

APPLICATION OF REGRESSION MODEL TO IDENTIFY STABLE FINGER MILLET GENOTYPES FOR DAYS TO 50 PERCENT FLOWERING

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INTRODUCTION

The frequent occurrence of genotype-environment (GE) interaction effect on yield responses and its hindering effect on crop genetic advance have long been recognized. With reference to improvement for a target region, the part due to GE interaction can be either minimized through breeding for specific adaptation to sub-regions in which genotype responses are relatively uniform or taken into account by identifying widely adapted materials through selection for stable yield across a few test sites capable of maximizing GE interactions. Studies of genotype adaptation including a sizeable number of varieties and locations may provide useful information not only on datedness and stability of materials but also on similarities of locations for genotype adaptive responses.

Several methods have been developed to analyze and interpret genotype x environment interaction (Lin *et al.*, 1986; Peephole, 1998). These methods can be univariate (based on regression or variance analysis) or multivariate. The earliest approach was the linear regression analysis (Mooers, 1921; Yates and Cochran, 1938). The regression approach was popularized in the 1960s and 1970s (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966 and 1969; Tai, 1971). In this approach, regression graphs are used to predict adaptability of genotypes. Some other univariate stability parameters (based on variance analysis) are the environmental variance (Lin *et al.*, 1986), the Shukla stability variance (Shukla, 1972), Wricke's ecovalence (Wricke, 1962) and the coefficient of variability (Francis and Kanenberg, 1978). As multivariate, the additive main effects and multiplicative interaction (AMMI) model have been extensively applied in the statistical analysis of multi environment cultivar trials (Kempton, 1984; Gauch, 1988; Crossa *et al.*, 1990; Gauch and Zobel, 1997; Akcura *et al.*, 2009; Ilker *et al.*, 2011). In Tai's stability analysis (Tai, 1971), the interaction term is partitioned into two components: the linear response to environmental effects, which is measured by a statistic.

Genotype show wide fluctuation in their yield ability when grown in different environments. The capacity of a crop to perform well over a range of environmental conditions, Stability in productivity, therefore, is a major and important consideration for the plant breeder. Study of phenotypic stability parameters is useful to identify genotypes suitable for low, marginal, average and high yielding environments. A number of statistical tools are available to estimate stability parameters with varying degree of efficiency and limitations.

Realizing the importance and need for such a comprehensive study in finger millet, the present investigation was undertaken To study the Genotype and Environment Interaction and To identify stable genotype across the locations and

ABSTRACT

All India Co-ordinate Varietal trails conducted in different testing centers of India during Kharif season of 2006, 2007 and 2008, ten elite genotypes of finger millet (Ragi) tried in 9 locations with a simple randomized block design with three replications in each location. Genotype X Environment interactions were highly significant indicating the presence of variability among genotypes over different environments may be attributed to variations in temperature, relative humidity, soil type, sunshine hours etc. It was observed that the genotype PR202 performed uniformly well over all the locations and years ($\bar{X} = 73.95$, CV=7.06), where as HR374 showed greater variation ($\bar{X} = 65.07$, CV=12.89) for Days to 50 percent flowering. Among the locations Mandya (L5) had uniform performance over all the genotypes and years ($\bar{X} = 86.19$, CV=5.16), where as Coimbatore (L8) had greater variability ($\bar{X} = 73.42$, CV=11.62). None of the genotypes were well adapted to all environments, poorly adapted to all environments and specially adapted to unfavorable environment. The genotype GPU65 was specially adapted to favorable environment.

KEY WORDS

Stability
Regression
Pooled ANOVA
Significance and Maturity

Received : 05.02.2015

Revised : 04.03.2015

Accepted : 17.07.2015

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years for days to 50 percent flowering.

MATERIALS AND METHODS

The material for this study was taken from an evaluated data of finger millet genotypes Conducted under All India Co-ordinate Varietal trails in different testing centre’s in India , Project coordinating unit (Small Millets), All India Coordinated Small Millets Improvement Project, University of Agricultural Sciences, GKVK, Bangalore during the Kharif seasons of 2006,2007 and 2008.The original experimental set up included 10 genotypes of finger millet (Ragi) tried in 9 locations all over India under the co-ordinate scheme. The experimental design employed was a simple randomized block design with three replications in each location.

