Advances in Crop Science and Technology

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Received: 'HF 0DQXVFULSW 1R Editor Assigned:

Keywords: AMMI; GGE-Biplot; Mega-environment; Ideal genotype

Introduction

Sugarcane is a eld crop plant mainly having high G x E interaction and high heterozygosity (Tena et al., 2019). e production of sugarcane is a ected by the environment, genotype and the interaction of both e ect (GEI); of which the GEI e ect causes signi cant variations in pattern), with the scores of the genotypes and the environments of the PC1 scores against their respective scores for the PC2 scores (Burgueno et al., 2009; Crossa et al., 2002; Ding et al., 2009; Yan and Kang 2003) when many genotypes are tested across locations for more than one year and/or cropping cycles(Yan et al. 2007; Vaezi et al., 2017) [4,5].

e users always need the varieties that with high yield performance and other essential agronomic traits in commercial crop production. In most cases, in Ethiopia, the sugarcane varieties under use in a commercial farm as well as under the research are introduced from foreign countries. Besides, the locations in which these cultivars tested are also vary in soil fertility, temperature range and irrigation types. us, statistical evaluation of this genotype is fundamental to identify the response of genotypes in relation to the environments of the experimental conditions. erefore, it is important to understand the causes of GEI for the determination of high-yielding genotypes and identi es sites that best represent the target environment. e objective of this study was to evaluate G x E interactions of sugarcane genotypes for sugar yield across six environments using AMMI and GGE biplot models and identify genotypes with high yield and stable performance [6].

Materials and Methods

Experimental site

e experiment was conducted at two most popular sugar estates of Ethiopia; Finchaa and Metehara. Finchaa was located at latitudes 90 30'N to10000'N and longitudes 370 15' to 370 30'E and an elevation between 14550-1600 m.a.s.l. An average annual precipitation of the area reaches about 1309 mm and the average maximum and minimum temperature was 31.50C and 14.60C respectively. Metehara sugar estate was located at latitude 80 53' N and longitudes 390 52' E and at an elevation of 950 meters at sea level. It receives an average of 554mm

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Result and Discussions

AMMI analysis of variance

e results of combined ANOVA and AMMI analysis of variance for sugar yield showed that highly signi cant (p 0.001) di erence among genotypes (G), environments (E) and genotype by environment interaction (GEI). Based on the AMMI result, the sugar yield of the genotype were in uenced by environments which explained 73.77% of the total phenotypic (G + E + GEI) variation while the genotype (G) and genotype by environment interaction (GEI) accounted 8.65% and 17.58% respectively indicating the contribution of environmental main e ects over genotypic main e ects for the variation of sugar yield due to diverse environmental conditions of the testing locations. Similar to this result, the higher donation of environment than the genotype and their interaction was reported in sugar yield by Tena et al. (2019) and by Legesse et al. (2019) in grain yield of maize [15]. e magnitude of sum squares of GEI is greater than that of genotype e ects, indicating that there are more di erences in genotypic response across environments. is result was not con rm with Erol et al. (2018) that reported the highest genotypic e ect than GEI in the study undertaken for the selection of the best barley genotypes to multi and special environments by AMMI.

e GE interactions e ect in the AMMI model has been partitioned into two Interaction Principal Component Axes (IPCA1 and IPCA2) [16]. e rst-IPCA1 showed highly signi cant level whereas the second-IPCA2 were not signi cant recording 59.08%, and 18.66%, respectively with a decrease in the subsequent axes and totally explained 77.74% of the variations observed. e rest 22.26% of the interaction e ect was residual, therefore, not interpreted (Purchase et al., 2000). e signi cance level of the rst-IPCA1 indicates that the sugarcane clones and the six environments were considerably di erent from one another. is end result was in agreement with Vaezi et al. (2017) and Regis et al. (2018). According to Legesse et al. (2019), such research result shows the performances of the genotypes used were varied di erently in sugar yield (Table 2) [17].

Mean performance of genotypes

e sugar yield mean values of an introduced sugarcane genotypes

mega-environments which comprise one or more environments. Consequently, the environments were grouped into two mega-environments [24]. e rst mega-environment made up by three environments: E1 (plant cane at Finchaa), E2 (rst ratoon at Finchaa and E4 (plant cane at Metehara). e second mega-environment was made up by E3 (second ratoon at Finchaa), E5 (rst ratoon at Metehara) and E6 (second ratoon at Metehara). is GGE-biplot polygon view indicates that the ratoon crops were grouped together in the second mega-environments except E2 showing the uniformity of this group in evaluating the tested genotypes. is suggests that the environments which located in the same sectors are strongly correlated (Solonechnyi et al., 2015). e vertex genotype observed with the highest yield in the rst mega-environment was found to be only G10 while the vertex genotype G4 was obtained higher yield in the second mega-environment. Among the ve vertex genotypes, G7, G6 and G3 were out of the mega environments. And were the poorest-yielding because of the fact that these genotypes were observed far away from all of test environments, re ecting as they yielded lower at each location [25].

e winning genotype on the vertex of the polygon contained in a mega-environment had the highest yield in at least one environment and was one of the best-performing genotypes in the other environments (Yan and Rajcan, 2002). In another word, these genotypes indicated highly and positively correlated with these locations. Similarly, Adu et al. (2013) and Yan et al. (2007) reported the vertex genotype in each sector had the highest yielder in the environment that falls within that particular sector. e other genotypes which had smaller vectors are contained within the polygon and this means, they are less responsive in relation to the interaction with the environments within that sector (Tena et al. 2019; Mattos et al., 2013; Yan and Rajcan, 2002) (Figure 2).

e GGE-biplot ranking

An average environment coordination (AEC) was used for ranking and identifying the top yielder and stable genotypes by GGE-biplot based on the principles suggested by Yan and Rajcan (2002). e AEC is a line crosses through the biplot's origin based on genotype focused single value portioning (SVP = 1) and helps to simplify the genotype assessment based on the mean performance and stability under a wide range of environment. When moving away from the axis of AEC ordinate and from the biplot origin, it indicates the instability of the genotype increases and hence, the interaction e ect with the environments will also increases (Tena et al., 2019) [26,27].

