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RESEARCH ARTICLE

INFLUENCE OF ENVIRONMENT AND ITS INTERACTION EFFECTSON NEW POTATO [(Solanum tuberosum (L.)] MUTANT LINES

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ABSTRACT

Potato (*Solanum tuberosum* L.) is an important food and income crop in Kenya. Potato growing regions in Kenya are diverse with similar to contrasting environmental conditions. Multi-location trials are necessary when determining agronomic response of new improved lines to environment - genotype interaction. The objective of the study was to determine the yield stability of new improved potato mutant lines under genotype by environment interaction effects. Eight genotypes, consisting of four mutant lines and four commercial varieties were obtained biotechnology seed Unit at the University of Eldoret. The study was carried out in five regions in Eldoret, Burnt Forest, Mosoriot, Marakwet and Nyandarua. The experiment was laid out in a Randomized Complete Block Design (RCBD) in three replications at each site. Data on plant height, days to 50% flowering, stem number, tuber number and tuber weight. Classical ANOVA, AMMI and GGE were used in the analysis of yield stability. The effects of genotype, environment and genotype by environment interaction were significant for all the studied agronomic traits. The analysis revealed IP1 as most stable (widely adapted), IP2 as specifically adapted, IP3 & IP4 showed some stability. The new varieties will reduce the overdependence on Shangi by farmers at the same time giving stable high yields over various geographical regions.

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INTRODUCTION

Potato (*Solanum tuberosum*) is an important tuber crop which is used worldwide for human and animal consumption, and as raw a material for starch and alcohol productionIt ranks third after rice and wheat consumption-wise, globally (Devaux, 2020) with approximately one billion people utilizing it as food (Devaux, 2021) and a global production of 370million tonnes (FAO, 2021). In Kenya, Potato is the second most important staple food after maize in Kenya(Kwambai *et al*., 2023). Potato production, is often faced with many production challenges mainly associated with biotic and abiotic constraints leading to low yields of 9-10t/ha far below attainable yields of 40t/haMuthoni & Shimelis, 2023). To improve and sustain potato production, continuous breeding and availing of new potatovarieties addressing old and new production constraints (Chepkoech *et al*., 2018; Placide *et al*., 2022) is imperative in reducing potato yield gap in Kenya. Attempts by plants breeders at the University of Eldoretplant breeding unit led to development of new improved potato mutant lines. The four potential mutant lines were selected for adaptability study under multi-location trials as a requirement for variety release.

MATERIALS AND METHODS

Experimental field sites and their description: The study was carried out at the University of Eldoret (UoE), ATC Chebara-Marakwet, Ol-jororok-Nyandarua, Burnt Forest and Chemuswa-Mosoriot. UoE lies between 0° 34' N and 35°18' E at 2154 meters above sea level (masl), it receives 1055mm of annual rainfall (AR) with average temperatures of 16.8 °C. ATC Chebara in lies between 0° 53' N and 35° 30' E at 2448 masl and receives 1238mm of AR with average temperatures of 15.8 °C. Nyandarua (Ol-jororok) is located at 2390masl and lies between 0° 04' N and 36° 21'E receiving AR of 990mm and average temperatures of 14°C. Burnt forest lies between 0° 12′ N and 35° 25′E at 2406 masl with AR of 1168mm and average temperatures of 18 °C. Chemuswa (Mosoriot) is located at 2058 masl and lies between 0° 21' N and 35° 6' E. It receives AR of 1500mm and average temperatures of 17°C.

Experimental materials: Four potato mutant lines (IP1, IP2, IP3 and IP4) with different characteristic developed through mutation breeding by Chepkoech *et al*., 2018 were obtained from biotechnology seed Unit at the University of Eldoret. One parental variety(Sherekea), one check (Shangi) and two(Kenya

Land preparation and planting of the sites: Land preparation in both sites was done in the month of April, 2020 during the long rain season and planted in month of May, 2020. The potato genotypes were planted in a Randomized Complete Block Design (RCBD) in three replications at each site. Each replication contained eight plots with each plot representing a genotype. Each plot comprised of two rows of eleven hills for each. The hills in each row were separated by 0.30 m and rows separated by 0.75 m. The spacing between plots was 1 m as well as between the adjacent replication. Fertilizer, Diammonium phosphate (DAP) was applied at planting while other agronomic practices were applied during the crop growth and development applied according to National Potato Council of Kenya (NPCK, 2013) field manual.

