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Full Length Research Paper

# Genotype-environment interaction and correlation of some stability parameters of total starch yield in potato in Amhara region, Ethiopia

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This study was carried out to assess the nature and magnitude of genotype-environment interaction (GEI) and the correlation among some stability parameters. Eleven potato genotypes were evaluated during 2011 rainfed season at three locations with Randomized Complete Block design with three replications in Amhara region. Combined analysis of variance indicated that the main effect due to location, genotype and genotype by environment interaction were highly significant. Location and genotype were the most important source of variation accounted for 46.51 and 33.82% of the total variance respectively. The GxE interaction was further partitioned using GGE biplot model. The first two principal components obtained by singular value decomposition of the centered data of total starch yield (t/ha) explained 96.8% of the total variability caused by (G+GE). Out of these variations PC1 and PC2 accounted 81 and 15.8% respectively. GGE biplot view across test environments indicated that E1 (Adet) was ideal test location. The stability analysis identified Guassa as more stable and high yielder genotype and recommended for commercial production for Amhara region. Significant ( $P < 0.01$ ) and positive correlations were found among  $\delta^2_i$ ,  $W_i$  and ASV, implying that anyone of these parameters could be used to describe genotype stability.

**Key words:** Potato (*Solanum tuberosum* L.), genotype plus genotype by environment biplot, genotype-environment interaction, principal component, stability parameters.

## INTRODUCTION

Potato (*Solanum tuberosum* L.), is one of the most productive and widely grown horticultural food crops in the world. Potato is an important food and nutritional security option, particularly for the poor, at global level (Thiele et al., 2010). Africa has been the most rapidly

growing region in terms of potato production during recent past (Scott et al., 2013). Ethiopia is an important potato producing African nation, however, it possesses distinct agro-climatic conditions and indigenously developed potato varieties for sustainable

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national potato improvement and development.

The composition of the respective potato variety is genetically determined, but also dependent on extrinsic factors such as climate, atmospheric conditions, soil, fertilizer use, and diseases (Norgia et al., 2008).

Farmers and researchers want successful new 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 (G×E) interactions. To overcome G×E interaction 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 Amhara region as well as Ethiopia has diverse climatic conditions and soil types escalates the problem of G×E interaction even further. Thought study of G×E interaction is particularly relevant to areas that have diverse agro-ecologies, as is the case in the Amhara region.

Once the data generated over several locations and years, several statistical methods have been proposed to analyze G×E interactions. These methods can be divided in to two major groups, univariate and multivariate stability statistics (Lin et al., 1986). The most recent multivariate stability statistics 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 and it identifies mega environments (Ding et al., 2007).

To date, little information is available on total starch yield of potato and its adaptation pattern especially under Amhara region. Thus there is a need to study GEI by using the GGE biplot and other stability parameters to determine the response of different genotypes to varying environments, identify high yielding stable potato genotypes in the region. Thus, the objectives of this study were to assess the nature and magnitude GEI, identify stable and high yielder genotypes and determine the correlation among some stability parameters.

## MATERIALS AND METHODS

### Field study

The field experiment was carried out with 11 genotypes; CIP-396033.102, CIP-395120.36, CIP-396004.337, CIP-395096.2, CIP-395111.13, CIP-395011.2, CIP-396031.108, CIP-396004.225, Guassa, Gudenie and Ater Abeba. The experiment was conducted under rainfed conditions in three different potato growing locations during 2011 (Table 1). At each site, planting was done in May in plots of 9 m<sup>2</sup> with 4 rows measuring 3 m with randomized block design in three replicates. The tubers were planted 0.75 m and 0.3 m row and plant spacing, respectively. Fertilizer application was 117 kg N/ha for Adet and Injibara and 176kg N/ha for Debretabor

location's where as uniform rate of DAP (150 kg P<sub>2</sub>O<sub>5</sub>/ha) was applied for each testing site. Whole DAP was applied at planting. Nitrogen was applied by splitting out half after two week's full emergency and the reaming half at flowering stage (Tesfaye, 2010). Four hundred gram fresh marketable tubers samples per block of each genotype were taken for starch extraction. Starch content was determined by using current protocol in food chemistry (Vasanthan, 2001).

The data analysis was conducted using appropriate statistical software's; viz., AGROBASE 20 (Eberhart and Russell regression stability analysis, Wricke Ecovalence and Shukla stability variance and cultivar superiority measure), SAS (2002) (analysis of variance and mean separation) and GGE biplot (GGE biplot) and Genstat (2010) (ASV).

