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Assessment of Sugarcane Varieties for Their Stability and Yield Potential in Fiji

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Abstract

The Sugar Research Institute of Fiji breeds and produces new varieties of sugarcane for the Fiji sugar industry for commercial production. The development of sugar cane varieties that show superior performance in different environments is a major challenge for breeders due to the response of genotypes across environments. This study was to evaluate the relative performance the genotypes during breeding program and identify promising ones that could be released for cultivation. Thus, an investigation was carried out to determine the magnitude of Genotype Environment interactions and the stability analysis of the genotypes cultivated in Fiji. Seventeen genotypes including three commercial varieties were evaluated in five locations using a randomized block design with three replications. The pooled analysis of variance carried out for the effect of environments, genotypes, and their interactions. The stability analysis was also performed using the Eberhart & Russell's (1966) model. Further, a cluster analysis was proposed for identifying the similar and stable genotypes. The results showed that there were highly significant ($p < 0.001$) variations among the genotypes (G), environments (E) and GE interactions. Two genotypes LF82-2122 and LF60-3917 had higher yield and stability statistics for the two most important traits: cane and sugar yields. Thus, the genotypes can be recommended for adoption and cultivation on all soil types in Fiji.

1. Introduction

Sugarcane is one of the most important agricultural crops planted on both the main islands (Viti Levu and Vanua Levu) of Fiji and has been the backbone of Fiji's economy for most of the 19th and 20th centuries. Sugarcane was introduced in the late 1870's and the revenue generated through the sugar industry has dominated Fiji's commercial agricultural sector and contributed significantly to the Fijian economy and continues to do so as a major foreign exchange earner (Narayan and Prasad, 2003, page 14).

The quest for new sugarcane varieties is paramount for the success of any breeding program and sustainability of the sugar industry. New sugarcane varieties are needed in Fiji due to widespread cultivation of Mana, which is a mid-late season maturing variety that contributes approximately 65% of the total cane production. Commercial varieties differ substantially from one another and they have certain characteristics that distinguish them. A commercial cane variety is selected on its ability to produce sucrose, its resistance to pests and diseases and its ratooning ability. While other characteristics may not influence the selection procedure to any great extent, they may influence a grower's choice of variety. It is desirable to grow better varieties that produce more cane and higher sugar yield so that proper and effective varietals scheduling can be practiced to provide quality cane to factories during the crushing period. Thus, continuous efforts are being made to develop, identify, evaluate, and release superior sugarcane varieties suitable for varying soil and climatic conditions of Fiji (Sugar Research Institute of Fiji, 2010).

In any plant-breeding programme, determining the genotype environment (GE) interactions is of major importance when testing newly developed varieties. The relative performance of genotype differs due to the difference in GE interactions in different environments. Many authors, such as Kennedy (1978), Galvez (1980), Tai et al. (1982), Kang and Miller (1984), Jackson and Hogarth (1992), Ceccarelli (1996), Rattey and Kimbeng (2001), Khan *et al*. (2002), Kimbeng *et al*. (2002, 2009), Chapman (2004), Ferreira *et al*. (2006), Queme *et al*. (2010), Tiwari *et al*. (2011), Chen *et al*. (2012), Luo *et al*. (2015), Rea *et al*. (2015), Pereira *et al*. (2017) etc., reported significant genotype-environment interactions.

The GE interactions are important sources of variation in any crop and the term stability can be used to characterize the performance of a genotype in different environment. According to Sabaghnia *et al*. (2006) a genotype that shows a relatively constant yield with a minimal variance for yield across different environments over several seasons is considered stable. Pandey et al. (1981) reported that merely the productivity of a

genotype in favourable environments does not indicate its adaptability but the stable performance of the genotype in diverse environments is a true evaluation of its potential for adoption. Thus, the analyses of adoptability and stability are extremely important for identification and recommendation of superior genotypes.

There are different methods for analysis of GE interactions and the stability of genotypes available in the literature. Among the techniques the most commonly used is a linear regression approach suggested by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Tai (1971); and a cluster analysis approach Abou-El-Fittouh *et al*. (1969), Mungomery et al. (1974) and Byth *et al*. (1976).

The secondary variety adaptation trials have been a major component of the sugar cane breeding program in Fiji for many years and the magnitude of GE interactions have not been documented until now. Thus, this paper evaluates the relative performance of cane and sugar yields of genotypes and identifies the promising ones that could be released for commercial cultivation by sugarcane farmers of Fiji.