Data collection: Data was collected during vegetative and at maturity stage of the crop and was based on phenotypic traits viz; days to 50% flowering, plant height, tuber number, tuber weight and stem number, of which some have direct correlation to yield according to studies (Lamboro *et al*., 2014; Tessema *et al*., 2022; Rizvi *et al*., 2020). The data for days to 50% flowering was taken when 50% of plants had at least one open flower. Plant height at maturity was determined from three randomly selected plants from each plot by measuring from ground level to the tip of the plant. Tuber number was taken at harvest where three plants per plot were harvested separately and their tuber numbers counted. The weight (kg) of tubers of three selected plants per plot was taken and recorded. Stem number of selected three plants per plot was counted. Tuber yield data was collected at harvest on eight plants from the two central rows at harvest and the tubers weighed and converted to tonnes per hectare (t/ha) as per Rumbidza *et al* (2022).

Statistical data analysis: The collected data on phenotypic traits (days to flowering, plant height, tuber number, tuber weightstem number and tuber yield) was subjected to analysis of variance (ANOVA) in order to determine the genotypic, environmental and interaction effects on the phenotypic traits using system analysis software (Genstat version. 14). The AMMI and GGE models were further used to determine the yield adaptability of the genotypes.

RESULTS

Performance of genotypes under genotypic, environmental and genotype by environment interaction effects: The analysis of variance for number of days to 50% flowering, plant height, number of stems, tuber number tuber weight and tuber yield showed highly significant (P<0.001) differences due to the influences of environments, genotypes and the interaction. The percent contribution to the variation by each component was further calculated using total percent sum of squares to highlight how each component affected the traits' expression (Table 1). Environmental effects led to variation in plant height and stem number contributing 59.9 and 52.7% total sum of squares (%SST) respectively. Genotypic effects influenced tuber number and number of days to flowering leading to 44.5 and 90 %SST mean while G x E interaction led to variation in tuber weight per plant hence final tuber yield.

Yield adaptability and stability analysis: The AMMI method is a single analysis that employs traditional ANOVA and PCA (principal component analysis) (Gauch, 1992).

GGE graphically displays G x E interaction data in GGE biplots (Pobkhunthod *et al*., 2022). These two methods were therefore used to analyze the yield stability of the genotypes using AMMI analysis of variance for the significance of the effects of G, E and GXE and percentage contribution of the components to total sum of squares, AMMI biplots, AMMI stability values (ASV) and GGE biplots. The ANOVA from AMMI analysis for the tuber yield of the eight genotypes across three environments divided treatment main effects into environment (E), genotype (G) and their interaction (Table 2). Both the environment, genotype and Genotype by environment interaction had high levels of significance (< 0.001) contributing to 17.4%, 32.6 % and 46 % total sum of squares respectively. IPCA1, IPCA2 and IPCA3 were also significant (< 0.001) accounting for 46.3%, 33.5% and 17.1% respectively to the total observed variation as a result of G x E interaction. Genotype and environment additive main effects were also plotted against their main IPCA scores in AMMI biplot and depicted as points on a plane.

Table 1. Analysis of variance for different traits of potato genotypes

TRAIT	Source	d.f	SS	MS	Pr>F	%SST
Number of days to 50% flowering	E	4	6786.7833	1696.6958	<.001	**8.4**
	G	7	1195.8833	10437.6714	<.001	**90.0**
	G X E	28	1195.8833	42.7101	<.001	**1.5**
Plant height	E	4	2909.467	727.367	<.001	**59.9**
	G	7	625.525	89.361	<.001	**12.9**
	G X E	28	1010.267	36.081	<.001	**20.9**
Number of stems per plant	E	4	35.3333	8.8333	<.001	**52.7**
	G	7	7.3917	1.0560	<.001	**6.9**
	G X E	28	44.4000	1.5857	<.001	**43.9**
Tuber number per plant	E	4	338.0333	84.5083	<.001	**19.4**
	G	7	773.5917	110.5131	<.001	**44.5**
	G X E	28	592.3667	21.1560	<.001	**34.1**
Tuber weight per plant	E	4	4.573333	0.908667	<.001	**15.4**
	G	7	9.580000	0.653333	<.001	**34.7**
	G X E	28	4.11889	0.342143	<.001	**46.3**

Table 2. AMMI analysis for tuber yield in 5 environments

Source	df	SS	MS	F	F_prob	%TSS	%GxE
Treatments	39	46246	1185.8	49.12	< 0.001	96.0	
Genotypes	7	15713	2244.7	92.98	< 0.001	32.6	
Environments	4	8365	2091.3	84.16	< 0.001	17.4	
Block	10	248	24.8	1.03	0.42848	0.5	
Interactions (GxE)	28	22168	791.7	32.79	< 0.001	46.0	
IPCA1	10	10266	1026.6	42.52	< 0.001		46.3
IPCA2	8	7426	928.3	38.45	< 0.001		33.5
IPCA3	6	3791	631.8	26.17	< 0.001		17.1
Residuals	4	685	171.2	7.09	< 0.001	1.4	
Error	70	1690	24.1	*	*		
Total	119	48184	404.9	*	*		

d.f-Degree of freedom, ss-sum of squares, ms-mean squares, %TSS-percentage total sum of squares, %GxE-percentage genotype by environment interaction

The biplot space was divided into four sections, with the low yielding environments and genotypes placed on the left upper and left lower section of the biplot whereas the higher yielding genotypes and environments were placed on the upper right and lower right of the biplot (Figure 1).

