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Research Article

Genotype by Environment Interaction and Stability Analysis for Potato (Solanum Tuberosum l.) Genotypes in North Shewa Zone of Oromia Region

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Abstract

Studying genotype-by-environment interaction and determining representative testing environments are important for releasing new varieties with high mean performance and stability. The experiment was laid out in randomized complete block design with three replications. Ten potato genotypes were evaluated to study their adaptability and stability in six environments of North Shewa Zone of Oromia Region. Multivariate methods (AMMI and GGE biplot) were used to identify high yielding and stable genotypes. The result of AMMI`s analysis of variance showed that genotype, Environment and genotype-by-environment interaction, and interaction principal component analysis (IPCA-I and IPCA-II) had significant effects on tuber yield. Genotype variance was the most significant source of variation, accounting for 53.43% of the total variation. The AMMI model's first two IPCAs (IPCA-I and IPCA-II) explained about 84.18% of the total GE interaction. GGE biplot analysis grouped the six test sites into one mega environments. CIP-313022. 68 (G07), CIP-313022. 218 (G05), and CIP-313034. 03 (G02) were the most stable and high-yielding genotypes across test environments, whereas G03 was a low-yielded and unstable variety. G04 was highly stable in tested locations and high yields. AMMI and GGE bi-plot analysis identified that CIP-313022. 68 (G07) and CIP-313022. 218 (G05) are high-performing and stable across test sites. The highest-yielding and stable genotypes, CIP-313022. 68 (G07) and CIP-313022. 218 (G05), were proposed and recommended for release in North Shewa Zone Oromia Region.

Keywords

AMMI-biplot, GxE, GGE-biplot, Potato, Stability

1. Introduction

Potato (Solanum tuberosum L.) is a tuber crop that produces more yields per unit area than any other crop on the planet. It is a key economic crop all over the world. Potatoes are the third most important food crop for human consumption after rice, and wheat, and they feed over a billion people [9]. China, India, and the United States account for more than 80% of global potato production, whereas Africa accounts for only approximately 5% [9]. Human population in Ethiopia is increasing, so enhancing the productivity of potato crop is critical for the country's food security. The development of improved potato varieties in Ethiopia started around 1987, with all efforts prior to 2015 directed towards evaluating germplasm devel-

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oped elsewhere for its suitability here. Most smallholder farmers in Ethiopia still cultivate low yielding table varieties that were released before 2013. Local and previously released improved varieties are becoming less productive and more prone to serious disease as the climate has begun to change. Enhancing potato yield and other desirable qualities through crossing could help generate high yielding varieties for the wide range of environments in Ethiopia, as well as varieties adapted to future environments as the climate changes. A sustained increase in yield is required for food security in a nation undergoing substantial human population growth [5].

Since potato is grown from mid altitudes to very high mountain tops, and from humid to dry areas in the country, improvements in productivity will require the development of varieties best adapted to a wide range of environments [13]. Plant breeding programs primarily focus on improving a crop's adaptability and tolerance to biotic stress in order to increase yield. Crop improvements made since the 1950s coupled with inexpensive agronomic inputs, such as fertilizers, pesticides, and water have allowed agricultural production to keep pace with human population growth [6].

In Ethiopia, potato ranks first in the category of root and tuber crops (RTCs) in terms of area coverage and total production. Crop production survey results of private peasant holding of the year 2019/20 indicated that of the total land areas of about 248,357.51 hectares covered by RTCs, 70,362.22 hectare (~28.33%) and over 1 million tons of potato was produced [7] with an average national yield of 13.140 t ha-1 [7]. Currently, potato is produced mainly in the North western, Central and Eastern highlands of Ethiopia [3]. Its production is constrained by a wide range of factors that resulting in low yields. These factors include lack of high yielding varieties tolerant to late blight, poor soil fertility, climatic limitation, inadequate seeds, lack of appropriate cultural practices, poor post-harvest management & storage problems, high cost of farm inputs, diseases and insect pests [10].