Depending on the goal and the desirable character under consideration, there are two different concepts of stability that exists, namely, the static concept of stability and the dynamic concept of stability. Both concepts of stability are valuable, but their application depends on the trait under consideration (Becker & Leon, 1988). In the static concept, genotypes with a minimum variance for yield across the different environments are considered stable. For cane and sugar yield, selection is focused on genotypes which are stable as well as high yielding. In the dynamic concept of stability, the response of a genotype to environments is predictable where genotypes with high mean yield will have the potential to respond to agronomic inputs or better environmental conditions. In this research, the stability analysis of genotypes was carried out by employing the Eberhart and Russell (1966) model and a cluster analysis that use the mean yield and the standard deviation.

2. Materials and Method

Seventeen sugarcane genotypes including 3 commercially cultivated were planted at five different locations to achieve the following objectives:

i) Determine the nature of GE interactions,
ii) Study the adaptation of the sugarcane genotypes using stability parameters and
iii) Identify potential genotypes based on yield potential.

2.1. Experiment sites

The five different locations used in the trial are Labasa, Legalega, Penang, Rarawai and Waqadra. The trial locations represented the different soil types of Fiji's sugar belt. Soil samples were taken from each site prior to planting and analysed to determine fertilizer recommendation to obtain optimum cane and sugar yield. The results on the soil analyses for each location are shown in Table 1.

2.2. Sugarcane cultivars used in the study

Seventeen sugarcane genotypes including 3 commercially cultivated varieties were planted in replicated secondary variety adaptation trials in 2010. The commercial genotypes Aiwa, Mana and Mali were used for comparative purposes, which are early, mid and late season maturing varieties respectively. Mana is the dominant variety grown in Fiji and accounts for approximately 70% of the total production.

2.3. Experimental Design Used in the Study

The trials were planted in a randomised complete block design (RCBD) during April-May of 2010. Each trial had three replications and the plot size was six rows by eight metres long. The between row spacing was 1.40m. The genotypes were placed randomly in the blocks and each block consisted of a total of 17 treatments (including 3 commercial varieties). The trials received well-distributed rainfall, which contributed to a healthy cane growth and were harvested between 14-15 months of age. The inner four rows were harvested for measuring yield tonnes cane per hectare. An 18 stalk sample was randomly taken from each plot and replication, and shredded. The shredded sample was thoroughly mixed and used for determining the biochemical parameters brix, fibre, %pocs and purity that are used in the determination of the sucrose yield for the plant crop. The method used to determine the biochemical parameters are that used by Sugar Research Institute of Fiji, Central Laboratory. The formula used to calculate the potential sucrose yield (tsh) was as follows:

$$\text{tsh} = \frac{\text{tch} \times \%\text{POCS}}{100}$$

Table 1. Soil analysis data for trial sites.

Location	Name of Location	pH	P (ppm)	K (ppm)	Ca (ppm)	Mg (ppm)	Soil Type
1	Labasa	6.5	21	95	521	49	F. L
2	Legalega	6.4	122	523	4077	781	A
3	Penang	5.3	71	322	1496	400	A
4	Rarawai	6.4	120	276	6801	1880	G
5	Waqadra	5.9	8	320	4398	896	A

Note F.L – Ferruginous latosols, A- Alluvial, G- Gley

2.4. Data analysis

The data were analysed to identify the effect of genotype, environment and their interaction by using analysis of variance, Post-Hoc test and pooled analysis of variance. The stability analysis was performed using Eberhart and Russell's (1966) model and a hierarchical cluster analysis.

2.4.1. Analysis of Variance (ANOVA)

Initially, an analysis of variance (ANOVA) test was carried out to test the difference of the mean of genotypes at each environment. The model of the test is:

$$Y_{ij} = \mu + G_i + \varepsilon_{ij} \quad (1)$$

where, Y_{ij} is the observation $j;(j=1,2,\ldots,n)$ receiving genotype $i;(i=1,2,\ldots,k)$, μ is the overall mean of the genotypes and ε_{ij} is the error terms that are normally distributed with mean zero and a constant variance.

2.4.2. Post-Hoc test for Multiple Comparison

For the multiple comparison, the Scheffe Test was used as a post-hoc test. The test corrects alpha for simple and complex mean comparisons. The formula to the test is given by:

$$\sqrt{(k-1)F_{\alpha}(k-1,\nu)MSE\left(1/n_i - 1/n_j\right)} \quad (2)$$

where, $F_{\alpha}(k-1,\nu)$ is the critical value of F with α level of significance, k is the number of genotypes, ν is the degrees of freedom and MSE is the mean square error.

2.4.3. Pooled analysis of variance

To study the genotype environment interactions effect, an analysis of variance of the combined data was used:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + \varepsilon_{ij} \quad (3)$$

where, Y_{ij} is the mean yield of the ith genotype in the jth environment; μ is the general mean; G_i, E_j and GE_{ij} represent the effect of the genotype-environment, and ε_{ij} is the average of the random errors associated with the *r*th plot that receives the *i*th genotype in the *j*th environment. The non-additivity interaction as defined in (3) implies that the expected value of Y_{ij} depends not only on the levels of G and E but also on the particular combination of levels of G and E.

