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# Joint Regression Analysis of Some Quantitative Characters of $F_1$ Sugarcane Genotypes

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## ABSTRACT

To determine the magnitude of the genotype-environment (G × E) interaction and stability in sugarcane (S*accharum officinarum* L.), 10 randomly selected $F_1$ genotypes were evaluated for two years at three locations in the North-Western zone of Bangladesh. Genotypes were developed from the crosses of North Carolina Design-I at the Bangladesh Sugarcane Research Institute. A joint regression analysis of variance for all the characters showed highly significant genotypic (G) and environment (E) items and their interaction. In most cases, both linear and non-linear regression accounted for the G × E interaction and the heterogeneity of regression showed non-significance for all characters. The G × E interaction was due to the slopes of non-linear relationship. Significant remainder but non-significant heterogeneity items makes the situation complex; non-linear type of component like linkage, epistasis etc are played important role in this interaction. The regression analysis of stability showed that genotypes 'G1' and 'G3' for germination percentage, 'G1' and 'G2' for leaf length,; 'G5' for number of millable canes per clump, 'G6', 'G7' and 'G8' for leaf breadth, 'G2' and 'G5' for Brix % and 'G4' and 'G9' for cane yield per clump character were the stable genotypes. These might be considered as stable genotypes to the changing environments. Regarding non-significant deviation mean squares (DMS, or $\overline{S}^2d_i$) and higher or lower regression coefficient ($b_i$) values some of the genotypes for different characters were recommended for favourable environments or poorly adaptable to all environments. Other genotypes were unpredictable due to their significant DMS values.

**Keywords:** stability, genotype × environment interaction

## INTRODUCTION

The genotype × environment (G×E) interaction is a widely recognized phenomenon in sugarcane clonal selection trials (Kimbeng *et al*. 2002). It complicates selection decisions because when G × E interaction is present, the definition of an elite genotype becomes conditional on the environment under which the genotype is evaluated (Rattey and Kimbeng 2001). The consequence is that, for quantitatively inherited traits such as sugar yield, genotypic performance and the relative ranking of genotypes changes from one environment to the other. This rank changing makes it difficult for the breeders to decide the true genetic value of prospective genotypes and to select among them because gene expression of an individual may occur with the changes of environments. Sugarcane (*Saccharum officinarum* L.) breeders are aware about the differences of its cultivars for yield and quality which varies from region to region. G × E interactions are important sources of variation in any crop and the term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. The phenotypic expression by the environment was first recognized by Johannsen (1909) while working with dwarf bean (*Phaseolus vulgaris* L.). He reported that heritable and non-heritable differences were jointly responsible for the variation in seed weight of beans and were of the same order of magnitude in effect. The different analyses of continuous variation over a number of years on many plant and animal species revealed the combination of heritable and non-heritable agencies in the determination of continuous variation. For the study of G × E interaction, joint regression analysis, a form of the analysis of variance has been used widely. The procedures and applications of joint regression analysis were reviewed by Freeman (1973) and Hill (1975). The effectiveness of the analysis in resolving the differences in genotypic response is related to the degree of linearity of response. Regarding these the present experiment was under taken to evaluate the magnitude of G × E interaction for nine agronomical characters of ten sugarcane genotypes to detect stable genotypes for different climatic conditions in Bangladesh.

## MATERIALS AND METHODS

The 15 sugarcane varieties / genotypes including 5 males [(I 149-00 (released as Isd 40), Isd 35, I 101-66, Co 642 and I 17-01] and 10 females [Isd 31, Isd 29, Isd 25, I 4-71, I 157-94, I 216-92, I 34-95, I 324-86, Co 1148 and CPI 85-80] were mated as North Carolina Design I (NCD I) of Comstock and Robinson, 1952. Following this NCD I each male mated with two different females and produces 10 progeny families. Each family consists of randomly selected five $F_1$. The mean values of selected $F_1$ of a family was considered as a genotype's value and calling them genotype1 (G1) to genotype10 (G10) for 10 families. These ten $F_1$ genotypes were subjected in this study as materials. The whole crossing work was done at Breeding Division of Bangladesh Sugarcane Research Institute (BSRI), Ishurdi, Pabna, Bangladesh in the cropping year of 2006-2007 under a higher study programme. The field trials of these $F_1$ genotypes (G1 – G10) were conducted under three different locations in two consecutive years 2008-2009 and 2009-2010 following RCB Design with three replications. The locations were 1.BSRI, Ishurdi under Pabna, 2. Horian, Rajshahi and 3. Regional Sugarcane Research Station, Thakurgoan districts of Bangladesh. These locations are geographically situated at 24°, 24.37° and 26.03° N latitude, 89.25°, 88.6° and 88.47° E longitude

