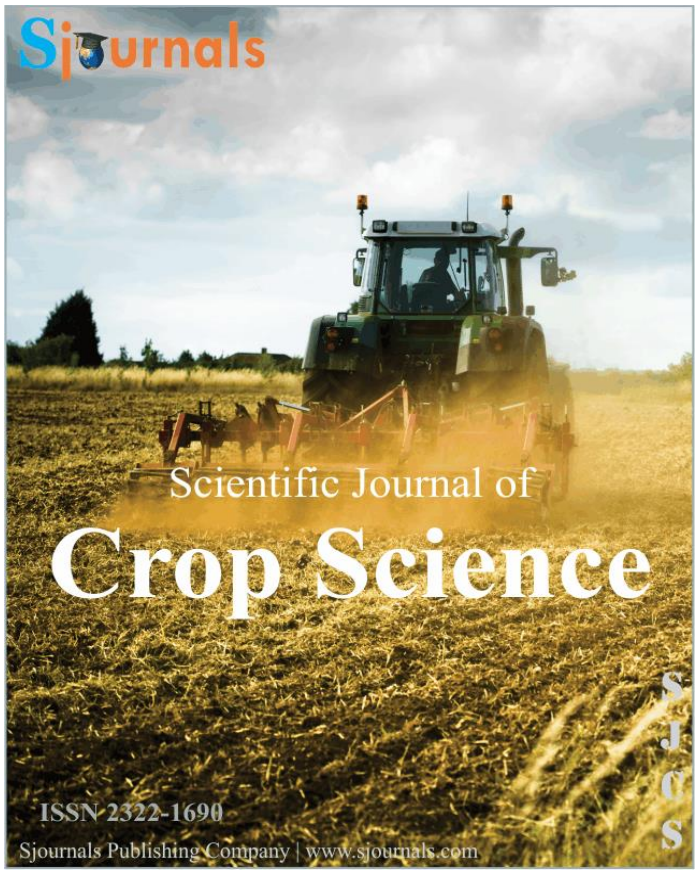

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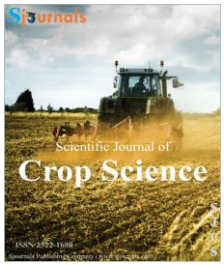

Original article

Genotype-environment interaction and stability analysis for tuber yield of potato (*Solanumtuberosum* L.) genotypes

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ABSTRACT

Yield data of 12 potato (*Solanumtuberosum L.*) genotypes tested across 9 rain-fed environments during the 2016-2018 growing season using RCBD in 3 replications were analyzed using the AMMI model. The AMMI analysis tested in nine environments (years) were showed that the yield was significantly affected (P<0.001) by genotypes and environment main effects as well as GxE interaction. The model revealed that differences between the environments accounted for about 57.73% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 16.87 % and 25.41% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 56.44% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 13.67% of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at P=0.01 and cumulatively contributed to 70.11% of the GxE interaction SS, leaving 29.89% of the variation in the GxE interaction in the residual. The AMMI and AMMI stability value (ASV) identified G3 and G12 as the stable and high yielding genotypes.

1. Introduction

Plant breeders invariably encounter genotype x environment interactions (GEIs) when testing varieties across a number of environments. Depending on the interactions or the differential genotypic responses to

environments, the varietal ranking can differ greatly across environments. In field crop trials, this interaction is often analysed with the aim of determining the stability of the genotypes especially when there is a reasonable genotype by environment interaction (GEI). A combined analysis of variance (ANOVA) can quantify the interactions, and describe the main effects. However, analysis of variance is uninformative for explaining GEI. Various statistical methods (parametric and non-parametric) have been proposed to study Genotype × environment interactions (Mohammadi and Amri, 2008; Mohammadi et al., 2010). The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (Hohls, 1995). The reason is that a genotype's response to varying environments is multivariate (Lin et al., 1988) whereas the stability indices are usually univariate (Gauch, 1988; Crossa, 1990).

