Genotype by Environment Interaction Analysis for Tuber Yield of Potato (*Solanum tuberosum* L.) using a GGE Biplot Method in Amhara Region, Ethiopia

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doi: 10.6088/ijaser.020500011

**Abstract:** Potato is one of the important crops grown in mid and high altitude areas of Ethiopia. Several potato genotypes has been introduced and tested in different parts of the region. However, the stability and performance of these genotypes under different parts of the region is not yet assessed. Therefore, the objective of this study was to determine the effect of genotype, environment and their interaction for tuber yield and identify stable potato genotypes. The study was conducted using eight potato genotypes under rainfed production season of 2010 and 2011 at five potato growing areas of the region. Randomized complete block design with three replications was used for the experiment. Among the testing locations, the superior mean tuber yield (25.43t/ha) was obtained from Adet while the inferior (13.89t/ha) was from Injibara. Similarly, among the genotypes CIP-396004.337 had high mean tuber yield(25.66t/ha), while CIP-395011.2 had inferior mean tuber yield. Combined ANOVA indicated that the main effect due to environments, genotype and genotype by environment interaction were highly significant for tuber yield. The contribution of *E, G* and *GEI* for the total variation in tuber yield was about 47.11%, 8.83% and 44.07% respectively. The *GEI* was further partitioned using GGE biplot model. The first two principal components obtained by singular value decomposition of the centered data of tuber yield explained 71.04% of the total variability caused by (*G*+*GE*). Out of these variations PC1 and PC2 accounted 50.98% and 20.07% respectively. Generally, GGE biplot view of this study identified Serinka and CIP-396004.337 as ideal testing location and genotype respectively in the region.

**Keywords:** G; GxE; GEI; Ideal environment, Ideal genotype

1. Introduction

Potato (*Solanum tuberosum* L.), a member of the family *Solanaceae* and the genus *Solanum*, is one of the most productive and widely grown horticultural food crops in the world. The relative high carbohydrate and low fat content of the potato makes it an excellent energy source for human consumption (Dean, 1994). The potato has its origin in the high Andes of South America and was first cultivated in the vicinity of Lake Titicaca near the present border of Peru and Bolivia (Spooner et al. 2005). It was introduced to Ethiopia in 1858 by the German botanist Shimper (Berga et al.,1992). Since then, it serves as food and cash crop for small scale farmers. Among root and tuber crops in Ethiopia, potato ranks first in volume produced and consumed followed by Cassava, Sweet potato and Yam (CSA, 2010). In Ethiopia, about 70% of the available agricultural lands is located at an altitude of 1800-2500 m.a.s.l and receives an annual rainfall of more than 600mm, which is suitable for potato production (Yilma, 1989).

Even thought the country has suitable environmental condition the regional (9.35t/ha) as well as national (7.99t/ha) (CSA, 2010) productivity of potato during 2010 season is very low as compared with world average of 17.16 t/ha (FAO, 2012). A number of production problems that accounts for low regional as well as national yield have been identified. The major ones are lack of stable, well-adapted, disease and insect pests’ tolerant varieties (Tesfaye and Yigzaw, 2008). Farmers and researchers want successful potato varieties that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions but also over years. The
basic cause of differences between genotypes in their yield stability is the occurrence of genotype-environment interactions (GEI).

To overcome GEI problem, the universal practice of scientists in most crops is to plant them in performance trials over several environments and years to ensure that the selected genotypes have a high and stable performance over a wide range of environments. Since the region as well as country has diverse climatic conditions and soil types escalates the problem of GEI even further.

Once the data generated over several locations and years, several methods have been proposed to analyze GEI. The most recent method, GGE biplot model, provides breeders a more 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 it identifies mega-environments (Ding et al., 2007). To date, little information is available on marketable tuber yield of potato and its adaptation pattern especially under Amhara region/Ethiopia. Thus there is a need to study GEI by using the GGE biplot models to determine the response of different genotypes to varying environments, identify high yielding stable potato genotypes in the Amhara region/Ethiopia. The objectives of this study were to assess the nature and magnitude GEI, identify stable and high yielder genotypes.