2.4.4. Stability analysis using Eberhart and Russell's (1966) model

The stability parameters were calculated by Eberhart and Russell's (1966) joint regression model:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij} \quad (4)$$

where, Y_{ij} is the mean of the *i*th variety at the *j*th environment, μ_i is the mean of the *i*th variety over all environments, β_i is the regression coefficient that measures the response of the *i*th variety to varying environments, I_j is the environmental index obtained as the mean of all varieties at the *j*th environment minus the grand mean and δ_{ij} is the deviation from regression of the *i*th variety at the *j*th environment.

The stability parameters regression coefficient and mean square deviations were estimated as described below.

i) The regression coefficient $\left(\beta_i\right)$:

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2} \quad (5)$$

ii) The mean square deviations $\left(\delta^2 d_i\right)$:

$$S^2 d_i = \frac{\sum_j \delta_{ij}^2}{s} - \frac{e}{r} \quad (6)$$

Where, *t* = number of varieties, *s* = number of locations, *e* = estimate of pooled error and the environmental index (I_j) is computed as:

$$I_j = \frac{\sum_j Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{ts}. \quad (7)$$

Eberhart and Russell defined a stable genotype as the one which produced high mean yield with regression coefficient (b_i) around unity and deviation from regression residual variance $(S^2 d_i)$ near to zero. The estimate of deviations from regressions 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 genotype cannot be predicted confidently or reliably. When deviations are not significant, the conclusion may be drawn by jointly considering the mean yield and regression values proposed by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) that are summarised in Table 2.

Table 2. Regression values, stability type in relation to mean yield.

Regression	Stability	Mean yield	Remark
β_i **=1**	Average	High	Well adapted to all environments
β_i **=1**	Average	Low	Poorly adapted to all environments
β_i **>1**	Below average	High	Specifically adapted to favourable environments
β_i **<1**	Above average	High	Specifically adapted to unfavourable environments

2.4.5 Stability analysis using hierarchical cluster analysis

Often, the Eberhart and Russell's model provides contrasting stability parameters that complicates the selection of the superior genotypes. Moreover, when the fitted lines were strongly influenced by some data points, the linear regression approach to analysing genotype-environment interaction cannot be regarded as trustworthy (Westcott, 1986). In such situation, a hierarchical cluster analysis approach is proposed for analysing the stability and adoptability of genotypes using variance-standardized squared Euclidean distance as dissimilarity measure. Comprehensive reviews of the applications of linear regression and cluster analysis can be found in Lin et al. (1986, 1988) and Westcott (1986).

It is considered that a genotype be stable (i) if its among-environment standard deviation is small and (ii) if its mean response is high. A set of dissimilarities for the 17 genotypes were clustered based on their mean

responses and standard deviations. Data were analysed in R software using the function hclust with the method="ward" option produces results that correspond to a Ward (1963) method. It is a nonparametric approach and the advantage is that the response is not expected to be linear to environment as it is assumed in regression based stability analysis.

3. Results

The study was carried out for one season only and the results show that the sugarcane genotypes performed differently in terms of cane yield and sugar yield across locations indicating GE interactions were present. Table 3 presents the average yield (tonnes per hectare) and the standard deviations of cane and sugar of the 17 genotypes (Genotypes 1-3 are commercial varieties and Genotypes 4-17 are test varieties) using 3 replications at 5 locations used in the study.

The average yields for both the cane and sugar due to each genotype are shown in Mean plots in Figure 1. From the Table 3 and Figure 1(a), it has been observed that the higher average cane yield was found in Genotype 2 (Mean = 121.47, SD = 7.03) and Genotype 10 (Mean = 126.73, SD = 10.32). Whereas, the minimum yield was found in Genotype 13 (Mean = 66.47, SD = 8.67) and Genotype 16 (Mean = 67.67, SD = 6.37). The ANOVA test revealed that there is significant difference in the average yields of the genotype with $F(16,232) = 63.001$ and $p < 0.001$. This implies that the effects of genotypes on the yields are not all same. Scheffe's test for multiple comparison was also performed, which reveals the significant difference between the genotypes, except the genotypes that fall within same category as shown in Table 6.

Similarly, from the Table 3 and Figure 1(b) for the sugar yield, the higher average sugar yield was found in Genotype 10 (Mean = 16.54, SD = 2.33) followed by Genotype 2 (Mean = 13.89, SD = 1.79) and Genotype 11 (Mean = 12.42, SD = 1.20). The lower yield was found in Genotypes 13-17. The ANOVA test revealed that the main effect of variety on yield was statistically significant, $F(16,170) = 55.497$ and $p < 0.001$. This implies that the effects of genotypes on the yields are not all same. The multiple comparison test reveals that there is significant difference between the genotypes, except

the genotypes that fall within same category as shown in Table 7.