### Stability analysis

The method of Eberhart and Russell (1966) was used to calculate the regression coefficient (bi), deviation from regression ( $S^2 di$ ). It was calculated by regressing mean tuber yield of individual genotypes genotypic index. Shukla stability variance ( $\sigma^2 i$ ) (1972) where genotypes with minimum values are considered stable. Ecovalence (Wi) suggested by Wricke (1962) and cultivar superiority measure were computed to further describe stability. Lin and Binns (1988) proposed a superiority measure ( $P_i$ ), which is defined as the distance mean square between the genotype response and the maximum response. The smaller the value of  $P_i$ , the lesser its distance to the genotype with maximum yield and the better the genotype is (Crossa, 1990). The AMMI stability value (ASV) (Purchase, 2000) based on the AMMI model's IPCA1 and IPCA2 scores for each genotype was also computed. ASV is the distance from the coordinate point to the origin in a two dimensional scattergram of IPCA1 scores against IPCA2 scores. The larger the IPCA scores, either negative or positive, the more specifically adapted a genotype is to a certain environments; the smaller the IPCA scores, the more stable the genotype is over all environments studied.

Another effective tool for analyzing GE interactions is 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.

## RESULTS AND DISCUSSION

The analysis of variance over locations of total starch yield (TSY) revealed a highly significant ( $p \leq 0.01$ ) variations for the genotype and environment effect and genotype by environment interaction. Thus, multi-environment data of potato were subjected to different GEI stability analysis. The ANOVA result of this study indicated that the variation explained by environment (E) was about 46.51% of total variation (G+L+GL) while genotype (G) and GE were accounted 33.82 and 19.67 respectively (Table 2). This indicated that genotype and environment are important in governing the expression of this trait. It agrees with the finding of Bach (2011), quality traits of potato manly influenced by genotype and environment factors.

The mean total starch yield (TSY) (t/ha) of the 11 genotypes across individual environment varied from

**Table 1.** Description of the testing environments.

Experimental site	Geographical location	Elevation (m.a.s.l.)	Soil physical and chemical properties						Metrology data		
			Total N (%)	Available P (ppm)	Available K (%)	pH	Organic matter	Texture	Annual RF (mm)	Sunshine hour (h)	Temp. (°C)
Adet	11°16'30.3"N 37°30'1.8" E	2240	0.435	7.17	0.7808	5.20	1.48	Heavy clay	1005.54	6.12	18.60
Debretabor	11°51'0"N, 38°1'0"E	2630	0.202	17.18	0.3392	4.94	3.00	Clay	1416.15	5.65	17.14
Injibara	10° 57' 0" N, 36° 56' 0" E	2610	0.278	5.62	0.0000	4.50	1.35	Clay	2175.37	4.28	15.18

The mean rainfall data, temperature and sunshine hour shown above is only the average of the growing months from May through September.

**Table 2.** Genotype (G), Location (L), genotype by location (GL), variance terms for rainfed potato trials in 2011 growing season.

Trait	Source	DF	SS	MS	%(L+G+GL)
	Location (L)	2	73.709	36.855**	46.51
TSY	Genotype (G)	10	53.594	5.359**	33.82
	GL	20	31.166	1.558**	19.67

\*\*, Significant ( $p < 0.01$ ); TSY, total starch yield (t/ha); DF, degree of freedom; SS, sum of squares; MS, mean squares

2.100 t/ha for Injibara to 4.008 t/ha for Debretabor with an overall mean of 3.316 t/ha. This is mainly because of broad span of environmental conditions (Table 1). The TSY values had a greater range of values in Adet (4.031 t/ha) than Injibara (1.476 t/ha), which likely contributed to the significant location x genotype interaction (Table 3). The mean performance of the tested genotypes across locations showed that G3, G7 and G9 had the highest TSY values (4.296, 4.275 and 4.039 t/ha respectively) as well as they were showed highly significance difference with other genotypes.

Since we found significant GEI effect in the ANOVA source of variation multi-environment data were subjected to GGE bilpot analysis. The

partitioning of GGE of total starch yield through GGE biplot analysis showed that PC1 and PC2 accounted 81 and 15.8% of GGE sum of squares, respectively explaining a total of 96.8% variation (Figure 1). This result revealed that there was a differential total starch yield performance among potato genotypes across testing environments due to the presence of GEI. Highest mean values fall on the positive end of PC1 and lowest mean values have negative values (Yan, 2001). High stability across environments is reflected in a small PC2. Genotypes that are stable over all environments fall very close to the PC2 origin, while genotypes that are highly variable are on the extreme positive or negative ends of PC2 (Yan, 2001). Thus biplot analysis showed that, G7, G9

and 10 had high stability, especially compared to G4 and G11 (Figure 1). Genotype G11, G4 and G2 had below average TSY levels (3.316 t/ha) across testing locations. Genotype G1, G5, G8 and G10 had nearly average mean TSY (t/ha). Among the tested genotypes, G7 had high stability as well as high mean yield in the trial while G4 had low stability. Biplot also separated the three environments into two groupings.