2. Materials and Methods

The experiment was carried out with eight potato genotypes; CIP-396033.102, CIP- 395120.36, CIP-396004.337, CIP-395096.2, CIP-395111.13, CIP-395011.2, CIP-396031.108, and CIP-396004.225. All genotypes were introduced from international potato center (CIP). The experiment was conducted under rainfed seasons of 2010 and 2011 in five different potato growing locations with a total of 10 environments (Table 1). Planting was done in May in plots of 3m*3m with randomized complete block design with three replicates. The tubers were planted 0.75m*0.3m row and plant spacing respectively. Fertilization and crop management were applied per the recommendation of the specific location (Tesfaye, 2010). Tuber yield was taken from 16 plants of middle rows and computed to hectare. Tubers which are healthy and greater than 30mm diameter considered as marketable tubers (Bonierbale et al., 2007). The collected data was analyzed by using SAS V9 (2002) (ANOVA) and Genstat 14th ed (2011) (GGE biplot). LSD was used for mean separation.

The locations were considered random and Genotype as a fixed effects and a mixed effect model ANOVA was used for statistical analysis. In the ANOVA, sources of partitioned variances include blocks, treatments and error terms. The treatment was broken down into three components: G, E and GEI effects in the following equation (Ding et al, 2007):

\[
Y_{ijr} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + b_j + \epsilon_{ijr}
\]

Where \(Y_{ijr}\) is the average value of the dependent variable of genotype i in environment j and block r, \(\mu\) is a grand mean, \(\alpha_i\) is the effect of the \(i^{th}\) genotype. \(\beta_j\) is the effect of the \(j^{th}\) environment, \(\alpha\beta_{ij}\) is the effect of the \(i^{th}\) genotype by the \(j^{th}\) environment, \(b_j\) is the block effect at the \(j^{th}\) environment and \(\epsilon_{ijr}\), is the residual error term.

Table 1: Description of the test environments of the field experiment

<table>
<thead>
<tr>
<th>Experimental Site</th>
<th>Geographical Location</th>
<th>Elevation (m.a.s.l.)</th>
<th>Soil properties</th>
<th>Climate data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adet</td>
<td>11°16’30.3”N</td>
<td>2240</td>
<td>5.20 Clay</td>
<td>1005.54</td>
</tr>
</tbody>
</table>
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Note: the mean rainfall data and temperature shown above is only the average of the growing months from May through September.

Stability Analysis: GE interaction analyzing is done by GGE Biplot, which uses singular value decomposition (SVD) to decompose GGE into two or more principal components. Each principal component consists of a set of genotype scores multiplied by a set of environment scores, and a two-dimensional biplot can be generated (Ding et al., 2007).

In GGE biplots genotype plus genotype × environment (G+GE) interaction is studied together and to achieve this G+GE effect is separated out from the observed mean from equation 3.1 (by omitting random error and block effect) and eventually model becomes as

$$Y_{ij} - \mu - \beta_j = \alpha_i + \alpha \beta_j$$

(2)

The GGE (G+GE) effect is partitioned into multiplicative terms by using SVD. The model based on singular value decomposition (SVD) of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{ij1} \eta_{j1} + \lambda_2 \xi_{ij2} \eta_{j2} + \epsilon_{ij}$$

(3)

Where $Y_{ij}$ the measured mean of genotype $i$ in environment $j$, $\mu$ is the grand mean, is the main effect of environment $j$, $\beta_j$ being the mean yield across all genotypes in environment $j$, $\lambda_1$ and $\lambda_2$ are the singular values (SV) for the first and second principal components(PC1 and PC2), respectively, and $\xi_{ij1}$ are eigenvectors of genotype $i$ for PC1 and $\xi_{ij2}$ PC2, respectively, $\eta_{j1}$ and $\eta_{j2}$ are eigenvectors of environment $j$ for PC1 and PC2, respectively, $\epsilon_{ij}$ is the residual associated with genotype $i$ in environment $j$ (Ding et al., 2007).