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**Table 1** Results of joint regression analysis for different characters in $F_1$ sugarcane genotypes.

| **Source** | **df** | **Germi%** | | | **NT/C** | | | **NMC/C** | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ |
| Genotypes (G) | 9 | 39.5918 | 10.7978** | | MS | $V_R$ | | 0.3245 | 3.2731** | |
| Environment (joint regression) | 5 | 102.455 | 27.9424** | | 0.9085 | 5.4442** | | 1.9095 | 19.2634** | |
| Genotype × Environment | 45 | 9.6453 | 2.6305** | | 3.6519 | 21.8840** | | 0.2189 | 2.2085** | |
| Heterogeneity between regression | 9 | 5.9229 | 1.6154 | | 0.3982 | 2.3861** | 1.4056 | 0.3429 | 3.4590** | 1.824 |
| Remainder | 36 | 10.5759 | 2.8843** | | 0.5177 | 3.1023** | | 0.1879 | 1.8959** | |
| Within Error | 120 | 3.6667 | | | 0.3683 | 2.2071** | | 0.0991 | | |
| **Source** | **df** | **CSH** | | | **CSG** | | | **LL** | | |
| | | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ |
| Genotypes (G) | 9 | 0.0333 | 3.6142** | | 0.0379 | 4.1542** | | 0.0384 | 2.0909** | |
| Environment (joint regression) | 5 | 0.1488 | 16.1344** | | 0.1752 | 19.2330** | | 2.1885 | 119.1963** | |
| Genotype × Environment | 45 | 0.0238 | 2.5780** | | 0.0269 | 2.9568** | | 0.0547 | 2.9790** | |
| Heterogeneity between regression | 9 | 0.0267 | 2.8970** | 1.1596 | 0.0421 | 4.6201** | 1.8182 | 0.0121 | 0.6570 | |
| Remainder | 36 | 0.0230 | 2.4982** | | 0.0232 | 2.5410** | | 0.0654 | 3.5595** | |
| Within Error | 120 | 0.0092 | | | 0.0091 | | | 0.0184 | | |
| **Source** | **df** | **LB** | | | **Bix %** | | | **CY/C** | | |
| | | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ | **MS** | $V_{R1}$ | $V_{R2}$ |
| Genotypes (G) | 9 | 0.0384 | 2.0909** | | 1.1828 | 6.2707** | | 0.3180 | 8.4275** | |
| Environment (joint regression) | 5 | 2.1885 | 119.196** | | 3.9025 | 20.6896** | | 1.4791 | 39.1932** | |
| Genotype × Environment | 45 | 0.0547 | 2.9790** | | 0.5598 | 2.9678** | | 0.1142 | 3.0258** | |
| Heterogeneity between regression | 9 | 0.0121 | 0.6570 | | 0.5552 | 2.9433** | 0.9897 | 0.0778 | 2.0623* | 0.6313 |
| Remainder | 36 | 0.0654 | 3.5595** | | 0.5610 | 2.9739** | | 0.1233 | 3.2667** | |
| Within Error | 120 | 0.0184 | | | 0.1886 | | | 0.0377 | | |