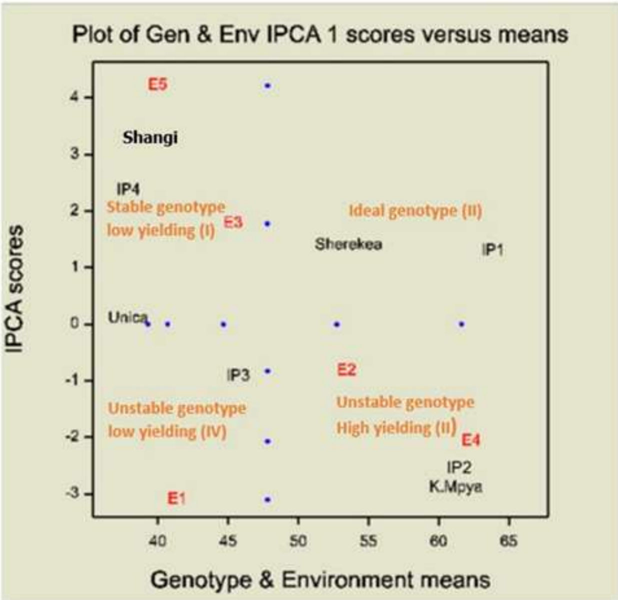


Figure 1. AMMI biplot for tuber yield stability analysis for eight potato genotypes in five environments

AMMI stability value (ASV) and IPCA scores were used to further study the stability of the genotypes (Table 3).

Table 3. Overall tuber yield means, IPCA scores and ASV values

Genotype	NG	Gm	IPCA [1]	IPCA [2]	IPCA [3]	ASV
IP1	1	63.04 (1)	0.81302	0.70771	1.29180	1.64
IP2	2	59.47(2)	3.29003	2.94689	-3.51132	5.4
IP3	3	44.87(5)	2.14093	-3.59526	-0.92525	4.7
IP4	4	37.07(6)	0.96204	3.78143	2.36321	4.1
K.Mpya	5	59.33(3)	-5.67603	0.35717	-2.89454	2.8
Shangi	6	31.00(8)	-2.45668	-0.71536	2.18613	3.5
Sherekea	7	51.20(4)	-0.72422	0.08088	1.39329	1.0
Unica	8	36.47(7)	1.65092	-3.56347	0.09669	3.9

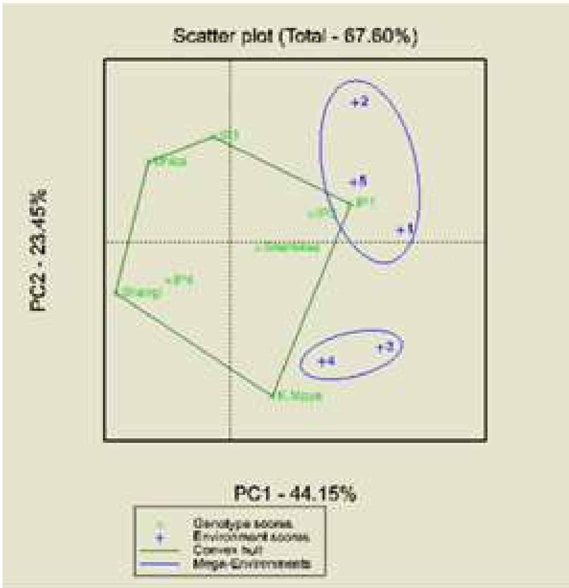
Lower IPCA score (positive or negative) - More stable, vice versa

Lower ASV score –More stable

Further, the AMMI model selected the best four genotypes for each of the five environments based on the tuber yield (Table 4). The best two genotypes in Eldoret were IP2 and IP1, IP3 and IP2 the best two in Nyandarua, in Marakwet, IP1 and Kenya Mpya were the best two, Kenya Mpya and IP1 the best two in Burnt Forest whereas IP1 and Sherekea were the best two in Chemuswa. A GGE polygon was additionally drawn to visualize yield stability (Asfaw *et al*., 2009; Yan, 2011). Like AMMI biplots, GGE biplots helps to determine which varieties are specifically and widely adapted and in recommendation of appropriate environments (Mattos *et al*., 2013), this is done through "which-won-where" approach. GGE polygon view are the best way to visualize and identify best performing and well adapted genotypes together with environments (Yan *et al*., 2000, Yan & Kang, 2003).