PC1 and PC2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors. Singular-value partitioning is implemented by,

$$g_{ij} = \lambda_1^{f_i} \xi_{ij} \text{ and } e_{ij} = \lambda_2^{1-f_i} \eta_{ij}$$

(4)

Where $f_i$ is the partition factor for PC1. Theoretically, $f_i$ can be a value between 0 and 1, but 0.5 is most commonly used.

To generate the GGE biplot, the formula (3.4) was presented as:

$$Y_{ij} - \nu - \beta_j = g_{ij1} e_{ij1} + g_{ij2} e_{ij2} + \epsilon_{ij}$$

(5)
3. Results and Discussion

3.1 Analysis of Variance

The analysis of variance for marketable tuber yield (t/ha) for each year/seasons and combined over years of tested genotypes revealed a highly significant variations for the genotype, environment and genotype by environment interaction effect (Table 2). The table also indicates that, location was the most important source of yield variation, accounted for 51.51 and 46.07% for the total variation (G, L and GL) during 2010 and 2011 season respectively. Similarly, the contribution of GL was about 38.50 and 42.23% respectively. GL was greater than G in both testing years. The same is true in combined data across years/seasons. The combined data analysis of variance across years and locations indicated that mean marketable tuber yield (MTY) was significantly influenced by environments (L+Y) which accounted for 47.11% of the mean MTY(t/ha) variation(G, L, Y, GL, GY, LY and GLY), while G and GEI explained 8.83% and 44.07 % of the variation, respectively(Table 2). Out of main effect, the contribution of year was about 0.21% (Table 2) this indicated that relatively year effect had minimal contribution for the total variation of MTY of potato .

The mean performance of tested genotypes across testing years and locations ranged from 18.78t/ha for G6 to 25.66t/ha for G3 (Table 3). The table also indicates that G6 and G4 had superior MTY at Ad1 and Db1 while inferior at Db1 and Ij2 respectively. This indicates that presence of cross over interaction. Mean MTY (t/ha) of testing environments varied from 13.05t/ha for Ij1 to 27.02t/ha for Dt1 (Table 3) this indicates that the influence of soil propriety, temperature, precipitation or another factor of climate on MTY (t/ha) (Table 1). The larger yield variation due to L, which is irrelevant to cultivar evaluation and mega environment investigation (Yan et al., 2000), Justifies selection of site regression as the appropriate model for analyzing the multi environment trials data. The larger GL, relative to G, confirms the possible existence of different mega environments. Thus, the MTY (t/ha) data of potato was subjected for GGE biplot analysis.

Table 2: Genotype (eG), environment (L and Y), genotype by environment (GE), variance terms for rainfed potato yield trials in 2010- 2011 and combined over these years/seasons

<table>
<thead>
<tr>
<th>Year /s</th>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>%(L+G+GL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>Location(L)</td>
<td>4</td>
<td>3117.05</td>
<td>779.26**</td>
<td>51.51</td>
</tr>
<tr>
<td></td>
<td>Genotype(G)</td>
<td>7</td>
<td>604.26</td>
<td>86.32**</td>
<td>9.99</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>28</td>
<td>2329.62</td>
<td>83.20**</td>
<td>38.50</td>
</tr>
<tr>
<td>2011</td>
<td>Location(L)</td>
<td>4</td>
<td>2332.70</td>
<td>583.17**</td>
<td>46.07</td>
</tr>
<tr>
<td></td>
<td>Genotype(G)</td>
<td>7</td>
<td>592.43</td>
<td>84.63**</td>
<td>11.70</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>28</td>
<td>2138.06</td>
<td>76.36**</td>
<td>42.23</td>
</tr>
</tbody>
</table>