The standard deviations calculated for the different traits provide a basis for assessing the adaptation of potential genotypes to the different environments. Genotypes with low standard deviation are adaptable to a wider range of environments as compared to varieties with standard deviation that are adaptable to specific environments. The standard deviations calculated for cane yields and sugar yields are presented in Table 3. The standard deviation for cane yield ranged from 5.57 to 15.44. The broad interval range of the standard deviation for cane yield indicated that the environment had an effect on the cane yields of all the genotypes. The standard deviation for sugar yield ranged from 1.04 to 2.33. Normally, if the variance and mean yield of a genotype is low, then this indicates that the genotype has low yielding potential across all locations it is tested on. The Genotype 16 had the low means 67.67 and 7.53 and the low standard deviation values 6.37 and 1.17 for cane and sugar yield respectively and falls in this category. If the standard deviation is high and mean yield is also high for a genotype, then that genotype may be suited to a specific environment. From the analysis of the descriptive statistics presented in the table, the Genotypes 2, 10 and 11 are found to be higher yielding varieties with lower to moderate standard deviation with respect to both cane and sugar yields, and thus far can be identified as the potential genotypes across the locations.

3.1. Cane and sugar yield at different locations

The Table 4 shows the average cane yield and sugar yield and their standard deviations in five locations.

The results reveals that the higher average cane yield was found at Labasa (Mean = 88.76, SD = 19.95) followed by Penang (Mean = 84.02, SD = 22.71). Whereas, the minimum yield was found at Legalega (Mean = 80.80, SD = 20.33) and Waqadra (Mean = 80.63, SD = 18.36). The ANOVA test showed that the location effects are significant, $F(4,170) = 8.377$ and $p < 0.001$.

Similarly, for sugar yield the higher average yield was found at Labasa (Mean = 10.84, SD = 3.12) followed by Legalega (Mean = 9.57, SD = 2.85). The lowest yield was found at Waqadra (Mean = 8.12, SD = 2.50). The ANOVA test showed that the location effects are significant, $F(4,170) = 29.305$ and $p < 0.001$.

3.2. Pooled Analysis of Variance

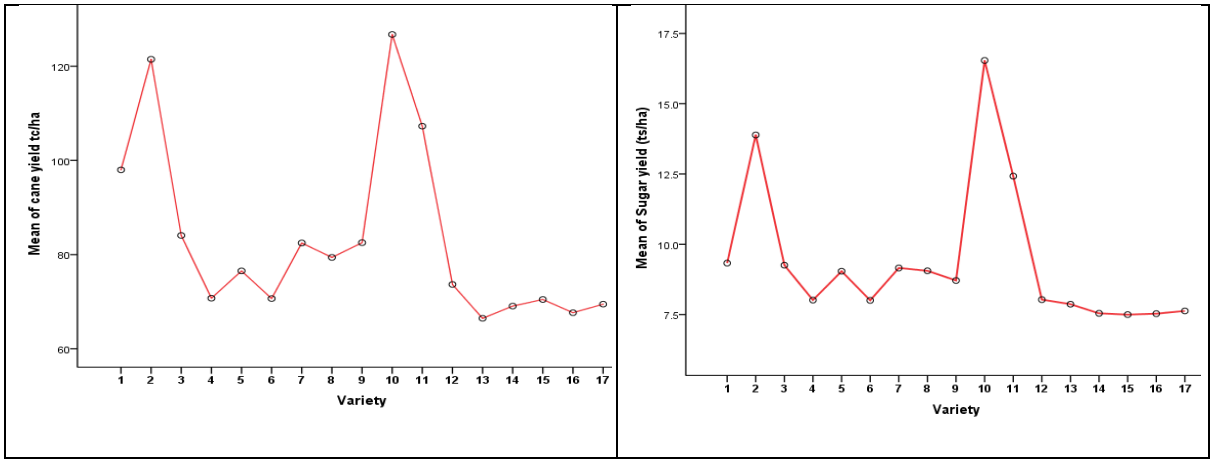
The analysis of variance of the pooled data for the cane yield and sugar yield from the five locations are presented in Table 5.

From Table 5, the pooled analysis of variance revealed that genotypes, environments and GxE interactions were significant for both cane yield and sugar yield. The relatively high mean sum squares indicated the significant difference. This implies that different genotypes and locations have different effect on both yields. The significance of GxE interactions implies that different environments have different effect on different genotypes. The nature of this interaction on cane yield and sugar yield is illustrated in Figure 2(a) and 2(b) respectively.