Table 4. First four AMMI genotype selections per environment based on tuber yield

Number	Environment	Mean	Score	1	2	3	4
2	E2	52.75	3.889	IP3	IP2	IP1	Unica
1	E1	40.70	2.762	IP2	IP1	K.Mpya	Sherekea
5	E5	39.28	0.548	IP1	Sherekea	IP3	Unica
3	E3	44.67	-1.416	IP1	K.Mpya	IP2	IP4
4	E4	61.63	-5.783	K.Mpya	IP1	Sherekea	IP3



DISCUSSION

Genotypic and environmental effects were all significant for all the traits indicating existence of variations among the genotypes and environments which in return leads to significant GE interaction(Table1). Significant G x E interactions are usually followed by adaptability and stability analysis since analysis of variance does not explain the details of GE interaction (Pupin *et al*., 2015; Oladosu *et al*., 2017; Yohannes *et al*., 2023). Significant effects of the components in AMMI model (Table 2) especially GE (46%) indicated that there was significant tuber yield variation among the genotypes.High (96%) contribution of treatments to total sum of squares is an indication of the reliability of the multi-environment testing. The points for environment and genotypes (Figure 1) are more scattered indicating variation of the test environments and genotypes. High yielding genotypes are placed farthest on the right side of the biplot and specifically adapted to the closest environment. The genotypes placed close to IPCA 0 point of origin indicate negligible or no GE interaction thus considered stable. Consequently, the AMMI biplots depicted Burnt Forest (E4) as the highest yielding environment having IP2 and Kenya Mpya, as the highest yielding genotypes. Nyandarua (E2) was depicted as the second highest tuber yielding environment and more stable for Potato production. IP1 and Sherekea were revealed as the most stable genotypes due to their closeness to the IPCA 0 point of origin.

Based on IPCA scores, Kenya Mpya and IP2 had the highest IPCA1 scores 5.6 and 3.2 respectively. This can as well be translated as having higher tuber yield in a specific environment or specifically adapted. IP1 and Sherekea had significant lower ASV ranking indicating their tuber yield stability. The genotypes with lower IPCA1 scores have less G×E interaction effect compared to those with higher IPCA1 scores indicating that they are more stable in tuber yield across environments (Oliveira *et al*., 2014). AMMI stability value (ASV) produced similar results with IP1 (1.64) and Sherekea (1.0) having lowest ASV numbers. Genotypes with lower calculated ASV have less Genotype by environment interaction hence more stable and widely adapted whereas those with higher ASV are have genotype-environment interaction thus specifically adapted. AMMI models also select best four genotypes in the test environments, in this study, only IP1 appeared in the top four in all environments revealing it as ideal genotype (stable and high yielding). The rest of the genotypes appeared either twice or thrice except Shangi (Table 4). The GGE biplot (Figure 2) captured 67.6% (PC1 44.15% and 23.45% PC2) of the genotype plus genotype by environment (GGE) variation. The genotype with the highest tuber yield in E1 (Eldoret), E2 (Nyandarua) and E5 (Chemuswa) was IP1. Kenya Mpya was highest yielding genotype in E3 (Marakwet) and E4 (Burnt Forest). This result indicates that those genotypes were more specifically adapted to those environments. Meanwhile, two mega environments were identified; ME1 (E1, E2 and E5) and ME2 (E3 and E4).
Generally, genotypes of wider adaptability tend to have lower yield whereas those of narrow or specific adaptability tend to yield more (Ng'ang'a, 2015). In this case, IP1 was an exception because it's an ideal genotype.

CONCLUSION

With climate change intensifying each year causing changes in the conditions in the farming environments, cultivar stability and adaptability is crucial now than ever. Stable cultivars, widely or specifically adapted with little to no GE interaction are a strong basis for food security and climate change mitigation. Therefore, there is need to intensify testing new crop lines and even the already released varieties under changing farming conditions in order to properly advice farmers on which cultivars to grow where based on stability and adaptability studies. Phenotypic performance trials of eight potato genotypes consisting of four new mutant lines and four commercial varieties in five environments was conducted. The results revealed that all genotypes had significant interaction with all environments based on the studied traits. IP1 and Sherekea were the most stable genotypes for they did not have much interaction with the environment therefore are recommended for farming in all five environments. IP2 and Kenya Mpya were the highest yielding and are recommended for environment 2 and 4 respectively.

ABBREVIATIONS

AMMI-Additive main effects and multiplicative interaction,
ANOVA-Analysis of variance
IPCA-Interactive principal component analysis
GGE-Genotype and genotype by environment,
GXE-Genotype by environment interaction.
RCBD-Randomized Complete Block Design
ASV -AMMI stability value

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