainfed	Irrigated	Irrigated	Irrigated
pH	7.8	6.4	7.16	7.4	7.5
EC (dsm ⁻¹)	0.39	0.26	0.42	0.33	0.33
Soil type	Non calcareous red soil	Red soil	Red soil	Red loamy soil	Red loamy soil

List 1: A pooled analysis of variance was carried out for 12 genotypes across five environments for five characters as follows:

Source of variation	Degrees of freedom	Mean sum of square	Expected mean sum of square
Environment	(e-1)	MS _e	
Genotype	(g-1)	MS _g	$\sigma^2_e + r\sigma^2_{ge} + r\sigma^2_g$
Genotype x Environment	(e-1)(g-1)	MS _{ge}	$\sigma^2_e + r\sigma^2_{ge}$
Pooled error	r(e-1)(g-1)	MSE	σ^2_e

Where,

- r = Number of replications
- g = Number of genotypes
- MS_e = Mean sum of squares due to environment
- MS_g = Mean sum of squares due to genotypes
- MS_{ge} = Mean sum of squares due to genotype x environment
- MSE = Pooled error
- σ^2_g = Genotypic variance
- σ^2_e = Error variance
- σ^2_{ge} = Variance due to genotype x environment

2.1.2 Eberhart and Russell [4] model

The linear model proposed by Eberhart and Russell [4] is

$$Y_{ij} = \mu + b_i I_j + \delta_{ij} \quad \text{Where, } i = 1, 2, \dots, g \quad j = 1, 2, \dots, e$$

Analysis of variance for stability as proposed by Eberhart and Russell [4]

Source	Df	Sum of squares	Mean squares
Total	(ge-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_i^2 / e$	
Genotypes	(g-1)	$1/e \sum_i Y_i^2 - \sum_i Y_i^2 / e$	MS1
Environment + (Genotype x Environment)	g(e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_i^2 / e$	
Environment (Linear)	1	$1/g \left(\sum_j Y_{.j} I_j \right)^2 / \sum_j I_j^2$	
Genotype x Environment (Linear)	(g-1)	$\sum_j \left(\sum_i Y_{ij} I_j \right)^2 / \sum_j I_j^2$	MS2
Pooled deviations	g(e-2)	$\sum_i \sum_j \delta_{ij}^2$	MS3
Deviation due to genotype 1	(e-2)	$\left[\sum_j Y_{ij}^2 - (Y_i)^2 / e \right] - \left(\sum_j Y_{ij} I_j \right)^2 / \sum_j I_j^2$ $= \sum_j \delta_{ij}^2$	
Pooled error	e(r-1)(g-1)	$\sigma^2 e$	

Where,

Y_{ij} = Mean of i^{th} genotype in j^{th} environment

μ = Mean of all genotypes overall environments

b_i = Regression coefficient of i^{th} genotype on the environmental index

I_j = Environmental index

$$= \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

δ_{ij} = Deviation from regression of the i^{th} genotype at j^{th} environment

g = Number of genotypes

e = Number of environments

r = Number of replications

Computation of environmental index (I_j)

$$I_j = \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge} \quad \sum_j I_j = 0$$

Where,

$\sum_i Y_{ij}$ = Total of all the genotypes at j^{th} location

$\sum_i \sum_j Y_{ij}$ = Grand total

g = Number of genotypes

e = Total number of observations

2.1.3 Estimation of stability parameters

Stability parameters namely (i) regression coefficient (b_i) and (ii) mean square deviation from regression (S_{di}^2) were computed as given by Eberhart and Russell [4].

2.1.3.1 Regression coefficient

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij} I_j$ = Sum of products of the environmental index (I_j) with the corresponding mean of genotype at each environment (Y_{ij})

$\sum_j I_j^2$ = Sum of squares of the environmental index (I_j)

Y_{ij} = Mean of i^{th} genotype in j^{th} environment

I_j = $\frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$

For each value of regression coefficient, $\frac{\sum_j I_j^2}{g}$ was common.

$\sum_j Y_{ij} I_j$ for each genotype was the sum of products of the environmental index (I_j) with the corresponding mean (\bar{X}) of that genotype in each environment.