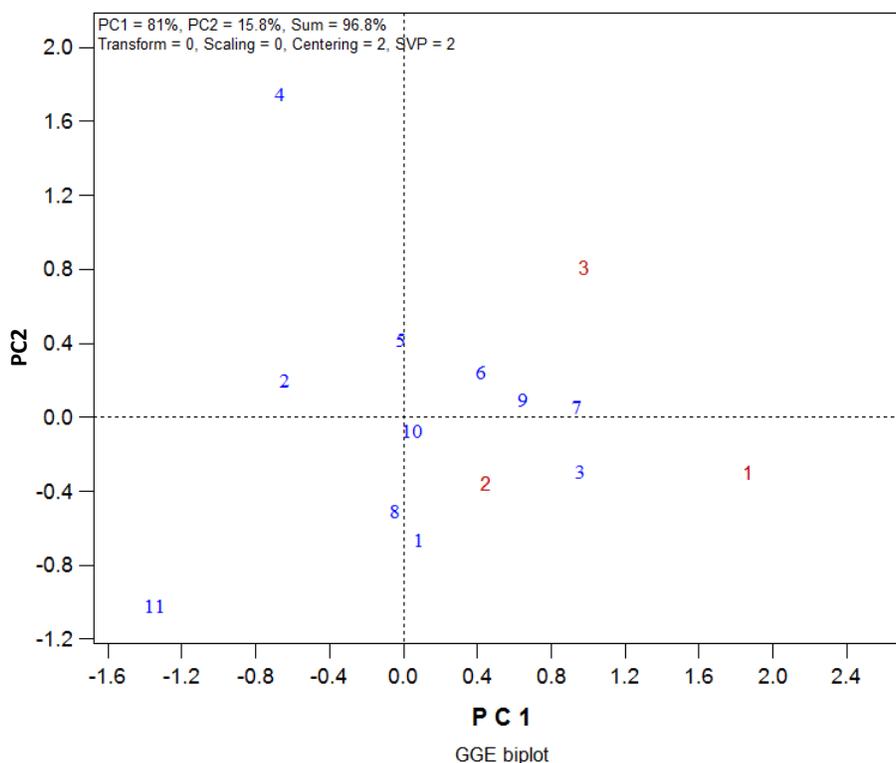
### Relation among test environments

GGE-biplot which depends on environment focused scaling was portrayed to estimate the pattern of environments (Figure 2). The figure

**Table 3.** Mean total starch yield (t/ha) of 11 genotypes over three locations, 2011 season.

G code	Genotype	Locations			Combined over locations
		Adet(E1)	Injibara(E2)	Debretabor (E3)	
1	CIP-396033.102	4.153 <sup>c</sup>	2.410 <sup>a</sup>	3.534 <sup>cd</sup>	3.366 <sup>b</sup>
2	CIP-395120.36	2.603 <sup>e</sup>	1.607 <sup>b</sup>	3.462 <sup>d</sup>	2.557 <sup>c</sup>
3	CIP-396004.337	5.644 <sup>a</sup>	2.603 <sup>a</sup>	4.640 <sup>ab</sup>	4.296 <sup>a</sup>
4	CIP-395096.2	2.0180 <sup>f</sup>	1.127 <sup>c</sup>	4.701 <sup>ab</sup>	2.615 <sup>c</sup>
5	CIP-395111.13	3.411 <sup>d</sup>	2.484 <sup>a</sup>	4.458 <sup>ab</sup>	3.451 <sup>b</sup>
6	CIP-395011.2	4.703 <sup>b</sup>	1.643 <sup>b</sup>	4.385 <sup>abc</sup>	3.577 <sup>b</sup>
7	CIP-396031.108	5.513 <sup>a</sup>	2.424 <sup>a</sup>	4.888 <sup>a</sup>	4.275 <sup>a</sup>
8	CIP-396004.225	3.802 <sup>cd</sup>	2.438 <sup>a</sup>	3.577 <sup>cd</sup>	3.272 <sup>b</sup>
9	Guassa	4.884 <sup>b</sup>	2.515 <sup>a</sup>	4.717 <sup>ab</sup>	4.039 <sup>a</sup>
10	Gudenie	3.910 <sup>c</sup>	1.991 <sup>b</sup>	3.881 <sup>bcd</sup>	3.260 <sup>b</sup>
11	Ater Abeba	1.614 <sup>f</sup>	1.856 <sup>b</sup>	1.840 <sup>e</sup>	1.770 <sup>d</sup>
	LSD value	0.4246	0.4035	0.8667	0.3395
	R-Square	0.99	0.92	0.90	0.97
	C. V	4.76	8.27	9.31	8.18
	Mean	3.842	2.100	4.008	3.316

