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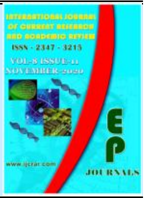

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Estimation of Components of Variances, Heritability and Genetic Advance in Sugarcane Genotypes at Finchaa and Metehara Sugar Estate, Ethiopia

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Abstract

Eight new sugarcane genotypes with two standard check varieties were tested in randomized complete block design (RCBD) with three replications for three cropping season at Finchaa and Metehara Sugar Estate of Ethiopia. The combined analysis of variance revealed that, variance due to location was higher than the other effects based on the relative contribution of sum of squares which is suggesting the existence of differences among the two locations and selection practices without considering location discourages breeding options. Although the difference is very small, the estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all traits indicating variation is not only due to genotypic but also due to environmental influences. The number of millable cane, number of tillers, cane yield, weight of single stalk and estimated sugar yield were revealed the highest genotypic and phenotypic coefficient of variation.

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Keywords

Genotype, Location, GCV, PCV, Heritability, Genetic advance

Introduction

The modern sugarcane varieties have arisen from the incorporation of genes of the wild *S.spontaneum* germplasm into the gene pool of domesticated *S. officinarum* (2n=80). The high polyploidy nature of sugarcane makes it a difficult species to work with at the genetic level (Robert and Chittaranjan, 2010).

According to singh *et al.*, (1994) cited by Crepin and Michael (2018), knowledge of genetic variability and heritability of traits are very important to identify those relevant for genetic improvement through simple selection. Genetic variability is the basic factor to be considered while making selection (Jamoza *et al.*, 2014; Silva *et al.*, 2007). Genetic variability is the cornerstone of sugarcane breeding for seeking traits with desirable agronomic importance for quality and or yield-related, resistance against biotic and abiotic factors.

Genetic studies in a wide range of sugarcane populations and diverse location indicates large estimates of heritability for sugarcane yield and its component traits (Masri *et al.*, 2015; Farrag *et al.*, 2017).

Thus, the objectives of the present investigation was undertaken to evaluate the information on genetic variability, heritability and genetic advance in sugarcane genotypes at Finchaa and Metehara.

Materials and Methods

Study area

The experiment was conducted at two among the oldest Ethiopian sugar estate. The first site was Finchaa sugar estate; located at latitudes 9^0 30'N to $10^0$00'N and longitudes 37^0 15' to 37^0 30'E and an elevation between 1350 and 1600 m.a.s.l. An average annual precipitation of the area reaches about 1309 mm and the average maximum and minimum temperatures were 31.5^0C and 14.6^0C respectively. The second site was Metehara sugar estate; located between 8^0 53' N latitude and 39^0 52' E longitudes and at an elevation of 950 m.a.s.l. It receives an average of 554mm annual rainfall with minimum and maximum temperature of 17.4^0c and 32.6 ^{0}c.

Treatments and experimental design

The experiment includes a total of ten sugarcane genotypes. Eight new introduced genotypes designated by 2-111, 2-222, 2-333, 2-444, 2-555, 2-777, 2-888, 2-999 and two standard check varieties, B52-298 and NCo-334 were tested on Luvisol of Finchaa and Metehara Sugar Estate. The activity was done from 2014 – to - 2019 harvesting year; plant cane-2014/2015, first ratoon-2016/2017, second ratoon-2017/2019. At each location, the trial was laid out in completely randomized block design (RCBD) with three replications. Each experimental plot composed of six rows of five meters length. The spacing was 1.45m for furrows; 1.5m between adjacent plots; 2.9m between replications; and 3 meters from the border crop. Equal number of two budded set of each variety was planted. Except the variation of the treatments (the sugarcane genotype) all agronomic management practices were applied uniformly throughout the growing season.

Data collection and analysis

Data were collected from the four middle rows of each plot for number of tillers, number of millable cane, number of internodes, cane diameter, cane height, cane length, cane yield, sucrose percent and estimated sugar yield for three cropping cycles at (plant cane and two successive ratoon crops) at both locations. The collected data were subjected to statistical analysis by General Linear Models Procedure using SAS software statistical package (SAS, 2002) and those traits showed statistically different for the genotypes at each individual location were engaged for combined analysis over two locations and three cropping years.