These values might be obtained in the following manner

$$[\bar{X}][I_j] = \left[\sum_j Y_{ij} I_j \right] = [S]$$

Where

$[\bar{X}]$ = Matrix of means

$[I_j]$ = Vector for environmental index and

$[S]$ = Vector for sum of products, i.e.,

$$\sum_j Y_{ij} I_j$$

2.1.3.2 Mean square deviations (S^2_{di}) from linear regression

In a regression analysis, it is possible to partition the variance of the dependent variable (Y) into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity.

$\sigma_y^2 = \sigma^2_{\text{regression}} + \sigma^2_{\text{deviation from the regression}}$

The variance of the mean over different locations with concerning individual genotype might be obtained in the following way.

$$\sigma_{V_i}^2 = \sum_j Y_{ij}^2 - (Y_i^2 / g)$$

The variance due to deviations from regression

$\left(\sum_j \delta_{ij}^2 \right)$ for a genotype being

$$\sum_j \delta_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_i^2}{g} \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2}$$

Where,

$\sum_j \delta_{ij}^2$ = Variance due to deviation from regression for a genotype

$\sum_j Y_{ij}^2 - \frac{Y_i^2}{g}$ = Variance due to dependent variable

$\frac{\sum_j (Y_{ij} I_j)^2}{\sum_j I_j^2}$ = Variance due to regression

$$\frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2} = \frac{\left(\sum_j Y_{ij} I_j \right) \left(\sum_j Y_{ij} I_j \right)}{\sum_j I_j^2} = \frac{b \sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

From $\sum_j \delta_{ij}^2$ values, the stability parameter S^2_{di} for each variety was computed as follows:

$$S^2_{di} = \frac{\sum_j \delta_{ij}^2}{(e-2)} - \frac{S_e^2}{r}$$

$$\begin{aligned} & \text{Mean square deviation} \\ & \frac{\text{Deviation from regression}}{\text{Degrees of freedom for environment}} \\ & \frac{\text{Pooled error}}{\text{Number of replications}} \end{aligned}$$

Where,

S_e^2 = The estimate of pooled error

e = Number of environments

g = Number of genotypes

r = Number of replications

2.1.4 Tests of significance

To test the significance of the differences among genotype means namely,

$$H_0 = \mu_1 = \mu_2 = \mu_3 = \dots \mu_{10}$$

F' test used was

$$F = \frac{\text{Mean square due to genotypes}}{\text{Mean square due to pooled deviation}} = \frac{MS1}{MS3}$$

To test that the genotypes did not differ due to regression on environmental index, i.e.,

$$H_0 = b_1 = b_2 = \dots b_{10},$$

The 'F' test used was

$$F = \frac{\text{Mean square due to genotype x environment (linear)}}{\text{Mean square due to pooled deviation}} = \frac{MS2}{MS3}$$

Individual deviation from linear regression was tested as follows:

$$F = \left[\frac{\left(\sum_j \delta_{ij}^2 \right) / (e - 2)}{\text{pooled error mean sum of squares}} \right]$$

t value at (g-2) d.f at P=0.05 and 0.01 levels.

The hypothesis that any regression coefficient did not differ from unity or zero was tested by the appropriate 't' test, i.e.,

$$t = \frac{|1-b|}{SE(b)} = \sqrt{\frac{\left(\sum_j \delta_{ij}^2 \right) / (e - 2)}{\sum_j I_j^2}}$$

't' value at (g-2) d.f. at P = 0.05 and 0.01 levels

Population mean (μ) and standard error

$$\text{Population mean } (\mu) = \frac{\text{Grand total}}{\text{Number of observations}}$$

$$SE \text{ (mean)} = \sqrt{\frac{\text{Mean Square due to pooled deviation}}{\text{Number of environments} - 1}}$$

3. RESULTS AND DISCUSSION

The regression analysis proposed by Finlay and Wilkinson [6] to measure phenotypic stability was improved upon by Eberhart and Russell [4]. They

introduced (in addition to two parameters proposed by Finlay and Wilkinson) one more parameter, which accounted for unpredictable irregularities in response of genotypes to varying environments measured as the deviation from the regression lines, to characterize a stable genotype. The linear regression model of Eberhart and Russel [4] is most frequently used for the analysis of genotype x environment interaction, adaptability and stability of performance of genotypes in which the 'b' values give information about adaptability and 'S²d' values are used as measures of stability of performance.