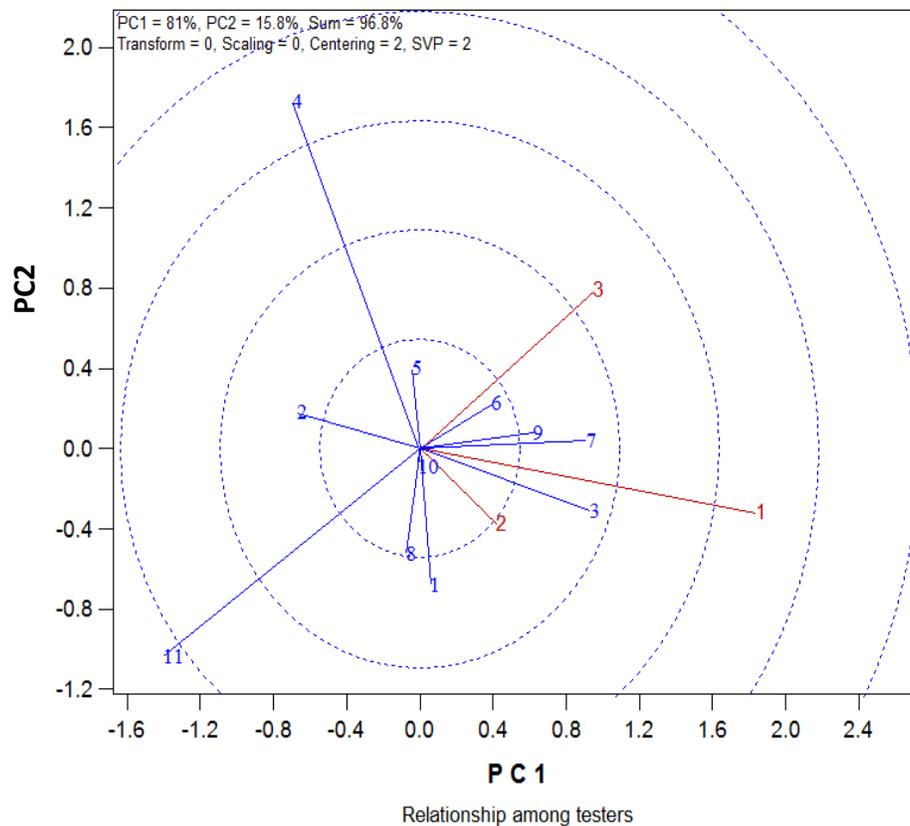
\*Means with the same letters within a column are not significantly different at  $p < 0.01$  based on Fisher LSD tests. G, Genotype.



**Figure 1.** GGE-biplot of total starch yield (t/ha) based on genotype focused scaling for genotypes.

shows that the angle between E1 and E2, E1 and E3 were less than 90 while the angle between E2 and E3 were nearly right angle. This indicates that E1 positively correlated to E2 and E3 whereas E2 and E3 were not

correlated to each other. Therefore, response to indirect selection for total starch yield (t/ha) of potato could be possible in E1 interims of E2 and E3. The figure also shows the performance of all genotypes in all



**Figure 2.** The GGE-biplot view showing total starch yield per ha of each potato genotype in each environment based on GGE-biplot.

environments. In this regard genotype G3 performed well in E1 and E2 than E3 while G7 performed well in E1 than the other locations. Genotype G2 and G11 had poor performance over tested environments.

### Relation among genotypes

Figure 2 shows the relationship among potato genotypes. The distance between two genotypes approximates the Euclidean distance between them and hence, is a measure of dissimilarity among the genotypes (Kroonenberg, 1995). Thus, G3 and/or G7 were quite different in their genetic make-up with G11, G2, G4 whereas very close to G9 and G6. A genotype located near the biplot origin has an average value in each of the environments. Such genotype has very minimum contribution to both G and GE interaction. Besides this, the length of genotypes vectors measures the contribution of the genotypes to either G or GEI or both (Yan and Tinker, 2006). Thus, genotypes G7 and G3 with the longest vector are the best genotypes while genotype G11 with the longest vector is the poorest or the most unstable (G4). On the other hand, G10 having very short vector and nearer to the biplot origin has very minimum

