Plant Archives Vol. 19 No. 1, 2019 pp. 978-982 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

STUDY OF GENOTYPE AND ENVIRONMENT INTERACTION ON YIELD ANALYSIS OF TUBER OF POTATO (*SOLANUM TUBEROSUM* L.) USINGAMMI IN IRAQ

Omar H. Muslah Almohammedi*, Maath M. AL-Abdaly and Saad A. Mahmod

Department of Horticulture, College of Agriculture,University of Anbar,Iraq.

Abstract

The additive main effects and multiplicative interaction (AMMI) model has been proposed for the analysis of genotype– Baghdad and Erbil, Iraq was evaluated based on the additive main effects and multiplicative interaction (AMMI) method.10 genotypes were evaluated via tuber yield means in four environments.Percentage of variation captured by genotypes, environments and GEI is 98.44%, 0.24% and 1.31%, respectively. Thus, genotypes were more effective than environments. The AMMI method allowed for easy visual identification of superior genotypes for each set of environments.

Key words : Solanum tuberosum L, AMMI, yield analysis, genotypes.

Introduction

Potato (*Solanum tuberosum* L.), represents as a tuber crop and member of the family Solanaceae, which considers as an important food and cash crop qualifying fourth rank after maize, wheat and rice annual production in the world (www.potato2008.org). It possesses necessary role in insurance of food security due to augmented demand (FAO, 2008). It produces an effective biomass that achieves an exceptionally high yield with more nutrition value per unit area per unit time than any other major crops. Thus, it can own an observed role in human diet as a supplement to other food crops such as wheat and rice (Badoni and Chauhan, 2010)). There are many factors contributing to minimum in yield of potato, one of them is unsuffience of improved cultivars withwide adaptability and stability in tuber yield. Consequently, assessing the genotypes over divergent environments relies on stability of performance and range of adaptation is focal and important component for any regional investigation programmed project. Evaluating genotypes over various environments is universal process to achieve the stability of performance of the genotypes (Sadeghi *et al*., 2011). Performance of genotypes stability is one of the most favortraits to be released as a cultivar for multi region growth (Singh and Chaudhry, 1977). However, the affectivity of identified, selected superior genotypes is complicated to be recommended and strongly determined by genotype× environment interaction (GEI) that is urgent in multi-environmental trials (Asfaw *et al*., 2009; Eberhart and Russel, 1966). Present GEI may confuse the performance of genotypes under with the effects of environment (Thillianathan and Fernandez, 2002). Multi statistical models and procedures had been improved and used for assessing the GEI effects, stability of genotypes and their associations in genotypic improved process (Finlay and Wilkinson, 1963; Crossa, 1990). Even though combined analysis of variance (ANOVA) can account the interactions and characterize the main effects, it is uninformative for explaining GEI. Thus, additive main effects and multiplicative interaction (AMMI) is the first applied model to maximize accuracy when main effects and interaction are both adopted (Zobel *et al*., 1988). Whereas, it is an effective tool for powerful analysis and explanation of multi-environment data set in breeding programmed projects and is fruitful for realizing GEI (Sadeghi *et al*., 2011). Crop breeders replicated conduct out AMMI model for interpreting GEI and extracting the performance of genotypes and test environments (Gauch,

---

***Author for correspondence:**E-mail : omar_hasham2000@yahoo.com

2006; Yan *et al*., 2007). This was clearly appeared when Almehemdi *et al*. (2017) used AMMI to fortify Ternary plot to test ten caraway genotypes extracted that AMMI Biplot precisely revealed that G7 (Iraqi genotype) was the most adaptable genotype depended on carvone yield. Furthermore, on the same crop Al-Rawi *et al*. (2018) recommended to apply suitable biplot as AMMI biplot fortified with facilitative statistical parameters as quartiles supplemented by ternary plot. Therefore, this paper assesses genotype x environment interaction and tuber yield stability of potato genotypes under Erbil northern and Mideast Iraq.

Materials and Methods

In this trial, ten genotypes of potato (1-Arizona, 2-Hermes, 3-Bureen, 4-Arnova, 5-Riviera, 6-Diamond, 7-Lusa, 8-Volare, 9-Agria and 10-Vouga) were assessment in randomized complete block design with three replicates at Baghdad in middle Iraq and Erbil in north Iraq during two successive seasons, spring and fall of 2016/2017. The plot area used was 3m x 3m with the spacing of 30 cm within rows and 75 cm between rows respectively. The sample data were recorded from the two middle rows. All agronomic and cultural processes were adopted as its necessary following recommendation. At physiological maturity, the tubers were harvested from two middle rows and washed with clean tap water to remove soils. The clean tubers were categorized and classed into large, medium and small based on their size. The yield of the tubers per plot (kg) was recorded and their mean was subjected to analysis.