In this model, the total variance is first divided into two components i.e., i) Genotypes and ii) Environment + G x E interaction. The second component (E + G x E) is further partitioned into three components viz., environments (linear), genotype x environments (linear), and deviation from regression (pooled deviation over the genotypes). The quantification of environments differs from that of Finlay and Wilkinson [6] in that means of all the genotypes at a site and or season was regarded by them as site mean. Eberhart and Russell [4] preferred to measure the environment as a deviation of the mean of all the genotypes at a location from the overall mean which is known as an environmental index.

The pooled analysis of variance demonstrated highly significant differences among genotypes for all the characters revealing that the presence of sufficient variability for these characters among the 12 littlemillet genotypes (Table 2). Significant variation due to environments represented adequate heterogeneity among the environments for all the yield component characters. Significant genotype x environment interaction for all the characters depicted differential expression of genotypes for the traits studied over different five agro-ecological zones.

MS due to E + (G x E) were significant for days to 50 percent flowering, plant height and single plant grain yield indicating the influence of the environments on the expression of these traits. Partitioning of this sum of squares, due to environment and environment (linear) were significant for all the characters except the number of basal tillers per plant and panicle length indicated significant environment mean sum of squares implying the significant influence of the environments on the genotypic expression,

but significant genotype x environment (linear) component was significant for days to 50 percent flowering and single plant grain yield suggesting predictable nature of the performance of genotypes taken over the environment. Pooled deviation was also found significant for all the characters. The significant value of both for G x E (linear) and pooled deviation confirms the presence of predictable and non-predictable components (Table 3). Even for the unpredictable factors, predictions can be made if one considers the stability performance of individual genotypes [7]. Linear predictable component showed significant G x E interaction indicated that genotypes differed considerably with their responsiveness and prediction of their performance over environment would be more reliable.

Environmental index directly reflects the poor or rich environment in terms of negative or positive values, respectively. Among the environments studied, environment 2 recorded the highest and positive index for all the characters studied except panicle length. Environment 1 showed a positive index for days to 50 percent flowering, plant height and basal tillers per plant. Hence, environment 2 and environment 1 appeared to be the most favourable for these characters. Environment 5 registered negative indices for all characters and environment 3 and environment 4 had negative indexes for all the characters except panicle length. Among the environments studied environment 2 had a favourable effect on single plant grain yield. Negative values of environmental indices indicated the unfavourable nature of the environments (Table 4).

Table 2. Pooled analysis of variance for five characters in 12 littlemillet genotypes

Source	df	Days to 50 % flowering	Plant height (cm)	Basal tillers per plant	Panicle length (cm)	Single plant grain yield (g)
Replication	10	0.53	17.22	0.65	2.90	2.62
Genotype	11	65.94**	972.5**	15.87**	108.36**	96.92**
Environment	4	38.77**	1102.92**	1.64**	6.34**	266.14**
Genotype x environment	44	6.14**	59.48**	2.25**	8.92**	10.98**
Pooled Error	110	1.40	1.77	1.01	3.45	0.48

* Significant at $P=0.05$ ** Significant at $P=0.01$

Table 3. Analysis of variance for stability performance for five characters in 12 littlemillet genotypes

Source	df	Days to 50 % flowering	Plant height (cm)	Basal tillers per plant	Panicle length (cm)	Single plant grain yield (g)
Genotype (G)	11	65.93**++	972.50**++	1.61++	108.36**++	10.76++
Environment + (G x E)	48	8.86**++	146.43**++	1.48++	8.70	29.47*++
Environment (linear)	1	155.07**++	4411.67**++	6.45++	25.37	686.80**++
G x E (linear)	11	12.81**++	35.73	1.40++	5.99	6.85++
Pooled deviation	36	3.60++	61.78++	1.30++	9.07++	12.44++
Pooled Error	110	1.40	1.77	0.36	3.45	0.95

* Significant at $P=0.05$ ** Significant at $P=0.01$ against pooled deviation
++ Significant at $P=0.01$ against pooled error

Table 4. Environmental indices for five characters in 12 littlemillet genotypes

Environments	Days to 50% flowering	Plant height (cm)	Basal tillers per plant	Panicle length (cm)	Single plant grain yield (g)
Environment 1	1.67	7.80	0.44	-0.13	-0.59
Environment 2	2.18	11.05	0.31	-0.97	8.13
Environment 3	-0.76	-1.88	-0.22	0.23	-3.98
Environment 4	-1.71	-4.19	-0.11	1.03	-1.75
Environment 5	-1.37	-12.79	-0.43	-0.16	-1.81