Estimation of phenotypic and genotypic variances

The phenotypic and genotypic variances of each trait were estimated from the RCBD analysis of variance using the methods suggested by Johnson *et al.,* (1955), the expected mean squares under the assumption of random effects model was computed from linear combinations of the mean computed as:

$$\sigma^2 g = (Msg-Mse)/r$$

$$\sigma^2 e = Mse$$

$$\sigma^2 ph = \sigma^2 g + \sigma^2 e$$

Where σ^2g, σ^2ph and σ^2e was genotypic variance**,** phenotypic variance and environmental variance; Msg and Mse were the mean square for the genotypes and error in the analysis of variance respectively and r was the number of replications. The phenotypic variance was estimated as the sum of the genotypic and environmental variances.

Coefficients of variation

Genotypic coefficient of variation and phenotypic coefficient of variation were calculated according to Singh and Chaudhary (1985).

$$GCV = (\frac{\sigma g}{GM}) * 100$$

$$PCV = (\frac{\sigma ph}{GM}) * 100$$

Where GCV, PCV, σg, σph and GM were genotypic and phenotypic coefficient of variation; standard deviation of the genotype and phenotype respectively and GM stands for grand mean. After the separation of components of variance, phenotypic and genotypic variances were computed. The PCV and GCV values are ranked as low, medium and high with 0 to 10%, 10 to 20%, 20% and above respectively (Deshmukh *et al.,* 1986; Shivasubramanian and Menon, 1973).

Estimation of heritability

Heritability estimates were computed from components of variance (Butterfield and nuss, 2002). Heritability in broad-sense for mean values was the ratio of genotypic variance to phenotypic variance using PABSTAT (Utz, 2007) following the formula described by Hill *et al.*, 1998; Allard *et al.*, 1960 and Hanson *et al.*, 1956.

$$H^2b = \left(\frac{\sigma^2 g}{\sigma^2 ph}\right) * 100$$

Where σ^2g, σ^2ph and H^2b are genotypic variance, phenotypic variance and heritability in broad-sense respectively. Heritability values are categorized as low (0- 30%), moderate (30-60%) and high (60% and above) as stated by Robinson *et al.*, (1949).

Genetic advance

Genetic advance is the expected gain in the mean of a population for a particular quantitative character by one generation of selection of a specified percent of the highest-ranking plants (Rolf, 2010). The expected genetic advance represents the shift in a population towards superior side under some selection pressure after single generation of selection. It could be calculated by using the methodology suggested by Allard (1960) at 5 per cent selection intensity using the constant 'K'.

$$GA = H^2(b) \times K \times \sigma p$$

Where, GA = Genetic advance

$H^2(b)$ = Heritability (broad-sense)
K = Selection intensity at 5 per cent =2.06
σp = Phenotypic standard deviation

Genetic advance as per cent of mean could be classified as low (<10%), moderate (10-20%) and high (>20%) according to Deshmukh *et al.*, (1986).

Results and Discussions

Analysis of variance

As presented in (Table: 1), the combined analysis of variance across locations and over copping cycles showed statistically highly significant ($P \leq 0.01$) for all traits among locations except for sucrose % indicating that studying on a single environment would be insufficient for the tested genotypes. Significant effects ($P \leq 0.01$) were detected for analysis of variance due to genotypes (Table: 1) showing the existence of the genetic variability among the studied clones. This research result was similar with Patil and Patel (2017); Swamy *et al.*, (2016); Tyagi *et al.*, (2011) who reported all the traits revealed the significant differences among genotypes for cane and quality trait studied. Cropping cycles also revealed highly significant for all traits indicating that the materials under study were performed differently among the cropping cycles (plant cane and the ratoon crops) in agreement with the results obtained by Farrag *et al.*, (2019) and Abu-Ellail *et al.*, (2018) and there could be a production determining factors during cropping years giving a chance of practicing selection in the forwarding breeding program.

The interaction of genotype by crop revealed significant for all traits at ($p \leq 0.01$) except numbers of millable cane which is non-significant. The genotype by crop interaction was important in determining sugarcane yield and its component traits, therefore, necessary to identify genotypes with the good ratooning ability for specific conditions. The interactions of genotype by location observed highly significant for estimated sugar yield, sucrose %, cane height and tillers at the third months after planting (Table: 1) in agreement with Tena *et al.*, (2016) who reported significant genotype × location interactions for most of the traits suggesting the genotypes were prejudiced by the locations to perform better. The variance due to genotype x crop x location interaction were significant for number of tillers at the third month, cane height, pol percent, purity percent and sucrose percent which indicates their good ratooning ability and more than one site should be considered to access final stages of genotype selection whereas the rest traits showed non-significance. This research result was similar with the former activity reported by Feyissa *et al.*, (2014) in the study conducted at the three pioneer sugarcane plantations of Ethiopia on ten introduced sugarcane genotypes.