Yield Attributing characters considered were Plant Height (X1), Number of Productive Tillers/Plant (X2), Main Ear Length (X3), Number of Fingers per Ear (X4), Days to 50% Flowering (X5), Grain Yield (X6) and Fodder Yield (X7).

Genotypes considered in the present investigation were GPU65, GPU66, GPU67, OEB265, OEB211, VR888, OEB57, PR202, VL333 and HR374. Locations were Vizianagaram (L), Jagadapur (L2), Ranchi (L3), Bangalore (L4), Mandya (L5), Kolhapur (L6), Berhampur (L7), Coimbatore (L8) and Waghai (L9).

Pooled analysis of variance was done on grain yield that obtained from nine environments according to the Comstock and Moll (1963) Method. Three stability parameters were applied to assess stability performance of genotypes and to identify superior genotypes; b_i , the linear regression of the phenotypic values on environmental index (Finlay and Wilkinson, 1963), S^2_{di} , the deviation mean square from regression (Eberhart and Russell,1966). Finlay and Wilkinson’s joint regression model (1963) and Eberhart and Russell’s method (1966) were applied and the regression coefficients (b), determination coefficients of the regression equations (R²), and residual MS values (s_d^2) were calculated.

Pooled Two-way Analysis of Variance: 10 genotypes over 9 locations was subjected to pooled two way analysis of variance. This was done to find out the variation due to genotypes and environments to reveal the existence of genotype x environment interaction, if any. Only after ascertaining the significance of genotypic x environment interaction in the two way analysis of variance, the data was further subjected to stability analysis

The structure of pooled two-way analysis of variance

Source of variation	d.f.	MSS	Expected value of MSS	Cal F.
Environments	(e-1)	-	-	-
Genotypes	(g-1)	M1	$\sigma_e^2 + \sigma_{ge}^2 + e\sigma_g^2$	-
Genotypes x environment	(g-1) (e-1)	M2	$\sigma_e^2 + \sigma_{ge}^2$	-
Pooled error	M*	M3	σ_e^2	-

*Degrees of freedom pooled over environments

MSS due to Genotypes x Environment/MSS due pooled error = Calculated F

If Calculated F is greater than Table F values at corresponding to level of significance, then GXE is significantly different.

Eberhart and Russell Model

The stability model proposed by Eberhart and Russell (1966) was adopted to analyze the data over nine environments. The model involves the estimation of three stability parameters like mean (\bar{y}), regression coefficient (b_i) and deviation from regression (S^2_{di}), which is defined by the following mathematical formula

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Where,

Y_{ij} - Mean of the ith genotype at the jth environment

(i = 1..... 10, j = 1..... 9)

μ_i : The mean of ith genotype over all the environments

β_i : The regression coefficient that measures the response of ith genotype to varying environment

δ_{ij} : The deviation from regression of the ith genotype of jth environment and

I_j : jth environmental index obtained by subtracting the regression of the ith genotype grand mean from the mean of all genotype at jth environment Stability parameters

The mean (μ_i), the regression coefficient (b_i) and mean square deviation from linear regression line (S^2_{di}) are the three stability parameters proposed by Eberhart and Russell (1966) in their stability model. These parameters were computed by using the following formula

$$\mu_i \text{ (mean)} = \frac{\sum_j Y_{ij}}{n} \text{ b}_i \text{ (regression coefficient)} = \frac{\sum_j Y_{ij}}{\sum_j I_j^2}$$

$$S^2_{di} \text{ (deviation from the regression coefficient)} = \frac{\delta_{e}^2}{r} - \frac{\sum_j \delta_{ij}^2}{n-2}$$

Where, $\frac{\delta_e^2}{r}$ - Mean square for (estimate of) pooled error, n - Number of environments

Y_{ij} : Performance of ith genotype in jth environment

$\sum_j \delta_{ij}^2$: Sum of squares of deviations from the regression

$$\text{line } I_j = \frac{\sum_j Y_{ij}}{v} - \frac{\sum_i Y_{ij}}{nv}$$

I_j - Environmental index (i.e., environmental mean - grand mean)

Where, n: Number of environments, v: Number of genotypes with $\sum_j I_j = 0$

The total variation is partitioned into genotypes, environment, environment (linear), genotype x environment (linear), pooled deviation and pooled error.