Table 5. Stability parameters for days to 50 % flowering and plant height in little millet genotypes

Genotype	Days to 50 % flowering				Plant height (cm)			
	Mean	Rank	b_i	S^2_{di}	Mean	Rank	b_i	S^2_{di}
TNPsu 12	53.73	5	1.54	0.41	109.41	1	0.90	46.97**
TNPsu 17	54.60	6	0.35	6.80**	120.65	2	0.69	152.31**
TNPsu 18	54.87	7	3.17**	1.27	123.22	5	1.21	21.36**
TNPsu 25	57.33	9	0.19	7.96**	122.86	4	0.68	117.47**
TNPsu 28	57.03	8	0.95	4.21*	121.43	3	1.18	24.19**
TNPsu 141	51.60	2	-0.19*	1.03	125.68	6	1.27	27.66**
MS 1826	51.93	3	0.42*	-0.07	133.87	8	1.47	29.92**
MS 4684	51.33	1	-0.13	1.75	139.60	10	1.16	9.64**
PM 29	59.47	10	1.76	5.19*	146.07	11	0.74	41.96**
IPmr 886	60.07	11	1.45	2.76*	162.22	12	0.41*	10.82**
CO (Samai)4	52.20	4	1.91	6.19**	128.41	7	1.11	8.93**
OLM 203	62.00	12	0.58	0.02	136.40	9	1.17	243.00**
Mean	55.51				130.82			
SE	1.05				4.02			

* Significant at 5 % level, ** Significant at 1% level of probability
 b_i - Regression coefficient S^2_{di} - Deviation from regression coefficient

According to Eberhart and Russell's stability model, three parameters explain the stability of a genotype the mean, regression co-efficient(b_i), and deviation from regression (S^2_{di}). A stable genotype is one which has a high mean, unit regression ($b_i = 1$), and the deviation from the regression as small as possible ($S^2_{di} = 0$).

3.1 Days to 50 Percent Flowering

Test of significance for regression coefficient equal to unity was non-significant for three genotypes such as TNPsu 12, TNPsu 28, and IPmr 886 and deviation of regression from zero was non-significant for genotypes TNPsu 12, MS 1826, and OLM 203. A significant deviation of regression from zero indicated the unpredictability of performance of these genotypes over environments. For days to 50 per cent flowering only one genotype, TNPsu 12 was found to be stable among the 12 genotypes studied. The genotype TNPsu 18 could be recommended for optimum conditional environments because of its high regression coefficient and non-significant deviation from regression. Low mean, regression coefficient less than unity and non-significant deviation from regression were observed in the genotypes TNPsu 141, MS 1826 and MS 4684. High mean, regression coefficient less than unity, and non-significant deviation from regression were observed in the genotype OLM 203. These genotypes would be suitable under sub-optimum environments. Because of the negative non-significant regression coefficient and non significant deviation from regression the

genotype MS 4684 could be considered for poor or extreme stress environments. The stability parameters for days to 50 % flowering are presented in Table 5.

3.2 Plant Height

The stability parameters of plant height was given in table 5. Non-significant regression coefficients were observed for all the genotypes except IPmr 886. Among the genotypes studied, MS 1826, MS 4684, and OLM 203 possessed a high mean with a regression coefficient equal to unity while genotypes, TNPsu 18, TNPsu 28, TNPsu 141, and CO(Samai) 4 showed low mean and regression coefficient equal to unity. All the genotypes tested had a significant deviation from regression, indicating the stability of these genotypes over the environments but performance is not predictable for this trait.

3.3 Basal Tillers Per Plant

Test of significance for regression coefficient equal to unity was non-significant for three genotypes such as MS 1826, IPmr 886 and OLM 203 and deviation of regression from zero was non-significant for genotypes TNPsu 17, IPmr 886 and OLM 203. A significant deviation of regression from zero indicated the unpredictability of performance of these genotypes over environments. The genotype, IPmr 886 showed a regression coefficient near to unity, high mean, and non-significant deviation from regression. This genotype would be stable and suitable for all environmental conditions. Because of the high regression coefficient and

non-significant deviation from regression, the genotype TNPsu 28 and MS 4684 might be more adapted to better environments. The genotype OLM 203 can be recommended for stress environments due to its negative non-significant regression coefficient and non significant deviation from regression. Regression coefficient less than unity and non-significant deviation from regression observed in the genotype TNPsu 141 would be suitable under poor environments. The stability parameters for basal tillers per plant were given in Table 6.