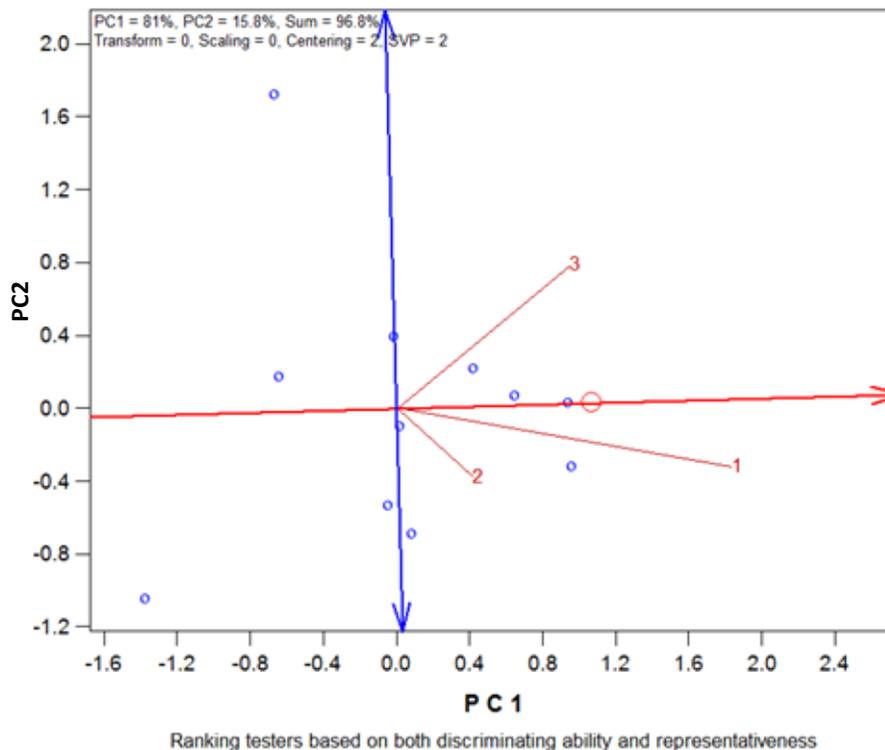
contribution to both G and GEI.

### Discriminating ability and representativeness of test environments

Discriminating power and representativeness view of the test environment of GGE-biplot view of the trait total starch yield is presented in Figure 3. Thus, among the testing environments E1 (Adet) with the longest vector was the most discriminating, while E2 (Injibara) was the least discriminating (shortest vector length) environment. E1 had long vectors and small angles with the AEC abscissa and was ideal for selecting superior genotypes. This result indicated that E1 (Adet) was ideal environment for selecting superior genotypes for the trait TSY of potato genotypes.

### Mean performance and stability of potato genotypes

Figure 4 shows the average tester coordination (ATC) view of the total starch yield GGE biplot. A solid line with a single arrow, called the average tester axis (ATA), passes through the biplot origin and the average



**Figure 3.** GGE-biplot of total starch (t/ha) showing a comparison of test environments with in ideal environment.

environmental coordinate (AEC). ATA line is used for categorizing cultivar mean performance such that cultivars further along the line, away from the biplot origin and in the direction of the arrow, exhibit a higher level of mean performance. In this manner, G can be assessed with the biplot. GE interaction can be determined as cultivar distance, in either direction, from the ATA such that cultivars closer to the ATA are more stable than cultivars with a greater distance from the ATA. A line bisecting the biplot origin and perpendicular to the ATA with arrows at each end, called the stability line, aids in the interpretation such that longer projections onto the stability line indicate greater cultivar instability. In this study, the shorter genotype vector lengths from ATA were obtained from G7 and G9. These genotypes also had better performances. G4 with the longest genotype vector was highly unstable (poorly performed genotype). The ATC ordinate separates genotypes with above average mean from below average means. Therefore, genotypes with above average means were from G7 to G6 on the graph, while genotype from 11 to 4 indicate genotypes with below average means while G1, G5, G8 and G10 gave average mean total starch yield.