The farmers need varieties that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions and also over years. The basic cause for difference in the performance of genotypes over environments is the occurrence of genotype-environment interaction (GEI). To overcome GEI problem, trials are usually conducted over several locations and years to ensure that the selected genotypes have a high and stable performance over a wide range of environments. The data generated in these trials are analyzed for GEI by various methods. The most recent method GGE biplot model [8], provides breeders with a complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents both mean performance and stability, optimized environments for specific genotypes and identifies mega-environments. To date, little information is available on marketable tuber yield of potato varieties and their adaptation under diverse environmental condition in North Shewa Oromia region. The present study was, therefore, conducted to generate relative information using GGE biplot model to assess the nature and magnitude of GEI and determine the response of different genotypes to varying environments to identify high yielding stable potato genotypes for the North Shewa Oromia region, Ethiopia.

2. Materials and Methods

The experiment was conducted at Three locations (Jida, Debra Libanos, and Girar Jarso) representing major Potato producing areas of the North Shewa Zone of Oromia region for two consecutive cropping years (2023 - 2024). A total of 10 Potato genotypes, comprising 8 advanced lines and two standard checks (Moti, and Wabi), were used (Table 1). In this trial design randomized complete block design with three replications were used. The experimental plot had an area of 11.25 m2 (3.75m width × 3m length). The space between replications and plots was 1.5 m and 1m, respectively.

The space between rows and plants was 75cm and 30cm, respectively. Fertilizer was applied at a rate of 195kg and 165kg ha-1 of NPS and UREA. All NPS and half of UREA were applied during planting, while the rest half splits were applied at vegetative stage of growth. The data were analyzed by using and Genstat 15th ed. [11] (GGE biplot). LSD was used for mean separation.

Table 1. *Lists of potato genotypes evaluated in the six test environments of North Shewa Zone Oromia Region during 2023-2024 main cropping season.*

Sr. No	Genotype	Genotype Code	Source
1	Aterababa x Dagim	G01	Adet ARC
2	CIP-313034. 03	G02	Sinana ARC
3	CIP13F2	G03	Sinana ARC
4	CIP-313037.04	G04	Sinana ARC
5	CIP-313022. 218	G05	Sinana ARC
6	Shenkola x Dagim	G06	Adet ARC

Sr. No	Genotype	Genotype Code	Source
7	CIP-313022. 68	G07	Sinana ARC
8	Abateneh x Ge. sh. 96	G08	Adet ARC
9	Moti	G09	Sinana ARC
10	Wabi	G10	Sinana ARC

Keys: G01up to G10 -genotype, Adet ARC= Adet Agricultural Reaserch center, Sinana ARC=Sinana Agricultural Reaserch center, CIP=International Potato Center (CIP)

2.1. Data Analysis

Different statistical software was used for data analysis. Combined analyses of variance and mean comparison with the LSD test were done using the General Linear Model (GLM) procedure of the Statistical Analysis Gen Stat 15th edition statistical package software. The chi-square test for homogeneity of variances was significant; however, no site has a CV value greater than 20%, so all six sites are included in the combined analysis of variance. The additive main effect and multiplicative interaction (AMMI) analysis was performed using the Gen Stat 15th software version. [11]

2.2. AMMI Analysis

Tuber yield was analyzed using the additive main effect and multiplicative interaction (AMMI) model, which was proposed for the AMMI analysis of variance (ANOVA) [10].

The AMMI model equation is as follows:

$$Yij=\mu + G_i + E_j + \sum_{K=1}^{n} \gamma_k \alpha_{ik} \delta_{jk} + pij + \varepsilon\ ij$$

Where, Yij is the mean tuber yield of the i^{th} genotype in the j^{th} Environment, μ is the grand mean;

G_i and E_j are the genotype and environment deviation from the grand mean, respectively; γ_k, α_{ik} and δ_{jk} are the eigenvalue of the k^{th} interaction PCA (IPCA) sustained in the AMMI model, the eigenvector for the i^{th} genotype from n^{th} IPCA, and the eigenvector for the j^{th}Environment from the n^{th} IPCA, respectively. n is the maximum number of multiplicative terms; pij is the GEI residual; ε_{ij} is the residual error term.