Statistical analysis

Analysis of variance (ANOVA) was carried out on tuber mean on plot basis and pooled over locations and seasons using the Generalized Linear Model (GLM) procedures of the GEA-R. The Additive Main Effects and Multiplicative Interactions (AMMI) statistical model was produced using GEA-R to analyze the yield data and to produce biplot that shows both main and interaction effects for both genotypes and environments.

AMMI model

The AMMI model was used to investigate GEI. The model AMMI equation is (7):

$$yger = \mu + \delta_g + \beta_e + \Sigma\lambda_n\gamma_{gn}\delta_{en} + P_{ge} + \varepsilon_{ger}$$

Where is the yield of genotype (G) in environment (E) for replicate (r), μ is the total yield mean, is the main effect of genotype or the genotype (G) mean deviation (genotype mean minus total yield mean), β_e is the main effect of environment or the environment (E) mean deviation, λ_n is the singular value for IPCA axis N (N is the number of remain PCA axis in AMMI model: . is the genotype (G) eigenvector value for IPCA axis N, is the environment (E) eigen vector value for IPCA axis N, is the residual or noise and is the error (if the test has repetition). It should be mentioned that Eigen Values and are without unit. But the single value of has a performance unit (Gauch, 1992).

Results and Discussion

Combined analysis of variance

Combined analysis of variance showed that there was a highly significant difference ($p<0.01$) among the genotypes for their tuber yield indicating that there is fluctuation of genotypes in their response to the different environments. Because of the highly significant difference existing in tuber yield among the genotypes, the AMMI analysis was used to estimate the highest stable genotypes. The majority of the total variation was accounted for by genotype (98.69%) while that of location is only 0.245%. This variability may be due to the variability of genotypes across locations. The AMMI analysis of variance showed that all the components were highly significant (table 1).

The environment had the greatest effect and accounted for 0.244% of the total sum squares; genotypes accounted for 98.44% and GXEI had accounted for 34.41%, which is the next highest contribution. A large sum of squares for environments indicates that the environments were diverse, with large difference among environmental means causing most of the variation in tuber yield.

The variation in soil moisture across the different environment was considered as the major underlying causal factor for the GXE interaction. The magnitude of the GEI sum of squares was 2.52 times larger than that for genotypes, indicating that there were substantial differences in genotype response across environments. Results from AMMI analysis (table 1) also showed that the first principal component axis (PCA 1) of the interaction captured 69.87% of the interaction sumof squares. Similarly, the second principal component axis (PCA 2) explained a further 23.58% of the GEI sum of squares. Furthermore, PCA 1 and PCA 2 had sum squares greater than that of genotypes. The mean squares for the PCA1 and PCA 2 were significant atp=0.01 and cumulatively contributed to 93.45% of the total GEI. Both the IPCA 1 and IPCA 2 scores revealed that genotype, 10 and4 was the most stable genotypes. Similarly, the calculated ASV indicated that genotype is the only stable genotype while others showed considerable interaction with the environments (table 1). So, genotypes 10 and 4

Table 1 : Partitioning of the sum of squares (SS) and mean of squares (MS) from the AMMI analysis of 10 potato advanced genotypes yield performance evaluated across 4 environments

	DF	SS	MS	F	PROBF	PORCENT	PORCENAC
ENV	3	27.33069	9.11023	.	.	0.24483	0.24483
GEN	9	10989.52	1221.058	.	.	98.444	98.68883
ENV*GEN	27	146.3687	5.42106	.	.	1.31117	100
PC1	11	102.2678	9.29707	185.9414	0.00001	69.86997	69.86997
PC2	9	34.50747	3.83416	76.6832	0.00008	23.57572	93.44569
PC3	7	9.59346	1.37049	27.4098	0.00107	6.55431	100
PC4	5	0	0	0	1	0	100
Residuals	0	0	.	.	.	0	0

Table 2 : Genotypes, mean, and interaction principal component of mean yield for potato genotypes.