3.2.1. Multiple comparison test for genotypes in cane yield

To identify specifically which genotype differs from others for cane yield, a Post-Hoc test for multiple comparison studies was conducted. As the Levene's test on the assumption of homogeneity was significant, Games-Howell test when equal variances cannot be assumed were used. The test results reveal the genotypes can be classified into five categories of homogeneous genotypes within which there is no significant difference as shown in Table 6.

Table 6 reveals that the Genotypes 2 (Mean = 121.47, SD = 7.03) and 10 (Mean = 126.73, SD = 10.32) were having similar genotype that produced maximum average yields. The Genotypes 2 (Mean = 121.47, SD = 7.03) and 11 (Mean = 107.27, SD = 5.57) fall in next category that were found to be similar and produced higher average yields and so on. Whereas, the Genotypes 3-9 and 12-17 can be classified as another category that have effect to produce lower average yields.



(a) **(b)**

Figure 1. Mean plot for (a) cane yield and (b) sugar yield of varieties (genotypes)

Table 3. Mean and standard deviation for the cane yield and sugar yield among 17 genotypes.

		Cane yield (t/ha)		Sugar yield (t/ha)	
Genotype	**Name**	**Mean**	**Std. Deviation**	**Mean**	**Std. Deviation**
1	LF57-5104	98.00	5.79	9.33	1.26
2	LF60-3917	121.47	7.03	13.89	1.79
3	LF73-229	84.07	15.44	9.25	2.00
4	LF79-640	70.73	9.65	8.01	1.87
5	LF79-1052	76.53	12.58	9.04	2.19
6	LF79-2964	70.67	9.63	8.00	1.40
7	LF80-127	82.47	9.61	9.16	1.72
8	LF82-1577	79.40	12.47	9.05	1.87
9	LF82-2031	82.53	10.78	8.71	2.17
10	LF82-2122	126.73	10.32	16.54	2.33
11	LF82-2244	107.27	5.57	12.42	1.20
12	LF82-2715	73.67	9.25	8.03	1.98
13	LF83-998	66.47	8.67	7.87	1.66
14	LF83-1058	69.07	8.36	7.54	1.04
15	LF83-2189	70.47	8.82	7.50	1.47
16	LF84-252	67.67	6.37	7.53	1.17
17	LF84-8077	69.47	8.30	7.63	1.52
Average		83.33	20.58	9.38	2.98

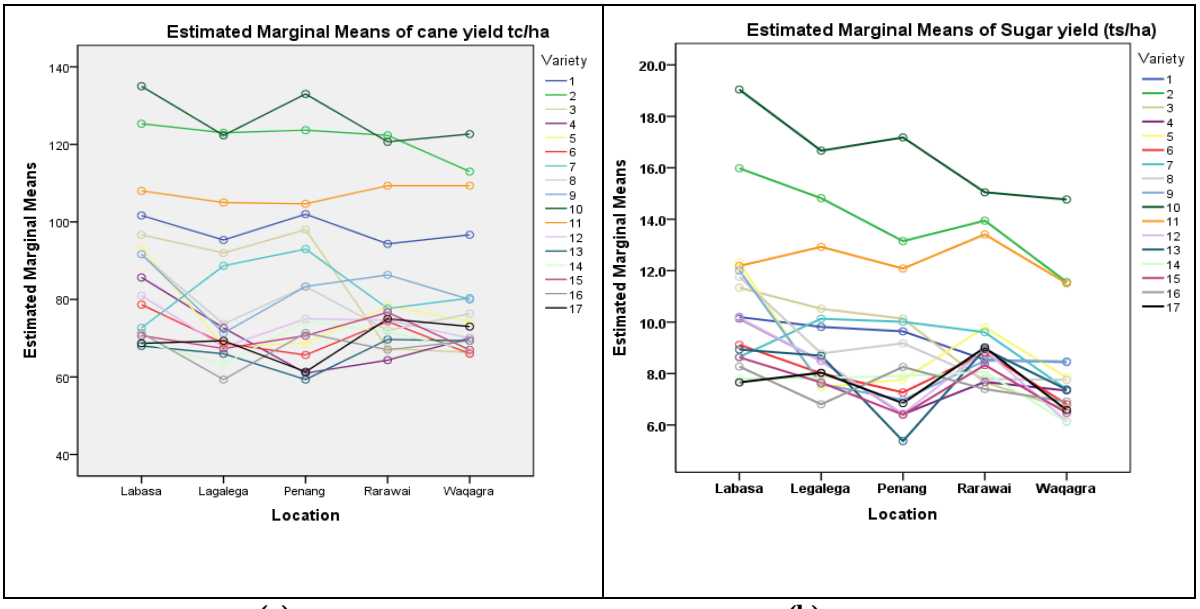
Table 4. Mean and standard deviation for the cane yield and sugar yield in different location.