$V_{R1}$, denominator is within error; $V_{R2}$, denominator is remainder

and 30, 24.37 and 37 m above sea level, respectively. The plot size of the experiment was 4 m × 4 m having a 1 m row-to-row distance. Fertilizers were applied according to the fertilizers recommended guides of Bangladesh Agricultural Research Council (BARC) 2005. Data were collected following nine agronomical characters such as germination percentage (G%), number of tillers/clump (NT/C), number of millable canes/clump (NMC/C), cane stalk height (CSH), cane stalk girth (CSG), leaf length (LL), leaf breadth (LB), field Brix percent (Brix%) and cane yield per clump (CY/C). Data of G% and NT/C were collected after 45 and 150 days of plantation, respectively and rest of the data were collected at the time of harvesting of cane. For the study of G × E interaction the 6 environments were classified as follows: Env. I- First year location-1 (2008-2009 at Ishurdi), Env. 2- First year location-2 (2008-2009 at Rajshahi), Env. 3- First year location-3 (2008-2009 at Thakurgoan), Env. 4- Second year location-1 (2009-2010 at Ishurdi), Env. 5- Second year location-2 (2009-2010 at Rajshahi) and Env. 6- Second year location-3 (2009-2010 at Thakurgoan). The joint regression analysis was done following the Perkins and Jinks (1968) model.

## RESULTS AND DISCUSSION

In this investigation the joint regression analysis of variance for nine quantitative characters of ten $F_1$ sugarcane genotypes at different environments are shown in **Table 1**. It was observed from the table that genotypic (G) and environment (E) items were highly significant for all the characters when tested against within error. Which suggested that there were real differences existed between the genotypes and between the effects of different environments on the genotypes. Similar findings were reported by Khatod *et al.* (2006) in sugarcane and Sagor *et al.* (2007) in wheat genotypes. Statistically significant environmental effects in the present investigation indicated that variability between environments was large enough for the proper estimation of $b_i$ values. Variability in environments is an important factor and in large part determines the usefulness of $b_i$ values (Pfahler and Linskens 1979).

The G × E interactions were operative in the present investigation. Here the joint regression analysis G × E interaction sum of square was partitioned into heterogeneity of regression sum of square (linear) and remainder sum of square (non-linear). Most of the cases both linear and non-linear regression was accounted for this G × E interaction. Here, the heterogeneity of regression was non-significant for all the characters. The non-significant heterogeneity of regression indicated that the G × E interaction was due to the slopes of non-linear relationship. A non-linear relationship was obtained by Alam *et al.* (2000) when working with soybean (*Glycine max* (L.) Merrill). The significant remainder item made complex the linear prediction for the G × E interaction was existed in the genotypes. Both linear and non-linear relationships with environments were reported by many investigators in different crops (Singh and Gupta 1983; Ghosh and Singh 1996; Khatods *et al.* 2006; Tiawari *et al.* 2011). The results of the present investigation are in agreement with the findings of Alam *et al.* (2000) and Khatods *et al.* (2006), who found both linear and non-linear interaction for some of traits, but are in disagreement with the findings of Tiawari *et al.* (2011), who found a linear regression for the G × E interaction for all the traits in their study.

Regression analysis measures the character of the genotype in relation to environment that how much genotypes depends on the environment to express its character. By the regression analysis method genotypic and environmental effects are estimated at the same time. In respect of stability measurement there are various suggestions given by different researchers in different investigations. Finlay and Wilkinson (1963) considered the linear regression ($b_i$) as a measure of stability. However, Eberhart and Russell (1966) suggested the criteria of a stable genotype that regression coefficient ($b_i$) should be 1.0 and deviation mean squares from regression (DMS or $\overline{S}^2 d_i$) need to be zero and having mean greater than grand mean. Further, Breese 1969 stated that regression coefficient is a measure of effects to varying environments of a particular genotype. From their observation it may be stated that a genotype which have high mean performance, a nearly unit regression coefficient ($b_i$ = 1.0) and non-significant DMS is stable for varying environmental conditions. The genotype which exhibited higher mean performance bellow average $b_i$ and non-significant DMS may be selected for poor environment. The genotype which have high mean performance and $b_i$ above unity and non-significant DMS indicating that its adaptability to unfavorable environment. The genotypes which have above average mean performance and $b_i$ higher than unity and non-significant DMS is sensitive to the changing environment may be selected for favorable environment. The genotype which exhibited less mean performance, $b_i$ value near to unity and non-significant DMS poorly adaptable to all environments. The genotype which exhibited significant DMS indicating their instability.