Since the genotype response to environmental variations is usually multivariate, therefore, a multivariate method of analysing genotype stability across environments will be the best option. One of the multivariate techniques is the AMMI (additive main effects and multiplicative interaction) model. AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two way data structure. The AMMI analysis is a combination of analysis of variance (ANOVA) and principal component analysis (PCA) in which the sources of variability in genotype by environment interaction are partitioned by PCA. The AMMI is, therefore, also known as interaction PCA (Gauch and Zobel, 1990), and can have several models: AMMI0, which estimates the additive main effect of genotypes and environments, and does not include any principal component axis (IPCA); AMMI1, which combines the additive main effects from AMMI0 with the genotype by environment interaction effects estimated from the first principal component axis (IPCA 1); AMMI2, and so forth, until the full model with all IPCA axis (Gauch,1988). It has both linear and bilinear component of GEI and hence very useful in visualizing multi-environment data (understanding complex GEI and determining which genotype won which environment) and gaining accuracy (improving cultivar recommendation and accelerating progress) (Gauch, 2006). The additive main effects and multiplicative interactions (AMMI) is defined powerful tool for effective analysis and interpretation of multi-environment data structure in breeding programs (Ebdon and Gauch, 2002a; Samonte et al., 2005; Yan et al., 2000; Zobel et al., 1988). The objectives of the study are: to evaluate, select and verify promising genotypes with desirable traits.

2. Materials and methods

Twelve potato genotypes were evaluated at three locations (Sinana on station, Goba and Dinsho) for three consecutive years (2016-2018) during *bona* production season following selection method. The trial was laid out in RCB design with three replications. Data was collected from central two rows. Data was subjected to analyses of variance using GENSTAT software program. Duncan's multiple range test was done for grain yield. The genotype by environment interaction analyses (GxE) and stability analyses were conducted using the AMMI model.

3. Results and discussion

Table 1
Combined analysis of variance of tuber yield data of potato genotypes tested across 9 environments.

Source	df	SS	MS	F	F_prob	% Explained
Total	323	176026	545	*	*	
Treatments	107	140070	1309	7.88	0	
Genotypes	11	23623	2148	12.93	0	16.87
Environments	8	80857	10107	59.24	0	57.73
Block	18	3071	171	1.03	0.43094	
Interactions	88	35589	404	2.44	0	25.41
IPCA(1)	18	20085	1116	6.72	0	56.44
IPCA(2)	16	4866	304	1.83	0.02933	13.67
Residuals	54	10638	197	1.19	0.20095	29.89
Error	198	32885	166	*	*	

The presence of significant differences for tuber yield among genotypes and environments reveals not only the amount of variability that existed among environments but also the presence of genetic variability among the genotypes.

The AMMI analysis tested in nine environments (years) were showed that the yield was significantly affected (P<0.001) by genotypes and environment main effects as well as GxE interaction. The model revealed that differences between the environments accounted for about 57.73% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 16.87 % and 25.41% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 56.44% of the interaction sum of squares. Similarly, the second principal component axis (PCA 2) explained a further 13.67% of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at P=0.01 and cumulatively contributed to 70.11% of the GxE interaction SS, leaving 29.89% of the variation in the GxE interaction in the residual (Table 1).

Table 2
Environment means and scores.

NE	Environment	Mean	IPCAe[1]	IPCAe[2]
E1	Dinsho2016	31.17	2.16013	2.72131
E2	Dinsho2017	24.96	-4.02097	1.13413
E3	Dinsho2018	17.53	-0.31763	-0.72134
E4	Goba2016	37.56	2.75013	1.79607
E5	Goba2017	16.57	-0.2955	0.6786
E6	Goba2018	25.29	0.3077	0.72516
E7	Sinana2016	67.89	0.9297	0.54188
E8	Sinana2017	50.39	-5.81314	-2.22988
E9	Sinana2018	43.12	4.29958	-4.64594

The AMMI model 1 biplot of the varietal trials was demonstrated in Figure 1. The abscissa shows the main effects while the ordinate shows the first PCA axis. The environments showed much variability in both main effects and interactions. However, the high potential environments were sparsely distributed in quadrant II and III, while the lower potential environments were also sparsely distributed in quadrants I and IV with high IPCA1 values (Figure 1).

Table 3
AMMI yield mean, AMMI stability values (ASV), and ranking orders of the 12 Genotypes tested across 9 environments.