### Mega environment classification and winning genotypes

One of the most attractive features of GGE biplot is its

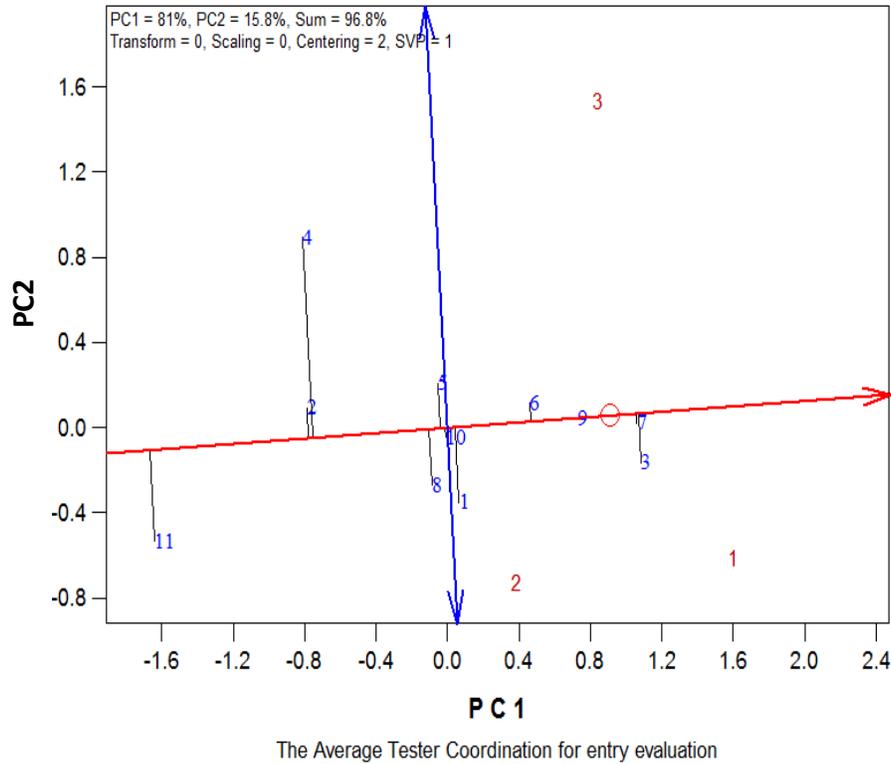
ability to show the “which-won-where” pattern of a genotype by environment dataset as it graphically addresses important concepts such as mega-environment differentiation, specific adaptation (Yan and Tinker, 2006). The polygon view of total starch yield (t/ha) a biplot is indicated in Figure 5. Five rays divide the biplot in to five sectors, out these; environments fall only in to two of them. The vertex genotype for mega I (E1 and E2) was genotype G3 and for Mega II (E3) is genotype G7 implying that this genotype was the winning genotype for these environments.

### Stability of total starch yield by other stability parameters

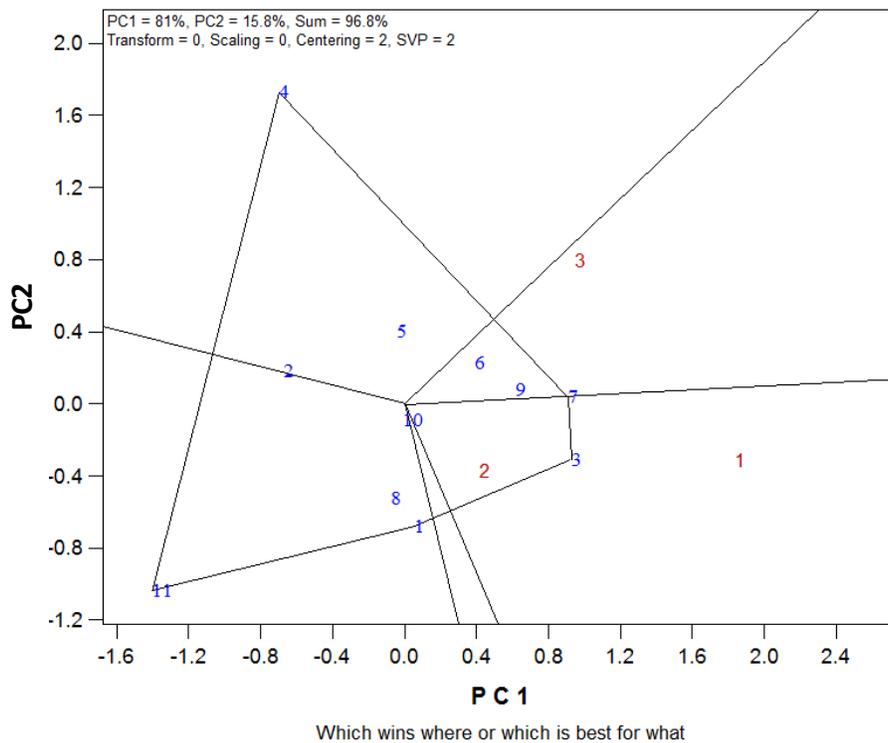
According to Eberhart and Resells deviation from regression model, G10 and G9 were the most stable genotypes across testing locations because they had small deviation from regression values.