Genotype and genotype by environment interaction (GGE-biplot analysis)

Tuber yield was analyzed using the genotype main effect and genotype plus environment interaction effect (GGE) model. The GGE model equation described according to [18] was used as below: -

$$Yij-\mu - \beta j = \lambda 1 \xi i1 - \eta j1 + \lambda 2 \xi\ i2 - \eta j2 + \varepsilon ij$$

Where, Y_{ij} is the mean for the i^{th} genotype in the j^{th}Environment, μ is the grand mean, β_j is the main effect of environment j, λ_1 and λ_2 are the singular values decomposition of the first and second principal components (PC1and PC2), ξ_{i1} and ξ_{i2} are the PC_1 and PC_2 scores, respectively, for genotype ith, η_{j1} and η_{j2} are the eigenvectors for the j^{th} Environment for PC1 and PC2, and ε is the residual error term.

3. Results and Discussion

3.1. AMMI Analysis of Variance (AMMI ANOVA)

AMMI ANOVA revealed that tuber yield performance of the genotypes across six test environments was significantly ($p<0.01$) affected by the impact from the environments (E), genotypes (G), interaction, and the first two IPCAs (IPCA-I and IPCA-II) (Table 2).

These results were in agreement with the works of [4] who reported the significant difference among potato genotypes, environments and their interactions that was attributed to variations in different climatic and edaphic conditions across the locations. This showed that the genotypes responded differently to different environments or that genotype responses were affected by the environment, and thus, the test environments were highly variable. The AMMI model (Table 2) explained five of the principal component axes, demonstrating the presence of G × E interaction. Many researchers witnessed that the most accurate AMMI model prediction can be made using the first two IPCAs [16]. The remaining interaction principal component axes captured mostly non-predictive random variation and did not fit to predict validation observations [10]. Based on this, the first and second interaction principal components explained 84.18% of the total variation (IPCA1= 56.60% and IPCA2 = 27.58%). The first two interaction principal components (IPCA1 and IPCA2) together captured above 50% interaction principal components. Several authors also reported for various crops that a significant and greater percentage of G × E interaction (>50) was explained by the first two IPCA scores [2] on sweet potato and [4] on potato.

Table 2. Analysis of variance for tuber yield using Additive Mean Effect and Multiple Interactions (AMMI) model.

Source of variation	Df	Sum Sq	Variance explained (%)	GxE explained (%)	Mean Sq
Environment (E)	5	1192.49	18.28		238.50***
Replication/E	12	256.50	3.94		21.38***
Genotype (G)	9	3485.09	53.43		387.23***
GxE	45	1112.23	17.05		24.72**
PC1	13	629.51		56.60	48.42**
PC2	11	306.76		27.58	27.89**
PC3	9	116.96		10.52	13*
PC4	7	41.99		3.78	6ns
PC5	5	17.02		1.53	3.40ns
Residuals	108	475.28			4.40

AMMI1 biplot projects genotypes onto the ordinate and the abscissa, representing the additive main effect of genotypes and the effects of interplay between genotype and Environment, respectively [12]. Therefore, it simultaneously allows one to visualize the mean performance of genotype, Environment, and stability using IPCA1. For the AMMI1 biplot, as a rule, tuber yield vs. IPCA-1 (AMMI plot) genotypes or environments located on the right-hand side of the midpoint of the axis main effects have higher yields than those on the left-hand side [1]. Therefore, CIP-313034. 03 (G02), CIP-313022. 218 (G05), and CIP-313022. 68 (G07) were positioned in the AMMI biplot on the right side of the perpendicular vertical line (Figure 1). These genotypes were considered highly productive, while the remaining varieties yielded less than the grand mean. Genotypes with IPC1 scores close to zero expressed general adaptation, whereas the larger scores depict more specific adaptation to environments with IPC1 scores of the same sign [10]. The genotypes CIP-313034. 03 (G02), CIP-313022. 218 (G05), CIP-313022. 68 (G07), G01, and G04 were found close to the origin with a lower contribution to the magnitude of genotype by environment interaction, indicating that these varieties were stable.