Location	Name of Location	Cane yield (t/ha)		Sugar yield (t/ha)	
		Mean	Std. Deviation	Mean	Std. Deviation
1	Labasa	88.76	19.95	10.84	3.12
2	Legalega	80.80	20.33	9.57	2.85
3	Penang	84.02	22.71	8.88	3.20
4	Rarawai	82.45	21.04	9.50	2.58
5	Waqadra	80.63	18.36	8.12	2.50

Table 5. ANOVA of the interactions among the pooled cane and sugar yields in 17 varieties tested at 5 environments (locations).

Source	d.f.	Mean sum of squares	
		Cane yield	Sugar yield
Genotypes (G)	16	1779.13***	32.157***
Environments(E)	4	566.98***	50.94***
G x E	64	131.44***	3.28**
E + (G x E)	68	52.35	2.026
E (linear)	1	755.97***	67.922***
G x E(linear)	16	52.51	1.003
Pooled deviation	51	38.50	1.055
Pooled error	170	17.43	0.512

** Significant at 0.01 level and *** Significant at 0.001 level



(a) **(b)**

Figure 2. The effect of variety and location on (a) cane yield and (b) sugar yield.

Table 6. Group of homogeneous genotypes for cane yield.

Genotypes (Ordered)	Category				
	A	**B**	**C**	**D**	**E**
13					66.47
16					67.67
14					69.07
17					69.47
15					70.47
6					70.67
4					70.73
12					73.67
5					76.53
8					79.40
7				82.47	82.47
9				82.53	82.53
3				84.07	84.07
1			98.00	98.00	
11		107.27	107.27		
2	121.47	121.47			
10	126.73				

A Post-Hoc test for multiple comparison studies was also conducted to identify which location differs from others in yielding the sugar cane. It reveals that the largest cane yield is produced at Labasa followed by Penang. However, there is no significant difference in the yielding at other three locations.

3.2.2 Multiple comparison test for genotypes in sugar yield

For the pairwise comparisons between the genotypes with respect to sugar yield, Games-Howell test when equal variances cannot be assumed were used as discussed above. The test reveals the genotypes can be grouped into 4 categories of similar genotypes as shown in Table 7.

The multiple comparisons test between the locations reveals that the largest sugar yield is produced at Labasa followed by Legalega and Rarawai. However, there is no significant difference in the yielding between Legalega and Rarawai.

Thus, the analyses carried out above reveal that the Genotypes 2 and 10 perform better in terms of both cane yield and sugar yield over all the environments.

3.3. Stability analysis using Eberhart and Russell (1966) model

Since the GE interactions were highly significant for both traits, the data were further processed for estimating the stability parameters using Eberhart and Russell (1966) model given in (4).

The three stability parameters viz., mean, regression coefficient (β_i) using (5) and mean square deviation $(\delta^2 d_i)$ from regression line using (6) were estimated by using the Eberhart and Russell's model for cane yield and sugar yield. The results are presented in Table 8.

3.3.1. Stability analysis for cane yield

From Table 8, it is found that the Genotype 10 with a mean of 126.73 had the highest cane yield and Genotype 13 with a mean of 66.46 had the lowest yield. The average yield over all the environments was 83.33. The regression coefficient value (b_i) of the Genotypes 1, 2 and 10 were close to one and the mean yield of these genotypes were higher than the grand mean of all genotypes over all the environments. Based on the regression value relative to type of stability as described in Table 2, these genotypes should be specifically adapted to all environments. On the contrary the mean square deviation values ($S^2 d_i$) for Genotype 1 very low and significantly deviating from zero that implies the yield potential cannot be predicted reliably. The Genotype 11 had a very high mean yield with regression coefficient of 0.01, which indicates that this genotype can be well adapted to favourable environments but cannot be predicted for it's stability as $S^2 d_i$ is very low and significantly deviating from zero. The Genotypes 6 and 16 had regression coefficients close to one, which indicates that these genotypes should be well adapted to all environments but the mean of these varieties were much lower than the grand mean. The values of regression coefficients and the mean square deviations for other genotypes suggested for not adopting these genotypes.

3.3.2. Stability analysis for sugar yield

The stability parameters for sugar yield are presented in the last three columns in Table 8. The Genotype 10 with a mean of 16.54 had the highest yield and Genotype 15 with mean of 7.50 had the lowest yield. The average sugar yield over all the environments was 9.38.

The Genotypes 1, 3, 4, 6, 8, 9, 13-15 and 17 had a regression coefficient close to one which implies that these varieties should be well adapted to all environments but the average yields of these genotypes were lower than the grand mean of 9.38.

The regression coefficient of the Genotype 2 was greater than one and sugar yield higher than the grand mean. This variety should be adapted to favourable environments. The regression coefficient of the Genotype 11 was less than one and sugar yield higher than the grand mean. These varieties should be adapted to unfavourable environments.