The combined analysis of variance revealed that, the variance due to location, genotype, cropping cycle, genotype by location interaction, genotype by crop and location by cropping cycles had an effects of 30.33%, 6.89%, 8.93%, 4.98%, 7.3% and 20.00% respectively, to the total variation based on the relative contribution of sum of squares which is an indication of the existence of differences among the locations in which the sugarcane varieties were evaluated as well as their interaction with the genotypes and crop patterns. Thus, in this experiment, the location effect was higher than the other effects, as indicated by Gauch (2006) and Pupin *et al* (2018). Genotype by location interaction is a big issue that discourages breeding activity since it complicates the proofing of superior cultivars by confusing determination of true genetic values for sugarcane crops to produce stable genotypes across different sites and cropping seasons and may cause changes in the relative ranking of genotypes.

Table.1 Combined analyses of variance for over locations and cropping cycles for sugar yield and related traits for eight new introduced sugarcane genotypes along with two standard checks.

		Traits											
Source V	DF	TC3	CH	CL	CD	BRX %	POL%	PRT%	SUC %	WSS	NMC	CY	ESY
Genotype	9	19185914929*	2648.73**	5713.81**	0.47**	5.99**	11.63**	31.37**	7.30**	0.88**	6548600933.7**	97.95**	0.65**
Location	1	189900923312**	120249.03**	25807.32**	10.37**	52.05**	27.60**	92.29**	1.80ns	2.43**	16104107939.00**	8287.19**	25.87**
Crop	2	47379170005**	27655.09**	42052.61**	1.60**	59.91**	135.52**	639.88**	87.68**	1.77**	8571754291.8**	743.62**	3.81**
Block(Rep)	2	961777107.6	92.64	285.27	0.02	3.66*	2.52	0.54	1.19	0.07	2803398240	36.21	0.22
Gen* Loc	9	12109262471**	1585.70**	1935.34	0.08*	3.10*	2.85*	7.12*	2.13**	0.19*	2112886264	34.96*	0.47**
Gen*Crop	18	2686046924.7**	1079.22**	2418.62**	0.07**	2.60**	4.80**	11.37**	2.48**	0.23**	1309688223.4	48.77**	0.35**
Crop* Loc	2	34206654837**	8151.77**	41968.79**	0.70**	61.92**	47.62**	81.28	27.73**	9.83	12681361655**	1007.71**	8.55**
Rep* Loc	2	1181506673.5ns	291.35	600.63	0.01	0.03**	0.91	9.83	0.83	0.02**	670560232.3	24.93	0.26
Gen*Crop*Loc	18	1773739281.9**	625.21*	964.46	0.03	2.35	3.69**	9.19*	2.37**	0.12	2170587665	21.79	0.13
Gen*Crop*Rep	58	483835087.15ns	339.05	909.26	0.02	1.25	1.58	5.70	0.96*	0.10	1737941142	13.92	0.13
Pooled Error	58	486769736.8	329.41	1032.77	0.02	0.95	1.19	3.36	0.62	0.08	1669238508	13.97	0.13
R-Square		0.963598	0.94	0.86	0.94	0.91	0.92	0.93	0.93	0.91	0.760222	0.95	0.91
CV		11.53604	7.41	12.07	6.02	4.81	5.92	2.02	6.16	16.19	42.29096	23.09	23.19

Keys:** and * =highly significant at p<0.01 and significant p<.0.05 probability level respectively; CV= Coefficient of variation, SE=Standard error, TC3 = Number of tillers per ha at the third months; CH= Average cane height(cm); CL= Average cane length; CD = Average cane diameter/Girth(cm); BRX = Field brix reading in %; POL = pol reading in %; PRT=purity in %; SUC%= sucrose %; WSS= average single Stalk weight(kg); NMC= number of millable cane/ha in 1000s; CY= cane yield(tone/ha/month); ESY=Estimated sugar yield (tone/ha/month

Table: 2. Combined components of variances, coefficients of variation, heritability, genetic advance of the traits for eight new introduced sugarcane genotypes across locations and cropping cycles (plant cane, first ratoon and second ratoon):