ANOVA for stability based on Eberhart and Russell model

Source	d.f.	M.S.S.	F test
Genotype (V)	(v-1)	MS1	MS1/ MS3
Environment (E)	v (n-1)		
Environment (E) (linear)	1		
Genotype x Environment(G x E) (linear)	(v-1)	MS2	MS2/MS3
Pooled deviations	v (n-2)	MS3	
Pooled error	n (r-1) (v-1)	Me	
Total	(nv-1)		

Where,

n: Number of environments

v: Number of genotypes

r: Number of replications

F test

(a) To test the significance of the differences among the genotypic means, the 'F' test is given by

$$F = MS1 / MS3$$

Where,

MS1: Mean sum of squares of varieties

MS3: Mean sum of squares of pooled deviation

(b) To test individual from linear regression, the formula is as follows,

$$F = \frac{1}{M_e} \left[\frac{\sum \delta_{ij}^2}{n-2} \right] \sim F_{[1, n(r-1)(v-1)]df}$$

Where,

n - Number of environments

$\sum j d_{ij}^2$ - Sum of squares of deviations from the regression line

Me - Pooled error

(c) To test the hybrids/varieties not differ for their regression on the environmental index, the appropriate' test is,

$$t = \frac{\hat{b}_1 - 1}{SE(b)}$$

t = t-distribution with 1 df

$$SE(b) = \left(\frac{\sum Y^2 - \{(\sum Y)^2 / n\} - b^2 \sum (X - \bar{X})^2}{(n-2) \sum (X - \bar{X})^2} \right)^{\frac{1}{2}}$$

Y : Variable or Character

X : Environmental index

n : Number of environments

\bar{X} : Mean performance of the genotype over the environment

A joint consideration of the three parameters that is,

The mean performance of the genotype over the environment (\bar{X})

The regression coefficient (b_1) and

The deviatîon from linear regression (S^2_d) is used to define stability of a genotype

The estimate of deviations from regression (S^2_d) suggests the degree of reliance that should be put to linear regression in interpretation of the data. If these values are significantly deviating from zero, the expected phenotype cannot be predicted satisfactorily. When the deviations (S^2_d) are not significant the conclusion may be drawn by the joint consideration of mean yield and the regression coefficient (b_1) values as below

Regression coefficient	Mean yield	Stability	Remarks
$\hat{b} = 1$	High	Average	Well adapted to all environments
$\hat{b} = 1$	Low	Average	Poorly adapted to all environments
$\hat{b} < 1$	High	Below average	Specially adapted to favorable environments
$\hat{b} > 1$	High	Below average	Specially adapted to unfavorable environments

RESULTS AND DISCUSSION

It is a known fact that the genotypes performing well under a particular environment may or may not perform well over other environments due to genotype-environment interactions (G X E). A genotype with low G X E interactions will have high yielding cultivar, if care is not taken to select for both yield and stability of performance, one may end-up with a high yielding genotype that is suitable only for a particular environment. It therefore necessitates the development of variety with wide adaptability. To assess the performance of genotypes under different environment, basic pooled Two-way ANOVA is carried out as follows

Pooled Analysis of Variance combined over the years (table1) revealed that the mean sum of square (MSS) due to genotype X environment interactions were highly significant indicating the presence of variability for Days to 50% Flowering, the variability among genotypes over different environments may be attributed to variations in temperature, relative humidity, soil type, sunshine hours etc.

Performance of Genotypes in different locations over years for Days to 50% Flowering is presented in table 2. It was observed that the genotype PR202 performed uniformly well over all the locations and years ($\bar{X} = 73.95$, CV=7.06), where as HR374 showed greater variation in Days to 50% Flowering over all locations and years ($\bar{X} = 65.07$, CV= 12.89).

Among the locations it was observed that Mandya (L5) showed uniform Days to 50% Flowering over all the genotypes and years (=86.19, CV= 5.16), where as Coimbatore (L8) showed greater variability with respect to genotypes (=73.42, CV=11.62) as presented in Table 2.

The important variations such as Varieties or genotypes, Environment + (Varieties X Environment), Environment (linear) and Pooled Deviation among the varieties are statistically significant at 1%.which are considered to be important for stability analysis (Table 3).