%(L+G+Y+GL +GY+GYL)

| Combined  | Location(L)| 4   | 987.91   | 141.13**| 46.90     |
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<table>
<thead>
<tr>
<th>Genotype(G)</th>
<th>7</th>
<th>5246.66</th>
<th>1311.66**</th>
<th>8.83</th>
</tr>
</thead>
<tbody>
<tr>
<td>Year (Y)</td>
<td>1</td>
<td>23.16</td>
<td>23.16**</td>
<td>0.21</td>
</tr>
<tr>
<td>GL</td>
<td>28</td>
<td>3699.38</td>
<td>132.12**</td>
<td>33.07</td>
</tr>
<tr>
<td>GY</td>
<td>7</td>
<td>208.25</td>
<td>29.75**</td>
<td>1.86</td>
</tr>
<tr>
<td>LY</td>
<td>4</td>
<td>223.76</td>
<td>55.94**</td>
<td>2.00</td>
</tr>
<tr>
<td>GLY</td>
<td>28</td>
<td>798.64</td>
<td>28.52**</td>
<td>7.14</td>
</tr>
</tbody>
</table>

** Significant at (P ≤ 0.01)

*Means with the same letters within a column are not significantly different at p<0.01 based on Fishers LSD. Where Ad1 & Ad2; Ij1&Ij2, Sr1& Sr2; Db1 & Db2 and Dt1 &Dt2 were 2010 and 2011 rain fed season in Adet, Injibara, Serinka, Debribirhan and Debretabor respectively.

Comparison between genotypes: on the GGE biplot, the performance of two genotypes can be visually compared by connecting their markers with a straight line and drowning perpendicular line/or equality line that pass through the biplot origin. Genotypes had better yield in environments that are located on its side of the equality line (Yan et al., 2000; Yan and Tinker, 2006). In figure 6, G3 and G6 were compared, the performance of G6 was better in Ad1, Ad2, Dt1 and Dt2 testing environments than G3 and vice versa in other testing environments. As table 3 indicated that Ad1, Ad2, Dt1 and Dt2 had mean MTY above average. This indicates that, relatively G6 was better adapted to high potential areas than G3.

4. Suitability of genotypes for particular environment using the “Which-Won-Where” function of a GGE biplot:

Figure 4 shows the which-won-Where view of this study. The vertex genotypes in this figure were G1, G2, G3, G4 and G6. Five rays divide the biplot into five sectors. The vertex genotype for sector which encompasses Db1, Db2 and Sr1 was G2 and sector content Dt1 and Dt2 was G4, for Ad1 and Ad2 was G6, for Ij1, Ij2, and Sr2 was G3/G1 these implying that these genotypes were the winning genotypes for respected environments. However, Which-won-where views of the GGE biplot of each year was not repeated across years (Figure 8). In this case GE cannot be exploited rather, it must be avoided by selecting high yielding and stable genotypes across target environments (Yan et al., 2007). Thus, G3 had high mean marketable tuber yield and stability across test locations and years, so G3 identified as high yielder and wide adaptable genotype.

Figure 1: GGE-biplot based on genotype focused scaling for the trait MTY (t/ha), 2010-2011
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N.b- Abbreviations in the biplot are as follows:

Table 3: Mean marketable tuber yield (t/ha) of eight potato genotypes across 10 environments in 2010-2011