However, G04, and G01, yielded low because they were located on the left side of the abscissa axis (Figure 1). Environments located on the right side of the midpoint of the axis are more productive than those on the left-hand side. The environments JD 24 (Jida 2024, DL23 (Debra Libanos 2023), and GJ24 (Girar Jarso2024) were located on the right side of the grand mean. In contrast, the remaining testing environments were located on the left side of the perpendicular line (Figure 1). JD24 (Jida 2024 and GJ24 (Girar Jarso2024) were found on the right side of the perpendicular line and far from the origin, implying that the testing locations contributed more to the magnitude of GEI and resulted in unstable genotype performance. DL23 (Debra Libanos 2023) was close to the origin with a lower contribution to GEI, implying that the testing location contributed less to the genotype by location interaction and contributed to the genotypes' stable performance. Overall, CIP-313022. 68 (G07) and CIP-313022. 218 (G05) are high-performing genotypes that are consistent across test sites.

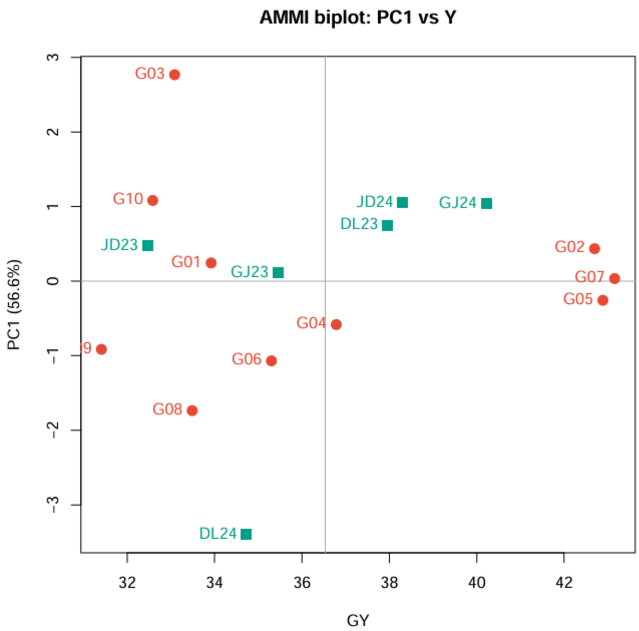

Figure 1. AMMI1 Biplot (tuber yield vs IPCA 1) illustrations for 10 potato genotypes tested across six locations.

Note G = genotype, DL23 (Debra Libanos 2023, DL24 (Debra Libanos 2024, JD23 (Jida 2023, JD24 (Jida 2024, GJ23 (Girar Jarso 2023), and GJ24 (Girar Jarso 2024)

3.2. GGE-biplot Analysis

3.2.1. Discriminative Power, Representativeness, and Test Environments Relationship

The GGE biplot indicating discriminating ability and representativeness of test environments is indicated in Figure 2. The biplot (ranking testers based on discriminating ability and representativeness) helps to visualize the length of the environment vectors which is proportional to standard deviation within the respective environments on the biplot and also shows the discriminating ability of the environments [20]. Thus, among the testing environments DL24 and DL23 (Debra Libanos 2024 and Debra Libanos 2023) with the longest vector were the most discriminating, while GJ23 (Girar Jarso 2023) was the least discriminating environments. Similarly, GJ24 and JD23 (Girar Jarso 2024 and Jida 2023) had the second longest vector mean hence they were the second best discriminating environments.

The best test environments for choosing superior genotypes are those with long vectors and small angles with the AEC abscissa. In contrast, test environments with long vectors and big angles with the AEC abscissa help screen out unstable genotypes [19].

Environment JD23 and DL23 (Jida 2023, and Debra Libanos 2023), which has a smaller angle with the AEA, is considered more representative than DL24 (Debra Libanos 2024), which has a significantly more considerable degree with the AEA. Since all test environments lie near the AEA, none of them show strong negative correlation or very different behavior, suggesting relatively consistent genotype performance across environments.

As shown in Figure 3, information was also provided regarding the connections among the test environments. Right (= 90°) and obtuse angles (>90°) show no correlation and a negative correlation, respectively, whereas acute angles (<90°) show a positive correlation among the test environments. The connections between the six test environments in the current investigation are shown in Figure 3. This graph demonstrates a positive relationship among the JD23, and DL23 (Jida 2023, and Debra Libanos 2023), sites since the angle between them is less than 90 degrees. It demonstrated that because test settings are closely connected, there is a higher chance of minimizing testing costs if the same information about the genotypes can be gained from fewer test environments. [19] also stated that if two test environments are tightly associated over time, one can be eliminated without losing a wealth of genotype-related data. As a result, genotypes that perform better in one Environment will perform worse in the other if environments are negatively correlated, and vice versa. However, if genotypes and environments have a positive correlation, then genotypes that thrive in one Environment will also thrive in the other.