3.4 Panicle Length

The stability parameters for panicle length were given in table 6. All the genotypes except TNPsu 17 had regression coefficient equal to unity was non-significant and deviation of regression from zero was non-significant for genotypes such as TNPsu 12, TNPsu 17, MS 1826, and OLM 203. For panicle length, genotype TNPsu 12 was found to be stable. This genotype would be suitable for all over environments. The genotypes such as TNPsu 17, MS 1826 and OLM 203 showed regression coefficients of more than one and non-significant deviation from regression and performed well under favourable environments.

3.5 Single Plant Grain Yield

Single plant yield is the most important trait in the development of little millet variety. Identification of

a genotype with a high single plant grain yield and average stability is of immense value. A perusal of stability parameter for single plant grain yield, potential genotypes TNPsu 141, and TNPsu 28 had possessed around unit regression coefficient ($b = 1.24$ to 0.82), thus displaying average stability and are adaptable to all the above five different agro-ecological zones. Also these genotypes had non- significant S^2_{di} values enabling it to predict the stability. Four genotypes TNPsu 17, PM 29, TNPsu 18, and IPmr 886 manifested significantly higher single plant grain yield than the standard check varieties along with regression coefficient values of greater than one expressing above-average stability. These can be relatively performed better in a favourable environment. However, they were classified as unstable due to their significant S^2_{di} values revealing that the performance of the genotypes was unpredictable for the given environment. These genotypes were performed better under optimum conditions. Out of 12 genotypes MS 1826 and MS 4684 had an average response and appeared unpredictable stability. However, among the genotypes studied, TNPsu 141 possessed low yield and perform better in sub-optimum environments which are inferred by less than unit regression. Thus, it could be inferred that their performance in respect of grain yield did not respond favourably to the improvement in the environment. The stability parameter for single plant grain yield was given in Table 7.

Table 6. Stability parameters for basal tillers per plant and panicle length in little millet genotypes

	Basal tillers per plant				Panicle length (cm)			
	Mean	Rank	b_i	S^2_{di}	Mean	Rank	b_i	S^2_{di}
TNPsu 12	8.09	6	1.72	3.49*	27.56	7	1.60	0.05
TNPsu 17	9.13	4	2.52	-0.19	38.94	1	-2.98*	1.64
TNPsu 18	7.63	9	1.14	6.21**	30.06	5	1.22	31.97**
TNPsu 25	9.27	3	-1.28	3.02*	26.73	9	1.16	15.84**
TNPsu 28	9.93	2	2.28	2.52	26.28	10	-0.13	4.30*
TNPsu 141	6.53	10	-0.56	2.12	26.76	8	1.87	2.55*
MS 1826	8.00	8	1.10	1.29	26.00	11	2.20	-0.21
MS 4684	8.71	5	4.31	1.51	28.30	6	2.13	18.43**
PM 29	8.03	7	0.17	2.40	33.06	3	0.98	6.44**
IPmr 886	10.27	1	1.62	0.91	38.24	2	1.50	8.63**
CO (Samai) 4	5.53	11	0.13	-0.00	32.19	4	-1.22	2.88*
OLM 203	4.22	12	-1.16	0.21	25.95	12	2.64	2.44
Mean	7.91				30.00			
SE	0.54				1.34			

* Significant at 5 % level, ** Significant at 1% level of probability
 b_i - Regression coefficient S^2_{di} - Deviation from regression coefficient

Table 7. Stability parameters for single plant grain yield in littlemillet genotypes