<table>
<thead>
<tr>
<th>Genotype Code</th>
<th>Genotypes</th>
<th>During 2010 season</th>
<th>During 2011 season</th>
<th>Combined mean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ad1</td>
<td>Ij1</td>
<td>Sr1</td>
<td>Db1</td>
</tr>
<tr>
<td>1</td>
<td>18.01</td>
<td>11.7</td>
<td>23.51</td>
<td>24.95</td>
</tr>
<tr>
<td></td>
<td>23.85</td>
<td>11.2</td>
<td>24.15</td>
<td>34.64</td>
</tr>
<tr>
<td>2</td>
<td>28.10</td>
<td>22.3</td>
<td>19.63</td>
<td>25.77</td>
</tr>
<tr>
<td>3</td>
<td>23.83</td>
<td>11.5</td>
<td>25.77</td>
<td>35.16</td>
</tr>
<tr>
<td></td>
<td>29.30</td>
<td>13.3</td>
<td>24.59</td>
<td>27.41</td>
</tr>
<tr>
<td>4</td>
<td>29.36</td>
<td>13.7</td>
<td>14.32</td>
<td>28.98</td>
</tr>
<tr>
<td></td>
<td>21.93</td>
<td>11.2</td>
<td>25.40</td>
<td>31.85</td>
</tr>
<tr>
<td>5</td>
<td>23.52</td>
<td>9.20</td>
<td>21.43</td>
<td>30.71</td>
</tr>
<tr>
<td></td>
<td>R square</td>
<td>0.87</td>
<td>0.95</td>
<td>0.96</td>
</tr>
<tr>
<td></td>
<td>P Level</td>
<td>0.000</td>
<td>1</td>
<td>0.000</td>
</tr>
<tr>
<td></td>
<td>LSD Value</td>
<td>4.688</td>
<td>2.73</td>
<td>2.748</td>
</tr>
<tr>
<td></td>
<td>CV</td>
<td>7.80</td>
<td>8.61</td>
<td>5.72</td>
</tr>
<tr>
<td></td>
<td>Mean</td>
<td>24.74</td>
<td>13.0</td>
<td>19.76</td>
</tr>
</tbody>
</table>
**Figure 2:** GGE-biplot view to show relationship among 10 testing environments, 2010-2011

**Figure 3:** GGE ranking biplot shows the mean marketable tuber yield and stability performance of eight tested genotypes
Figure 4: Comparison biplot views of marketable tuber yield of genotypes with the ideal genotype

Figure 5: Which won where view of GGE biplot of eight genotypes over five locations during 2010 (left) and 2011 (right)
5. Summary and Conclusion

Among testing environments, the minimum mean marketable tuber yield (t/ha) was obtained from Ij1 (Injibara first season) while the maximum mean was from Dt1 (Debretabor first season). The mean performance of tested genotypes across all environments ranged from 18.78 t/ha for G6 (CIP-395011.2) to 25.66 t/ha for G3 (CIP-396004.337) with an average mean yield of 21.72 t/ha.

The Analysis of variance across locations and years of this study indicated that location was the most important source of yield variation, accounted for 46.90% for the total variance (G, L, Y and GEI). The contribution of GEI for the yield variation was about 44.07% while G was about 8.83%. The GEI component partitioned by GGE biplot, the first two principal components (PC1 and PC2) obtained by singular value decomposition of the centered data explained 71.04% of the total variability caused by (G+GE). Out of these variations PC1 and PC2 accounted 50.98% and 20.07% respectively.

Biplot view of relation among test environments of this study showed that Environment Serinka (Sr1 and sr2) was more associations with environment Injibara (Ij1 and Ij2). Thus, indirect response to selection could be possible in these environments. Among the testing environments, Serinka (Sr1 and Sr2) is ideal testing location to identify stable and high yielder genotypes for the region.

Mean performance and stability biplot of tested genotypes across test environments indicates that G3 had highest mean yield as well as stability while G6 and G4 had mean minimum yield as well as less stability.

In this study crossover GEI not repeatable across years. Thus mega environment classification was not possible in this study. Therefore, based on high yield potential and stability across test environments, G3 (CIP-396004.337) selected as best genotype for testing sites.

Acknowledgements

The authors would like to acknowledge the financial support provided by Adet Agricultural Research Center, Spanish Agency for International Development Cooperation (AECID) and SWISHA. The authors also highly appreciate and acknowledge the efforts of potato team of respective agricultural research centers for managing the field trials and collecting data. We use this opportunity to thank Tesfaye Abebe (PhD) for his guidance and provision of materials. Our appreciation also goes to Miss Yemisrach Melkie for her help in providing computer service.

6. References


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