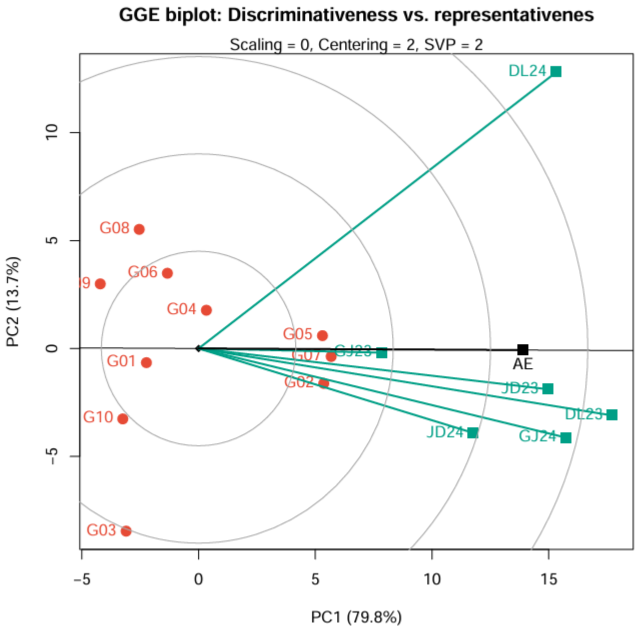

Figure 2. *GGE biplot view showing the relationship among the testing environments, discriminativeness vs representativeness.*

3.2.2. GGE Biplot Analysis

The GGE biplot simultaneously displays the genotype's main effect and the interaction effect of the genotype and Environment. The closeness between pairs of environments or genotypes in the biplot is proportional to their response to the genotype by environment interaction effects. The IPCA1 was plotted on the x-axis, whereas IPCA2 was plotted on the y-axis for tuber yield and yield components (Figure 3). The more IPCA scores approximate zero, the more stable the genotype across environments ([10], and the high magnitude of IPCA scores has specific adaptability [10]. Therefore, G04 and G01 attain IPCA values both (from positive and negative) relatively close to zero and are, hence, better stable and widely adaptable genotypes across locations (Figure 3). However, CIP-313022. 218 (G05), CIP-313022. 68 (G07), and CIP-313034. 03 (G02) attained IPCA values nearest to zero on both sides (positive or negative) (Figure 3) but was a high yielder.

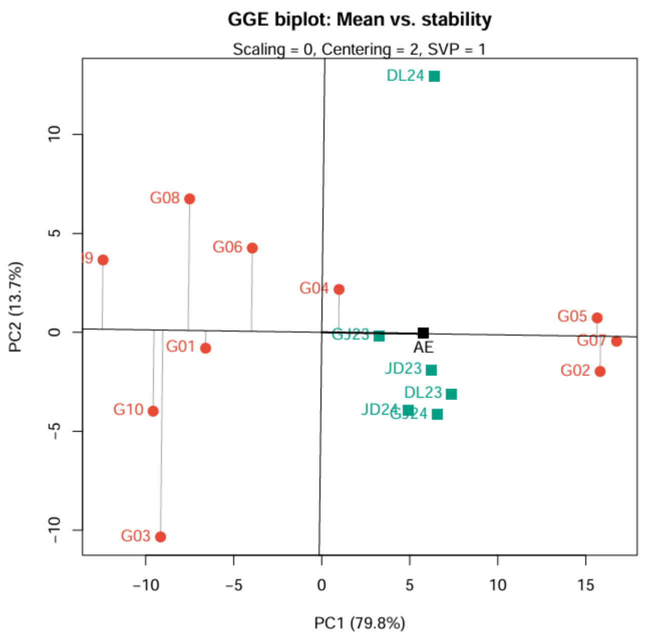

Figure 3. *"Mean vs Stability" GGE biplot for the potato trials yield data (tons/ha) with 10 genotypes (G) and 6 environments.*