Genotype	Single plant grain yield (g)			
	Mean	Rank	b_i	S^2_{di}
TNPsu 12	22.55	6	0.16*	3.96*
TNPsu 17	26.81	2	1.10*	0.84
TNPsu 18	23.03	4	1.38	23.91**
TNPsu 25	17.70	8	0.52	14.80**
TNPsu 28	15.58	11	1.24	2.52
TNPsu 141	17.27	9	0.82	2.55
MS 1826	15.14	12	1.07	1.37
MS 4684	15.63	10	0.87	6.14**
PM 29	22.82	5	1.42	0.76
IPmr 886	26.94	1	1.27	1.46
CO (Samai) 4	25.05	3	0.93	0.36
OLM 203	19.69	7	0.60	0.23
Mean	20.68			
SE	1.27			

* Significant at 5 % level , ** Significant at 1% level of probability
 b_i - Regression coefficient S^2_{di} - Deviation from regression coefficient

Table 8. Stability of genotypes for different traits (Eberhart and Russell Model)

Character	Genotypes for all environments	Genotypes for favourable environments	Genotypes for unfavourable environments
Days to 50 % flowering	TNPsu 12	TNPsu 18	TNPsu 141, MS 1826, MS 4684
Plant height (cm)	-	MS 1826, MS 4684, OLM 203	TNPsu 18, TNPsu 28, TNPsu 141, CO(Samai)4
Basal tillers per plant	IPmr 886	TNPsu 28, MS 4684	OLM 203
Panicle length (cm)	TNPsu 12	TNPsu 17, MS 1826, OLM 203	-
Single plant grain yield (g)	TNPsu 17	IPmr 886, PM 29	OLM 203

Eberhart and Russell [4] described a genotype as an ideal one that would have a high mean value over a wide range of environments, a regression coefficient around unity, and non-significant deviation from the regression coefficient. Genotypes based on their stability for different traits under study were categorized and tabulated (Table 8.) under the following three main criteria.

- Genotypes with a high mean, $b_i = 1$ with non-significant δ^2_{di} would be suitable for general adaptation, *i.e.*, suitable for all environmental conditions and they should be considered as stable genotypes.
- Genotypes with a high mean, $b_i > 1$ with non-significant δ^2_{di} might be considered as below average in stability. Such genotypes would respond better to favourable environments but give poor yield in unfavourable environments. Hence, they

would be suitable for favourable environments.

- Genotypes with a high mean, $b_i < 1$ with non-significant δ^2_{di} would not respond favourably to improved environmental conditions and hence, they could be regarded as specifically adapted to poor or stressed environments.

From the stability analysis, it could be inferred that the genotypes, TNPsu 17 and CO (Samai)4 showed general adaptation to all environments for single plant grain yield which would be categorized in category 1. The genotypes such as IPmr 886 and PM 29 responded better under favourable environments, but failed to perform well under stress conditions and hence, they would be suitable for high input conditions and grouped in category 2. Among the genotypes evaluated only two genotypes OLM 203 and TNPsu 141 showed adaptation for poor or the

stressed environment which were grouped under category 3. Single plant grain yield is the most important trait in the development of littlemillet variety. Identification of an elite genotype with a high grain yield and average stability is of immense value. A perusal of stability parameters for single plant grain yield indicated that both linear and non-linear components of genotype x environment interaction were found to be significant in the current study. Similar results were reported by Sreedhar et al. [8] in rice.

The present study brought out the fact, none of the genotypes was stable for all the characters, and stability for one character was independent of the stability of other characters. Any generalization regarding the stability of genotype for all the traits is quite difficult as many genotypes had average stability to the environments for single plant grain yield and its component characters. Eberhart and Russel [4] suggested that, if the traits associated with high yield show stability, the selection of genotype only for yield could be effective. A non-significant correlation between the deviation from regression and mean performance or regression coefficient indicated that these stability parameters might be under the control of different genes located on a different chromosome [9]. Earlier, Grafius [10] and Bradshaw [11] also reported that plasticity in one or more component characters might allow stability in the final character. It is inferred that alleles that confer broader adaptation might be involved to achieve yield and stability across environments. It is also clear that most of the genotypes exhibited stability for yield component characters in all environments. This might be due to plasticity in their traits and phenotypic stability could be the result of their high plasticity.

4. CONCLUSION

Superior varieties were identified concerning their phenotypic stability. TNPsu 141 and TNPsu 28 showed high mean performance, above-average response and unpredictable stability for most of the characters. It is interesting to note that most of these varieties exhibited their superior performance for at least two yield contributing characters such as duration and basal tillers per plant, which revealed that stability is imparted by its component traits.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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