**Table 2** Stability parameter for nine quantitative characters in ten $F_1$ sugarcane genotypes.

| Genotypes | Germi.% | | | NT/C | | | NMC/C | | |
|---|---|---|---|---|---|---|---|---|---|
| | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** |
| $G_1$ | 35.68 | 0.94 | 7.50 | 6.25 | 1.73 | -3.72** | 3.86 | 1.08 | -4.25** |
| $G_2$ | 34.13 | 0.99 | 8.15* | 5.09 | 1.20 | -3.96 | 3.48 | 1.15* | -4.24 |
| $G_3$ | 28.98 | 0.99 | 8.16 | 5.26 | 1.37 | -3.88* | 3.63 | 1.47* | -4.16 |
| $G_4$ | 36.17 | 1.03 | 8.71* | 5.36 | 1.11* | -4.00 | 3.45 | 0.75 | -4.33 |
| $G_5$ | 33.02 | 1.81 | 18.67* | 5.11 | 1.76* | -3.71 | 3.46 | 0.98 | -4.28 |
| $G_6$ | 30.72 | 0.67 | 4.10** | 4.81 | 0.86 | -4.12* | 3.31 | 0.81 | -4.32 |
| $G_7$ | 33.83 | 1.20 | 10.90* | 5.68 | 0.34 | -4.36** | 4.11 | 2.26 | -3.97** |
| $G_8$ | 32.90 | 0.74 | 4.98** | 5.46 | 0.43 | -4.32* | 3.53 | 1.10 | -4.23* |
| $G_9$ | 31.13 | 0.60 | 3.13** | 5.32 | 0.86 | -4.12* | 3.6 | 0.31 | -4.44 |
| $G_{10}$ | 37.08 | 1.03 | 8.65** | 5.31 | 0.33 | -4.362* | 3.74 | 0.09 | -4.49 |
| **Genotypes** | **CSH** | | | **CSG** | | | **LL** | | |
| | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** |
| $G_1$ | 2.64 | 1.59 | -4.49* | 2.64 | 1.42 | -4.48** | 123.43 | 0.94 | 614.17 |
| $G_2$ | 2.69 | 0.69 | -4.50* | 2.69 | 0.60 | -4.50* | 125.84 | 1.04 | 679.10 |
| $G_3$ | 2.55 | 1.02 | -4.49** | 2.55 | 0.82 | -4.491** | 123.92 | 1.12 | 732.94** |
| $G_4$ | 2.56 | 1.51 | -4.48** | 2.56 | 1.42 | -4.481** | 124.42 | 1.01 | 662.62** |
| $G_5$ | 2.76 | 0.92 | -4.49* | 2.74 | 0.82 | -4.49** | 126.11 | 1.05 | 685.65** |
| $G_6$ | 2.53 | 2.17 | -4.47** | 2.53 | 2.06* | -4.47** | 125.82 | 1.03 | 672.56** |
| $G_7$ | 2.67 | 0.38 | -4.50 | 2.66 | 0.18 | -4.51 | 127.00 | 1.01 | 662.60** |
| $G_8$ | 2.67 | 0.52 | -4.50 | 2.67 | 0.49 | -4.50 | 124.44 | 0.91 | 594.90** |
| $G_9$ | 2.56 | 0.94 | -4.49 | 2.49 | 2.01 | -4.47 | 119.81 | 1.14 | 746.42** |
| $G_{10}$ | 2.61 | 0.27 | -4.51 | 2.60 | 0.18 | -4.51* | 122.20 | 0.76 | 495.79** |
| **Genotypes** | **LB** | | | **Brix%** | | | **CY/C** | | |
| | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** | **Mean** | **bi** | $\bar{S}^2$**di** |
| $G_1$ | 3.26 | 1.03 | -4.23* | 18.48 | 1.97 | -3.55** | 2.17 | 0.91 | -4.34** |
| $G_2$ | 3.31 | 0.81 | -4.29 | 18.82 | 1.02 | -4.01 | 2.6 | 1.48* | -4.24 |
| $G_3$ | 3.32 | 1.12 | -4.21** | 17.86 | 0.35 | -4.34** | 2.58 | 1.14 | -4.30** |
| $G_4$ | 3.32 | 0.84 | -4.28** | 18.65 | 0.98 | -4.03** | 2.73 | 0.94* | -4.34 |
| $G_5$ | 3.5 | 1.13 | -4.20** | 18.17 | 1.06 | -3.10 | 3.05 | 0.33 | -4.45** |
| $G_6$ | 3.34 | 1.04 | -4.23 | 18.61 | 1.76 | -3.65** | 2.76 | 0.89 | -4.35** |
| $G_7$ | 3.44 | 1.01* | -4.24 | 19.13 | 0.78 | -4.13** | 2.82 | 1.24* | -4.28 |
| $G_8$ | 3.37 | 0.97 | -4.25 | 18.51 | 0.60 | -4.22* | 2.85 | 1.31* | -4.27 |
| $G_9$ | 3.23 | 1.07 | -4.22** | 17.79 | 1.10 | -3.97** | 2.8 | 1.04* | -4.32 |
| $G_{10}$ | 3.35 | 1.00 | -4.24** | 18.95 | 0.38 | -4.32** | 2.77 | 0.72 | -4.38** |