In this investigation, the ranking biplot AEC indicated that G2, G9 (standard check) and G4 observed with above-average means and wer always considered among the best genotypes. Particularly, G2 could be noted as the stable and best leading and an ideal genotype as compare to the others due to its nearness to the arrowhead. e genotype G10 was observed as above average sugar yield mean value, but positione at moderately stable direction. erefore, based on the genotype G2 could be selected because of superiority and stability followed by G10 due to its above mean value and moderate stability. Conversely, G6, G7, G3 and G5 were those genotypes scored with below-average mean performance [28,29]. is research result is con rmed with the report of Mebrahtom et al. (2018) and Tena et al., (2019) for GEI evaluation in sugarcane genotypes at the same location with this work and Legesse et al. (2019) in quality protein maize (Figure 3).

e GGE-biplot comparison

Genotype which is the highest sugar yield mean values in all test environments and well stable is said to be an ideal genotype (Yan and Kang, 2003). is is decided as in the center of the concentric circles or otherwise located closer to the ideal circle (Kendal et al., 2016). e center of the concentric circle is a point in the positive direction and has the longest vectors of the genotypes and helps to visualize the distance between each genotype and the ideal genotype [30]. Accordingly, depicts that G10 was located on very nearest to the concentric circle; thus, closest to the ideal genotype and therefore identi ed as the best genotype than the others. Genotype G2 and G9 (standard check) were categorized in the second and third desirability respectively, in terms of their higher yielding performance and stability [31]. is genotypes are ordered as G10>G2>G9 in their sugar yield performance and ordered as G2 > G10>G9 in their stability attraction. Consequently, it is very important to decide that G10 and G2 were recommended for commercial production and for broad adaptation than the others. On

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Figure 3: ...

Figure 4: 7KH **(&RPSDULVRQ RI VXJDU \LHOG RI WHQ JHQRW\SHV $ SDWWHUQ IRU HQYLURQPHQWDO IRFXV WKH GHVLUDEOH JHQRW\SHV WR WKH LGHDO FHQWHU

the contrary, genotype G3, G6 and G7 were extremely far away from the concentric circle and thus not in the category of ideal genotype. is implies they are poor yielding mainly because of their distance from the concentric circle. Other reports also found that an ideal genotype having the highest yield and stable; the genotypes with poor yielder and instable (Kendal et al., 2016, Tena et al., 2019, Legesse et al., 2019) [32].

Ideal environments have two features; discriminativeness (the ability of an environment to distinguish genotype) and representativeness (the ability of an environment to represent all other evaluated environments) [33]. Environment-focused scaling of comparison the GGE biplot is measured based on AEC and concentric circles which helps to evaluate the tested environments as this measures showed the distance of the environments from the biplot origin. e ideal environment is the one that is close to the center of concentric circles. In this case, E4(plant cane at Metehara followed by E2 (rst ratoon crop at Finchaa) were found for being an ideal environment as placed close to the concentric circles (representativeness of suitable environment) having the smallest vector length from the biplot origin. is implies that sugarcane genotypes selected in that environment as well as cropping cycle would have high probability to perform well in other locations of the same region [34].

e environments that were placed far from the comparison biplot origin indicated the discriminating ability of the environments as the discrimination power of an environment is proportional to the length of the environmental vector (Vargas et al., 2013). Hence, from the six-tested environments, E1 (plant cane at Finchaa) had strong ability to discriminate the genotypes for sugar yield as it was placed far from the biplot origin (longest vector). In line with these ndings reported on the discriminative and representative ability of the environments, Mebrahtom et al. (2018) and Tena et al. (2019) for sugar yield at similar locations and Enyew et al. (2021) analysis for grain yield and other agronomic traits in sorghum (Figure 4A and 4B) [35,36].

Conclusion

e variation due to environments explained 73.77% out of total phenotypic variation indicating the importance of environmental main e ects over genotypic main e ects to in uence sugar yield of the genotype. Analysis of the AMMI observed to be the genotypes G10 (1.928) had high mean sugar yield in ton/ha/month while G6 (1.282) recorded the least sugar yield.

e genotype labeled by G10 was considered as the rst cultivar in obtaining the highest sugar yield mean value in ton/ha/month in four environments: E1, E2, E3 and E4. e GGE-biplot grouped the target environment into two mega-environments in which both of them were made up by three environments indicating most probably the ratoon crops were merged together.

Both E4 (plant cane at Metehara and E2 (rst ratoon crop at Finchaa) were found for being representativeness of suitable environment while E1 (plant cane at Finchaa) had strong ability to discriminate the genotypes for sugar yield. In general, the GGE-biplot ranking analysis showed that G2 was categorized as an ideal genotype and stability followed by G10 due to its above mean value and moderate stability over location for making e ective selection. erefore, these two genotypes could be recommended for veri cation and release for commercial farm.

Acknowledgements

e authors genuinely thank for the material grants of Ethiopia sugar industry group.

Competing Interests

e authors declare that there is no con ict of interest.

References

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