The regression coefficient value of Genotype 10 was close to one and the yield of this genotype was on par and higher than the grand mean. This genotype can be well adapted to all environments.

Based on the standard deviation values the Genotype 16 was much close to zero but the yield of this genotype was 7.53, which was the second lowest and also lower than the overall mean. On the other hand, the yield of the Genotypes 5 and 7 were close to the overall mean but the regression coefficients were far away from one and the standard deviations were higher. Thus, these genotypes did not show yield stability for cane and sugar, and may not be well adapted to all environments.

3.4. Stability analysis using cluster analysis

3.4.1 Stability analysis based on cane yield

From the columns 3 and 4 in Table 3 and Table 6, one can see that the Genotype 10 is similar to the Genotype 2 with respect to the average cane yield but it has higher standard deviation, which implies that the Genotype 10 is less consistent. Similarly, there is not much difference in the consistency between the Genotype 1 and 11 as their standard deviations are almost same. However, the Genotype 11 produced higher average cane yield than the Genotype 1. Therefore, one may be interested to investigate which genotype is more stable with respect to both the average yield and the standard deviation. In this section, as discussed in Section 2 we propose a technique of stability analysis using Ward's Hierarchical cluster analysis method that determines the clusters of similar genotypes based on a set of dissimilarities in both averages and standard deviations. The Figure 3 shows the Dendrogram plot of five clusters within which the genotypes are stable.

Table 7. Group of similar genotypes for sugar yield.

Genotype	N	Category			
		1	**2**	**3**	**4**
15	15				7.50
16	15				7.53
14	15				7.54
17	15				7.63
13	15				7.87
6	15				8.00
4	15				8.01
12	15				8.03
9	15				8.71
5	15				9.04
8	15				9.05
7	15			9.16	9.16
3	15			9.25	9.25
1	15			9.33	9.33
11	15		12.42	12.42	
2	15	13.89	13.89		
10	15	16.54			

Table 8. Estimated regression coefficient (b_i) and mean square deviation (S^2d_i) for cane and sugar yields.

Genotype	Name	Cane yield (t/ha)			Sugar yield (t/ha)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	LF57-5104	98.00	0.82	-11.11	9.33	0.55	-0.12
2	LF60-3917	121.47	0.92	0.54	13.89	1.63	-0.36
3	LF73-229	84.07	2.71	209.08	9.25	1.49	1.89
4	LF79-640	70.73	1.74	57.83	8.01	1.20	0.17
5	LF79-1052	76.53	2.51	29.47	9.04	1.67	1.33
6	LF79-2964	70.67	1.22	1.98	8.00	0.90	-0.33
7	LF80-127	82.47	-1.16	52.47	9.16	0.33	1.08
8	LF82-1577	79.40	2.22	-3.81	9.05	1.33	0.67
9	LF82-2031	82.53	1.84	7.88	8.71	1.43	1.81
10	LF82-2122	126.73	1.72	-2.50	16.54	1.35	1.04
11	LF82-2244	107.27	0.01	-11.53	12.42	0.30	0.09
12	LF82-2715	73.67	1.46	-14.82	8.03	1.62	-0.15
13	LF83-998	66.47	-0.13	5.18	7.87	0.92	1.47
14	LF83-1058	69.07	0.47	2.04	7.54	0.53	-0.04
15	LF83-2189	70.47	0.29	0.32	7.50	0.91	-0.21
16	LF84-252	67.67	0.89	2.92	7.53	0.34	-0.02
17	LF84-8077	69.47	-0.54	13.79	7.63	0.50	0.39
Overall mean		83.33			9.38		

The figure reveals that the Genotypes 2 and 10 are similar in terms of stability as compared to the Genotypes 1 and 11. This implies that the Genotypes 2 and 10 are the potential varieties that can be predicted reliably and be adapted to all environments. It can be observed that the results found in cluster analysis are aligned with that of Eberhart and Russell's model of stability analysis discussed in Section 3.3.

3.4.2. Stability analysis based on sugar yield

From the columns 5 and 6 in Table 3 and Table 7, it can be seen that the Genotype 10 is similar to the Genotype 2 with respect to the average sugar yield but it has higher standard deviation, which implies that the genotype is less consistent. Similarly, there is not much difference in the average sugar yield between the Genotype 2 and 11 but the Genotype 2 is more inconsistence. Therefore, using the cluster analysis as discussed earlier we determine the clusters of similar genotypes. The Figure 4 shows the Dendrogram plot of 4 clusters within which the genotypes are similar and stable.

The figure reveals that the Genotype 10 is more stable as compared to the Genotypes 2 and 11. Thus, the Genotype 10 is the potential variety to be predicted reliably and can be adapted to all environments. The Eberhart and Russell's stability model discussed in Section 3.2 also revealed the similar results.