G	Genotype	Yield(Qt/h)	IPCAg[1]	IPCAg[2]	ASV
G1	Beleta	39.48	1.41042	0.37999	5.834355
G2	CIP-387967.3	41.98	3.20807	-2.1019	13.40813
G3	CIP-84866-5	48.62	0.6093	-0.87377	2.662541
G4	Gudane	34.86	0.09253	-1.65359	1.697128
G5	KP-170-5	32.15	-6.72753	-0.41318	27.77315
G6	KP-90116-1	28.32	-0.02066	-2.05808	2.059846
G7	KP-90147-2	32.63	2.14374	3.41648	9.485614
G8	KP-90162-3	34.63	2.13154	0.21313	8.801207
G9	Local	17.45	-3.43121	1.79934	14.27727
G10	Milki	37.24	-0.00678	-2.3536	2.353766
G11	Moti	24.87	1.48194	2.40133	6.571636
G12	ROBJIN	47.1	-0.89135	1.24385	3.883901

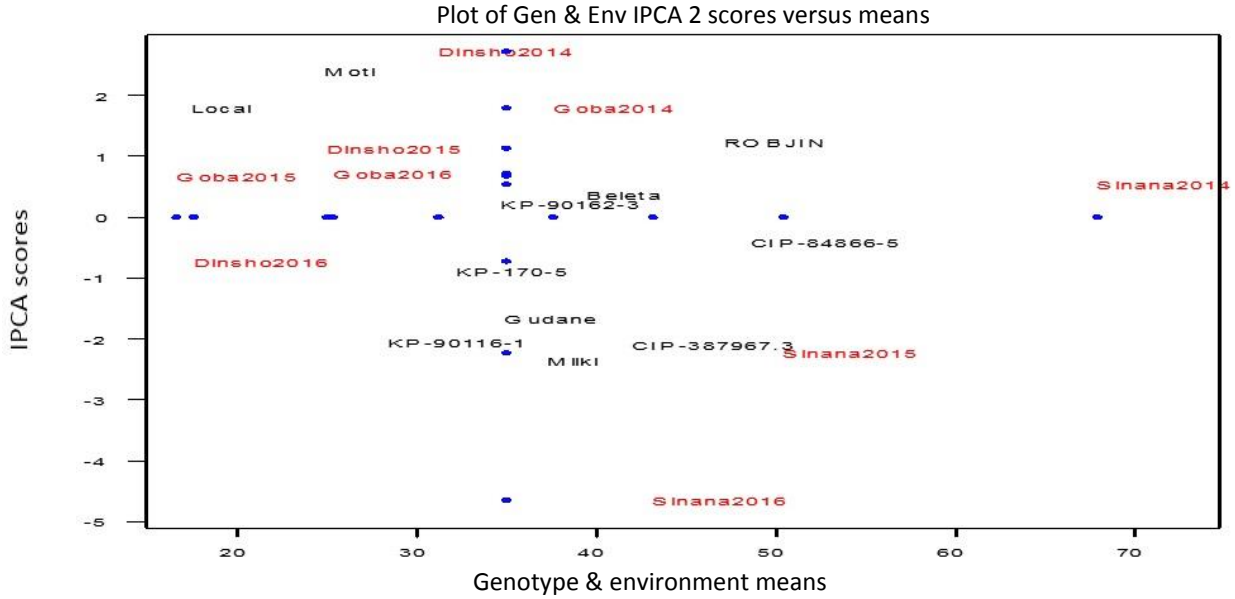

Fig. 1. AMMI model I biplot of the tuber yield of potato genotypes evaluated in 9 environments.

In ASV method, a genotype with least ASV score is the most stable, accordingly genotype G4 was the most stable. But G3 is high yielder and medium ASV. Therefore, release of this genotype (G3) for production in the mid and highlands of Bale will result in increased production and productivity of potato in the country.

4. Conclusion

AMMI analyses revealed the stable and high yielding genotypes over ranges of environments. That is genotypes G3. Therefore, release of this genotypes for production in the mid and highlands of Bale will result in increased production and productivity of potato in the country. It can be concluded and recommended from this study that genotypes should be selected for wider adaptations.

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