Traits	**σ^2g**	**σ^2ph**	**σ^2e**	**GCV (%)**	**PCV (%)**	**H^2b (%)**	**G.adv % mean**
TC3	6233048397.39	6719818134.22	486769736.83	41.28	42.86	92.76	81.90
NMC	1626454142.00	3295692649.70	1669238507.70	41.75	59.42	49.35	60.41
CH	773.11	1102.52	329.41	11.35	13.55	70.12	19.57
CL	1560.35	2593.12	1032.77	14.84	19.13	60.17	23.71
CD	0.15	0.17	0.02	14.95	16.12	86.06	28.57
BRX%	1.68	2.63	0.95	6.39	7.99	63.86	10.52
POL%	3.48	4.67	1.19	10.14	11.74	74.60	18.04
PRT%	9.34	12.70	3.36	3.37	3.93	73.56	5.95
SUC%	2.23	2.85	0.62	11.69	13.21	78.28	21.30
WSS	0.27	0.35	0.08	28.74	32.99	75.90	51.58
CY	27.99	41.96	13.97	32.68	40.02	66.71	54.99
ESY	0.17	0.31	0.13	26.41	35.14	56.46	40.88

Key: σ^2g=genetic variance, σ^2ph=phenotypic variance, GCV=genetic coefficient of variation, PCV=phenotypic coefficient of variation, h^2b=heritability in broad-sense and G.adv= genetic advance expressed as per cent of mean (Genetic gain). TC3 = Number of tillers per ha at the third months; CH= Average cane height(cm); CL= Average cane length; CD = Average cane diameter/Girth(cm); BRX = Field brix reading in %; POL = pol reading in %; PRT=purity in %; SUC%= sucrose %; WSS= average single Stalk weight(kg); NMC= number of millable cane/ha in 1000s; CY= cane yield(tone/ha/month); ESY=Estimated sugar yield (tone/ha/month)

The genotype by environment interaction may either promote or hampers the selection of superior cultivars Dutra *et al.,* (2014). Therefore, it is a major concern that measuring the interaction of genotype by location is important to determine optimum information for selecting genotypes adapted to specific or over locations Pupin *et al* (2018) and Esayas *et al.,* (2019).

Estimation of components of variance

The magnitude of genotypic variance exceeded the corresponding environmental variance in determining the expression of phenotypic variance for all traits except number of millable cane (as presented in Table: 2) in which environmental variance was higher than genotypic variance as opposed to the investigation reported by Tena *et al.*, (2016) for most traits tested under this study. In this case, number of tillers at the third month followed by number of millable cane were recorded the highest magnitude for genotypic and phenotypic variance. The lowest magnitude of phenotypic and genotypic variances was exhibited by cane diameter ($\sigma^2g = 0.15$ and $\sigma^2ph = 0.17$) followed by estimated sugar yield ($\sigma^2g = 0.17$ and $\sigma^2ph = 0.31$). High magnitude of genotypic variance shows the presence of high genetic variability among the studied genotypes for these traits and individuals in a population were less influenced by environmental factors. This research result were similar with Masri and Amein (2015) for cane diameter and cane yield, however opposed to Shitahun *et al.*, (2018) for number of tillers, cane height and sucrose %.

Genotypic and Phenotypic Coefficients of Variation

The combined results displayed that, traits such as number of millable cane, number of tillers at the third months after planting, cane yield, weight of single stalk and estimated sugar yield were revealed the highest genotypic coefficient of variation (GCV) in their decreasing order (Table: 2). Moderate genotypic coefficient of variation (GCV) was displayed in cane diameter, cane length, sucrose percent, cane height and pol percent. Earlier research, however obtained that low genotypic coefficient of variation for cane yield, cane height and cane diameter (Ebid *et al.*, 2015) as opposed to the present result. The most important yield contributing traits viz number of millable cane, numbers of tiller at the third months, single stalk weight, cane yield, and estimated sugar yield shows the highest estimates of phenotypic coefficient of variation(PCV) and this is similar with the works carried out by Ebid *et al.*, (2015) in the selected sixteen sugarcane clone for two growing season for the trait single stalk weight and with Guruprasad and Nagaraja (2016) for the trait cane yield and estimated sugar yield.