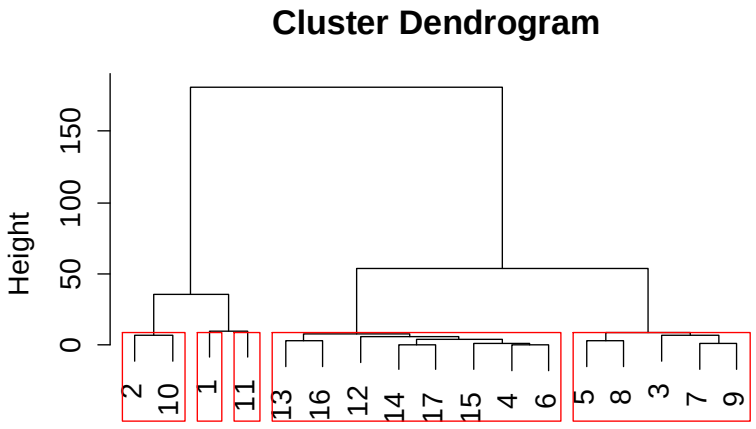


Figure 3. Clusters of stable genotypes for can yield.

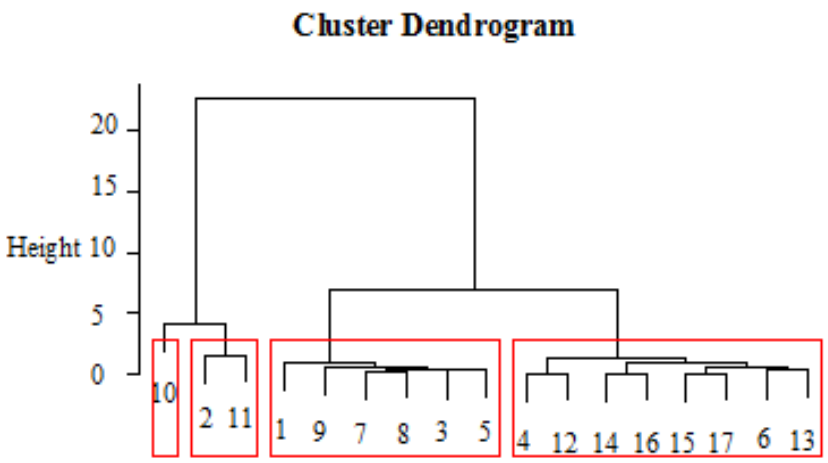


Figure 4. Clusters of stable genotypes for sugar yield.

4. Discussions

The yielding ability of sugarcane varieties varies when grown in different environments or climatic zones. In this paper, we present the results of an investigation to identify the stable genotype (s) over the five locations for yield and yield related traits in sugarcane.

The pooled analysis of variance revealed that the genotypes, environments, genotypes x environments were highly significant for cane and sugar yields. There were highly significant differences in the yields across all the locations. The yields of most of the varieties at Labasa were generally higher compared to the other locations, which is mainly due to the effect of the environment. Similar results were reported by Gilbert *et al*. (2006).

The study reveals that the two promising varieties LF82-2122 (Genotype 10), LF82-2244 (Genotype 11) and two commercials LF57-5104 ((Genotype 1) and LF60-3917 (Genotype 2) recorded higher yield at all the locations. The varieties LF82-2122 and LF60-3917 had significantly higher yields across all the locations and were adapted to all environmental conditions. Since cane and sugar yields are the most important traits and looking into the results on the performance of the genotypes on these traits, the two varieties LF82-2122 and LF60-3917 can be recommended for adoption as the two most superior promising varieties from this trial for cultivation in Fiji.

5. Conclusion

The purpose of this study was to evaluate the relative performance of promising sugar cane varieties across five locations that represented the different soil types and climatic conditions where cane is grown in Fiji and identify genotypes that could be widely adapted and provide stable yields under cultivation.

In this paper, we study the effect of GxE interactions that is accounted in most plant breeding program. We also assess the genotypes of sugarcane and determine the promising varieties that are more stable in several environmental conditions.

Pooled analysis of variance revealed significant differences among the genotypes for all the characters studied. GxE interactions were found to be highly significant for the yields. Stability analysis of the data was carried out by adopting the Eberhart and Russell (1966) model. A cluster analysis technique was also performed for identifying the variety, which is suitable for planting on all soil types.

The study revealed that two genotypes LF82-2122 and LF60-3917 proved to be most promising due to higher yield and stability statistics for both the traits: cane and sugar yields. This means that these two genotypes performed the best in the various locations, soil type and climatic conditions. Hence for breeding purposes these two genotypes can be used as promising parents.

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