Over the year the genotypes GPU66, GPU67, OEB265,

Table 1: Pooled Two-way Analysis of Variance over years for Days to 50 percent flowering

Source	df	Sum of square	Mean Sum of square	F
Genotypes	9	5517.38	613.04	60.16**
Environments	8	17282.67	2160.33	212.00**
G X E	72	11262.15	156.42	15.35**
Error	180	1834.68	10.19	
Total	269	35896.89		

Table 2: Performance of Genotypes in different locations over years for Days to 50% flowering

Genotypes	L1	L2	L3	L4	L5	L6	L7	L8	L9	Mean	CV (%)
GPU65	83.77	69.73	78.57	75.00	91.00	88.78	78.88	79.58	71.00	79.61	9.16
GPU66	82.10	69.77	81.31	74.57	81.88	88.00	75.22	76.70	67.56	77.47	8.39
GPU67	83.00	70.63	76.86	71.43	84.79	86.00	74.44	75.32	70.33	76.99	8.00
OEB265	81.63	68.10	74.77	68.78	92.77	87.12	76.00	76.44	68.22	77.09	11.26
OEB211	78.30	66.00	73.00	67.22	89.90	80.10	74.79	73.21	65.01	74.16	10.67
VR888	84.40	71.97	75.43	69.67	88.68	85.55	74.10	83.01	68.89	77.98	9.59
OEB57	80.77	70.53	73.56	66.89	87.68	83.22	73.90	81.32	67.67	76.19	9.65
PR202	79.87	71.07	75.21	67.79	84.43	72.77	73.32	70.65	70.43	73.95	7.06
VL333	70.73	60.77	59.09	61.23	80.57	79.88	67.67	61.67	62.57	67.13	12.32
HR374	66.20	56.20	64.08	60.01	80.33	76.12	66.04	56.30	60.22	65.07	12.89
Mean	79.03	67.27	73.20	68.26	86.19	82.75	73.43	73.42	67.20	74.56	0.00
CV (%)	7.56	7.64	9.13	7.21	5.16	6.50	5.19	11.62	5.29	7.56	0.00

Table 3: ANOVA for Eberhart and Russell model

Sources of Variation	DF	SSQ	MSQ	F
Varieties	9	2363	262.54	31.51**
Env. +(v x E)	80	7841	98.01	11.76**
Environment (linear)	1	5510	5510.36	661.50**
Varieties X Env. (linear)	9	68.1	7.56	0.23
Pooled Deviation	70	2264	32.32	3.87**
Variety 1	7	37.8	5.4	
Variety 2	7	57.6	8.23	
Variety 3	7	83.2	11.88	
Variety 4	7	5.69	0.81	
Variety 5	7	27.3	3.89	
Variety 6	7	251	35.81	
Variety 7	7	554	79.13	
Variety 8	7	37.2	5.32	
Variety 9	7	305	43.52	
Variety 10	7	635	90.68	
Pooled Error	180	1500	8.33	
Total	89	10204	114.65	

** Significance at 1 percent

Table 4: Stability Parameters of different models over years for Days to 50 Percent flowering

Genotypes	Eberhart And Russells		
	Mean	b_1	S^2_d
GPU65	79.46	0.75	10.13
GPU66	74.62	1.09	51.42*
GPU67	69.27	1.74	42.57*
OEB265	72.19	1.53	55.44*
OEB211	71.58	1.11	41.56*
VR888	78.00	0.73	15.86*
OEB57	76.22	0.73	13.84*
PR202	69.38	0.58	135.64*
VL333	67.14	0.83	17.61*
HR374	64.89	0.90	14.33*
Mean	72.27		

OEB211, VR888, OEB57, PR202, VL333 and HR374 are significant with respect to deviation from their respective regressions and GPU65 is non significant for Days to 50 % flowering (Table 4)

Genotype X Environment interactions were highly significant indicating the presence of variability among genotypes over different environments may be attributed to variations in temperature, relative humidity, soil type, sunshine hours etc. For Days to 50 Percent flowering, none of the genotypes were

well adapted to all environments as well as poorly adapted to all environments. The genotype GPU65 was specially adapted to favorable environment. None of the genotypes were specially adapted to unfavorable environment.

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