The most unstable genotype for this trait was G4. The regression coefficients  $b_i$  for the genotypes ranked from -0.06 to 1.57. The genotypes with the lowest  $b_i$ ; G11 and G8 were more adapted to marginal environments whereas genotype G6 and G7, were input sensitive and adapted to high potential environments (Table 4).

Using Wricke's ecovalence ( $W_i$ ) and stability parameter ( $\delta_i^2$ ), genotypes G10 and G9 with the lowest ecovalences



**Figure 4.** Average tester coordination (ATC) ranking biplot view to show the mean performance and stability of genotypes total starch yield (t/ha).



**Figure 5.** The which-won-where view of the GGE biplot to show which genotypes performed better in which location for total starch yield (t/ha).

**Table 4.** Genotype code, Stability value, means TSY and ranks of tested genotypes across testing locations.

G code	Yield (t/ha)		Eberhart and resells regression model				Others stability parameters						AMMI model			GGE biplot				
	$\bar{x}$	r	bi	r	$S^2_{di}$	r	Wi	r	$\delta^2_i$	r	Pi	r	IPCA1	IPCA2	ASV	r	GGE1	r	GGE2	r
1	3.367 <sup>b</sup>	6	0.76	5	0.25**	7	0.41	5	0.51	4	0.68	5	-0.145	-0.415	0.461	4	0.355	9	1.1	5
2	2.557 <sup>c</sup>	10	0.81	3	0.24**	6	0.35	4	0.43	3	2.04*	9	0.373	0.040	0.521	5	-0.14	5	1.9	9
3	4.296 <sup>a</sup>	1	1.35	8	0.73**	10	1.02	9	1.45	8	0.01	1	-0.644	-0.051	0.897	9	0.228	7	0.2	2
4	2.616 <sup>c</sup>	9	1.32	6	3.03**	11	3.28	11	6.58**	11	2.56*	10	0.743	0.960	1.410	11	-0.942	11	2.1	10
5	3.451 <sup>b</sup>	5	0.83	2	0.39**	9	0.48	6	1.14	7	0.86	8	0.430	0.110	0.609	6	-0.21	6	1.2	7
6	3.577 <sup>b</sup>	4	1.57	10	0.14**	5	0.89	7	0.59	6	0.34	3	-0.524	0.320	0.796	7	-0.087	4	0.6	4
7	4.275 <sup>a</sup>	2	1.49	9	0.36**	8	0.92	8	2.11*	9	0.34	3	-0.590	0.171	0.838	8	0.046	2	0	1
8	3.272 <sup>b</sup>	7	0.67	7	0.03	3	0.29	3	0.51	4	0.86	7	0.053	-0.372	0.379	2	0.265	8	1.2	8
9	4.039 <sup>a</sup>	3	1.24	4	0.04	4	0.20	2	0.14	2	0.10	2	-0.268	0.098	0.386	3	0.005	1	0.4	3
10	3.260 <sup>b</sup>	8	1.04	1	-0.005	2	0.02	1	-0.05	1	0.73	6	-0.094	-0.026	0.133	1	0.047	3	1.1	6
11	1.770 <sup>d</sup>	11	-0.06	11	0.003	1	2.55	10	3.67**	10	4.35**	11	0.666	-0.835	1.247	10	0.433	10	2.8	11
Mean	3.316																			

Means with the same letters within a column are not significantly different at  $p < 0.01$  based on Duncan multiple range tests. G, genotype code;  $\bar{x}$ , mean yield; bi, coefficient of regression;  $S^2_{di}$ , deviation from regression; Wi, Wricke's ecovalence;  $\delta^2_i$ , shukla stability variance; Pi, cultivar superiority measure; ASV, AMMI stability value; GGE1, distance of GGE Biplot (stability evaluation); GGE2, distance of GGE Biplot (stability evaluation plus mean performance); r, stability rank; \*, \*\* = significant difference at ( $p=0.05$ ) and ( $p=0.01$ ) with 1.79 and 3.10 cut off points respectively for shukla stability value.

were considered to be stable as they contributed low to the interaction sum of squares, whereas G4 followed by G11 with the highest Wi were unstable and made the highest contributions to Gx E interaction. According to shukla stability value, G3 and G9 identified as stable and high yielder genotypes (Table 4).