The phenotypic coefficient of variation was categorized under moderate level for traits viz cane, length, height and diameter, pol percent and sucrose percent in agreement with the study done by Rewati (2001) for sucrose percent. Quality measure traits like purity and brix percentage shows low estimates of genotypic and phenotypic coefficient of variation in agreement with the findings of Guruprasad and Nagaraja (2016) whose reported low genotypic coefficient of variation and phenotypic coefficient of variation values for the same traits in the investigation consisting of thirty five clones to estimate the genetic variability parameters for fourteen quantitative characters and whereas Jamoza *et al.*, (2019) recorded lower genotypic coefficient of variation value for qualitative traits. As anticipated, the estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all traits there-by showing variation is not only due to genotypic but also due to environmental influences in similar way of the finding of Boryana *et al.*, (2014). Nevertheless, the differences between phenotypic coefficient of variation and genotypic coefficient of variation for all traits were small indicating high prospects for genetic progress through selection under the situation of this investigation in agreement with the result reported by Jamoza, *et al.*, (2014).

Heritability and genetic advance

From Table: 2, it can be observed that heritability percentage of the studied traits ranges from 49.35% to 92.76%. Among the twelve traits measured, numbers of tiller at the third months(92.76), cane diameter(86.06), sucrose content(78.28), single stalk weight(75.9), pol percent (74.6), purity percent (73.56), cane height(70.12), cane yield(66.71), brix percent (63.86) and cane length(60.17) scored the highest heritability value showing the traits were not very often influenced by the environment. The only two rest traits viz number of millable cane (49.35) and estimated sugar yield (56.46) were categorized under moderate heritability in broad sense. This indicates that the effectiveness of simple selection method for sugarcane genotypes improvement in breeding program based on heritability results of these traits as one of the selection criterion for judging. These results are in conformity with the reports of Alam *et al.,* (2017) for number of tillers, number of internodes, number of millable cane, cane diameter, cane height with the highest heritability percentage. Conversely, Swamy *et al.,* (2016) reported a moderate percentage of heritability for single stalk weight and number of internodes in the experiment tested on thirty sugarcane clones to study the variability parameters for cane yield and quality traits in plant and ratoon crops.

Genetic advance

In the present study, number of tillers at three months (81.90%), millable cane (60.41%), cane yield (54.99), weight of single stalk (51.58) and estimated sugar yield (40.88) were categorized under the highest genetic advance as percent of mean suggesting that a large proportion of the total variance had heritable in the tested genotypes and selection of these traits would be effective. High heritability together with high genetic advance indicated that these traits were controlled by additive gene action. Hence, selection for these traits will be useful in the improvement of such traits to decide the best genotype.

The lowest genetic advance as percent of the mean was observed in purity percent(5.95%) together with high heritability percentage (73.56) indicates the non-additive gene effects for control of this particular trait. According to Abu-Ellail *et al.,* (2017) and Farrag *et al.,* (2019), traits with low genetic coefficient of variation, phenotypic coefficient of variation and genetic advance as percent of mean as in case revealed by purity percentage in the current research suggests that, planning for the improvement of sugarcane genotypes through selection would be less effective and or considerably impracticable because of the masking effects of environment on genotypic expression (Wunna *et al.,* 2009; Butterfield and Nuss, 2002). The result of this study observed that, number of tillers at three months, cane yield and weight of single stalk could be considered as an important trait for selection and sugarcane genotype improvement for that they were exerted high genetic coefficient of variation, high heritability percentage and genetic advance as percent of mean in agreement with Patil and Patel (2017) and Patel *et al.,* (2006).

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Genotype by location interaction is a major factor in breeding activity because it hinders the selection of superior cultivars by confusing determination of true genetic values for sugarcane crops. The combined analysis of variance revealed that, the variance due to location was higher than the other effects based on the relative contribution of sum of squares which is an indication of the existence of differences among the two locations. The higher values of phenotypic coefficient of variation than the genotypic coefficient of variation for all traits shows the observed variation is not only due to genotypic but also due to environmental influences. The results of the present study indicated, the importance of number of tillers, cane yield and weight of single stalk could be considered as one of the selection criterion and sugarcane genotype improvement for that they were exerted high genetic coefficient of variation, high heritability percentage and genetic advance as percent of mean. These traits also recorded high heritability together with high genetic advance indicating that they were controlled by additive gene action. Hence, selection for these traits will be useful in the improvement of such traits to decide the best genotype.

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