3.2.3. "Which Won Where" Polygon View of GGE Biplot

The polygon view of the GGE biplot is important for studying the possible existence of different mega environments in a region [10]. In the present investigation, the partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 79.8% and 13.7% of GGE sum of squares, respectively, explaining 93.5% of the total variance (Figure 4). The polygon view of GGE biplot was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. In GGE biplot-graph, various lines emanating from the origin and become perpendicular to the line connecting the vertex genotypes are useful to divide the testing environments and genotypes into different sectors. Therefore, the six testing environments were divided into three mega environments, while the 10 genotypes were divided into four genotype groups (Figure 4). The first mega environments consisted of one DL24 (Debra Libanos 2024) and one genotypes (G08). The second mega environments included one environments JD23 (Jida 2023) and one genotypes CIP-313034. 03 (G02). The third mega environments included four environments JD23, JD24, DL23, and GJ24 (Jida 2023, Jida 2024, Debra Libanos 2023, and Girar Jarso 2024). The genotypes that are placed far from the biplot origin (vertex genotypes) are the poorest or best performing in some or all tested environments [17]. The winning cultivar is located at the vertex where two sides of the polygon join, whose perpendicular lines form the sector's borderline. As shown in Figure 4, the vertex genotypes are G03 and G08. These genotypes perform better or worse in some or all environments because they are the furthest from the biplot origin [14]. They are thought to be especially suited genotypes because they are more sensitive to changes in the Environment and contribute a high magnitude of GE. Varieties fall in the vertex where no environment falls in the sector, showing that such genotype were less stable across the environments [15]. According to [15], G03, and G09 were the least stable across environments due to their position in the vertex, where no environment falls within the sector.

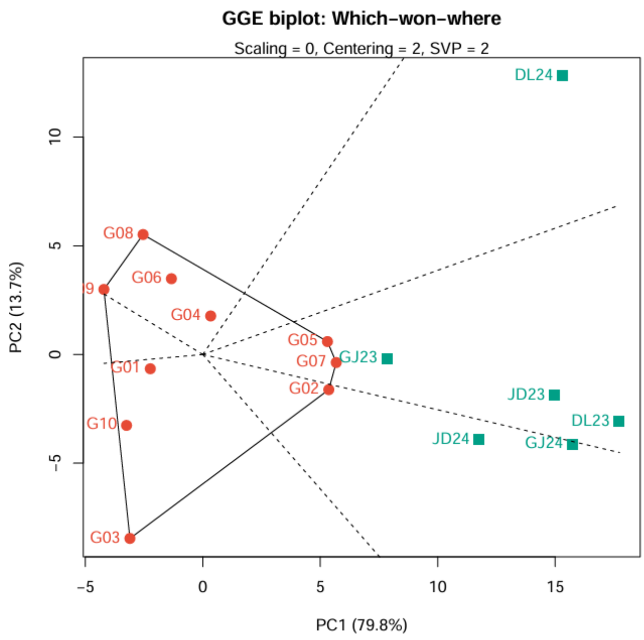

Figure 4. *The which-won-where view of the GGE biplot to delineate mega Environment and genotype performance in each mega Environment for tuber yield.*

4. Conclusion and Recommendations

The current study evaluated 10 potato genotypes grown under six environments in the north shewa zone Oromia region for genotype-environment interactions and tuber yield stability. The findings of this study revealed the presence of three mega environments and four potato genotypic groups. AMMI and GGE biplot models show that CIP-313022. 218 (G05) and CIP-313022. 68 (G07) genotypes have high mean performance across test environments. CIP-313034. 03 (G02) High yield but less stable can be considered for environments similar to those on the right side CIP-313022. 218" (G05) and CIP-313022. 68 (G07) " were the most promising regarding tuber yield and good stability. Hence, they were chosen as a prospective candidate for release in north shewa zone of Oromia region and similar agro ecologies throughout the country for production.

Abbreviations

G	Genotype

AMMI	Additive Main Effects and Multiplicative Interaction
GGE	Genotype Plus Genotype by Environment
ANOVA	Analysis of Variance
PCA	Principal Component Analysis
CIP	International Potato Center

Author Contributions

Zewdu Tegenu: Conceptualization, Data curation, Formal Analysis, Methodology, Project administration, Software, Supervision, Writing – original draft, Writing – review & editing

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Conflicts of Interest

Authors have declared that no competing interests exist.

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