On the basis of above criterion the genotypes ‘G1’ and ‘G3’ for G %; ‘G5’ for NMC/C; ‘G9’ for CSH ; ‘G1’ and ‘G2’ for LL; ‘G6’, ‘G7’ and ‘G8’ for LB; ‘G2’ and ‘G5’ for Brix %; and ‘G4’ and ‘G9’ for CY/C characters were selected as stable genotype from the present materials having $b_i$ values near to unity (0.94 – 1.06) and non-significant DMS (**Table 2**). The said genotypes might be considered as the most stable with the changing environments and could be used for the future breeding programme. The results are in agreement with the findings of Paroda and Hayes (1971), Islam (2002) and Khatod *et al.* (2006). Besides these, it was observed that ‘G2’ and ‘G5’ for NT/C, ‘G2’ and ‘G3’ for NMC/C, ‘G9’ for CSG and ‘G2’ ‘G7’ and ‘G8’ for CY/C were more responsive to changing environment, having non-significant DMS and high values of $b_i$. It suggested that these varieties might be recommended only for favourable environments. Khan *et al.* (2002) reported that the genotype AEC8 I-8415 might be advantageous for favourable environments for cane and sugar yield having $b_i$ values 1.206 and 1.364 and DMS values 0.024 and 0.006, respectively. While ‘G4’, ‘G6’, ‘G9’ and ‘G10’ for NMC/C, ‘G7’, ‘G8’ and ‘G10’ for CSH; ‘G7’ and ‘G8’ for CSG and ‘G2’ for LB were found poor adaptability to all environments because the regression coefficient is less than 1.0 and non-significant DMS values. Singh and Rai (1989) and Singh *et al.* (1993) found similar results in sugarcane. There were evidences that in sugarcane for different quantitative characters, some varieties were adaptable in favourable and some were adaptable in unfavourable conditions. Rests of the genotypes were found unpredictable due to their significant DMS values for different characters.

In this study G × E interaction was due to the slopes of non-linear relationship and significant remainder item made complex the linear prediction. The genotypes of ‘G1’ and ‘G3’; ‘G1’ and ‘G2’; ‘G2’ and ‘G5’; ‘G5’; ‘G6’, ‘G7’ and ‘G8’; ‘G9’ and, ‘G4’ and ‘G9’ were the stable genotypes for G%; LL; Brix %; NMC/C; LB; CSH and CY/C characters, respectively. These genotypes might be considered as stable to the changing environments. This study also suggests that the stability analysis can contribute with supplementary information on the performance of new sugarcane selections prior to release for commercial cultivation and can increase the efficiency of cultivar development programmes.

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