Lin and Binns cultivar superiority measure (Pi) value of TSY depicted G3, G7 and G9 as stable and G11 and G4 with limited adaptation in the tested environments (Table 4). Additive main effect and multiplicative interaction stability values (ASV) analysis for TSY identified that G10 was the most stable genotype across locations

because it had minimum ASV value. Similarly, G9 was the second most stable genotype as well as it had better yield than G10. This analysis also identified that G4 was the most unstable genotype Distance of GGE biplot based on the ATC coordinate (stability evaluation as well as stability evaluation plus mean performance) values identified G9 and G10 were identified as stable genotypes while G4 and G11 were unstable genotypes (Table 4).

#### Correlation of stability parameters

The ranks of 11 genotypes after applying the

methods of stability analysis were used to assess the relationships among stability parameters. Spearman's rank correlation was computed among eight stability parameters are revealed in Table 5. Significant ( $p < 0.01$ ) and positive correlations were observed between Wricke's ecovalence (Wi), AMMI stability value (ASV) and Shukla stability variance ( $\delta^2_i$ ) parameters. The same holds true between yield ranks, Lin and Binns cultivar superiority measures (Pi) rank and GGE2 rank order. This indicated that GGE2 is more of a genotype performance measure, rather than a stability measure. In this study GGE1 showed positive but none significant correlation

**Table 5.** Spearman's rank correlation for different stability parameters evaluated for total starch yield during 2011 main season.

	Yi	Pi	bi	$s^2_{di}$	Wi	$\delta^2_i$	ASV	GGE1	GGE2
Yi									
Pi	0.91**	1							
bi	-0.14	-0.09	1						
$s^2_{di}$	-0.40	-0.16	-0.06	1					
Wi	0.01	0.23	0.66*	0.51	1				
$\delta^2_i$	0.005	0.29	0.65*	0.48	0.97**	1			
ASV	0.01	0.22	0.62*	0.51	0.98**	0.93**	1		
GGE1	0.52	0.60*	0.26	0.20	0.56	0.56	0.46	1	
GGE2	0.94**	0.95**	-0.09	-0.24	0.15	0.18	0.14	0.66*	1

Yi, yield (t/ha); Pi, cultivar superiority measure; bi, coefficient of regression;  $s^2_{di}$ , deviation from regression; Wi, Wricke's ecovalence,  $\delta^2_i$ , stability variance; ASV, AMMI stability value and GGE1, distance of GGE Biplot (stability evaluation) ; GGE2, distance of GGE Biplot (stability evaluation plus mean performance); \*\*,\*\*\*; significant at (P< 0.05) and (P<0.01) respectively

with Wi, ASV and  $\delta^2_i$

Generally, Wi,  $\delta^2_i$  and ASV were significantly (P <0.01) correlated to each other. This indicates that, any of them can be used to identify stable and high total starch yield potato genotypes.

**Conclusions**

This multi-location study helped elucidate total starch yield and some of the factors affecting starch yield in potato. Among the tested genotypes across testing locations, the maximum total starch yield (t/ha) was obtained from G3 but it did not showed statistical difference with G9 (Guassa). The environmental mean of tested genotypes ranged from 2.10 t/ha from Injibara (E2) to 4.008 t/ha Debretabor (E3). This is mainly because of spanned a broad range of climatic and soil conditions.

The pulled analysis of variance of this study indicated that, GEI effects seem uncommon in total starch yield. This suggesting that, genotype and environment were the most significant factors contributing to variations in these traits.

Among the testing locations, Adet (E1) was the most ideal testing location for TSY of potato. Among tested genotypes, all most all stability parameters considered in this study identified G9, as the most stable as well as high yielder genotype while G4 as the most unstable genotype in total starch yield. There for G9 (Guassa) genotype is more appropriate for processing especially for new emerging small cheeps making industries in the region.

G9 is selected over G3 because of stability not because of yield. Positive and significant (P<0.01)

correlation obtained between Wricke's ecovalence (Wi), AMMI stability value (ASV) and Shukla stability variance ( $\delta^2_i$ ) stability parameters' in TSY of potato. This indicates that, any of these methods can be used to identify stable and high yielder potato genotypes.

GGE biplot polygon view of total starch yield (TSY) of this study indicated that, two possible mega environments of test locations (that is, E1 and E2 grouped together and E3 as other group). The wing genotype for E1 and E2 was G3 and G7 for E3. Thus, potato breeding program of the region should consider these two different mega environments separately to maximize yield potential of potato through exploration of positive GEI.

**Conflict of Interests**

The author(s) have not declared any conflict of interests.

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The background of the cover is a dark, rounded rectangle. In the upper half, there is a bowl filled with various fruits including apples, oranges, and grapes. In the lower right, there is a white bowl filled with a bright yellow liquid, likely juice. The title is centered in a white, bold, sans-serif font over a semi-transparent dark grey rectangular area.

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