	TYPE	NAME	YLD	DIM1	DIM2	DIM3
1	GEN	1	95.175	0.239057	0.39084	0.078844
2	GEN	10	76.125	0.123899	-0.34723	0.58104
3	GEN	2	61.375	-1	-0.4818	0.197857
4	GEN	3	93	0.729117	0.56545	0.29737
5	GEN	4	82.25	0.235102	-0.53609	-0.3267
6	GEN	5	90.8875	-0.09732	0.324283	-0.51896
7	GEN	6	54.75	-0.91536	0.622575	0.001281
8	GEN	7	49.875	-0.24877	-0.0705	-0.11441
9	GEN	8	91.375	0.53209	-0.35804	-0.24505
10	GEN	9	60.25	0.402193	-0.1095	0.048737
11	ENV	BAGHDF	75	0.900232	-0.56644	-0.59474
12	ENV	BAGHDS	74.705	0.927808	0.631139	0.545369
13	ENV	ERBILF	75.46	-0.82804	-0.81614	0.458151
14	ENV	ERBILS	76.86	-1	0.751447	-0.40878

showed negligible interaction and is found to be the most stable genotypes showing broad adaptation across environments. In AMMI model, principal component analysis is based on the matrix of deviation from additivity or residual, while pattern analysis employs both classification and ordination techniques. In this respect both the results of AMMI analysis, the genotype and environment will be grouped based on their similar responses (Gauch, 1992; Pourdad and Mohammadi, 2008). GEI was further partitioned by principal component analysis (table 1). Ordination technique using an approximate F-statistic (Gollob, 1968) revealed high significant differences for IPC1, IPC2 and IPC3. The Gollob's test most often retains the multiplicative axis terms of little practical relevance that is, axis with a low proportion of explained GE variation. In this study, the first three multiplicative axis terms explained 48.37, 25.54 and 16.17% of GEI sum of squares, respectively. The first three interaction principal components (IPC1, IPC2 and IPC3) retained by Gollob's F-test accounted for 90.08% of GE interaction. Corrected grain yield can be obtained by AMMI1, AMMI2 and AMMI3 for each environment and used as selection criteria in breeding programs. In general the importance of AMMI model is in reduction of the noise even if principal components do not cover much of the GESS (Gauch and Zobel, 1988; Gauch, 1992). The AMMI model revealed that there was a more complex GEI which could not facilitate graphical visualization of the genotypes in low dimensions, so it is essential to use an alternative procedure to interpret GEI using AMMI parameters. The three IPCAs accounted for 90.08% of the total interaction, the remaining 9.92% being the residual or noise, which is not interpretable and thus discarded (Purchase, 1997). The AMMI model used in this research exhibited a more complex interaction which required a maximum of two PC axes to account for considerable amount of variation in the GEI. Also eigen vectors and three first IPCs for each genotype over all environments are given in Table 2. The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments (Purchase, 1997; Martin and Alberts, 2004). The greater the IPCA scores, the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled.

Biplot analysis

The rest genotypes showing considerable interaction with the environments were highly interactive and were highly unstable across environments. According to SVA calculated, the most unstable genotype is 3 followed by 7, 9, 8 and1. The underlying causes of the interaction observed can therefore be based on both the genetic differences between these genotypes. Except the local check, which gave the lowest tuber yield, most of the unstable genotypes had the best performance in their tuber

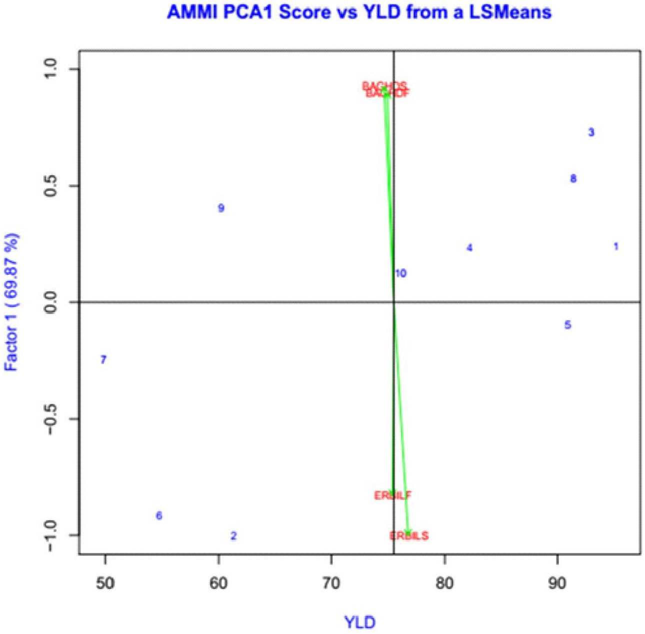

Fig. 1 : Biplot of the first interaction principal component axis (IPCA1) versus mean yields.

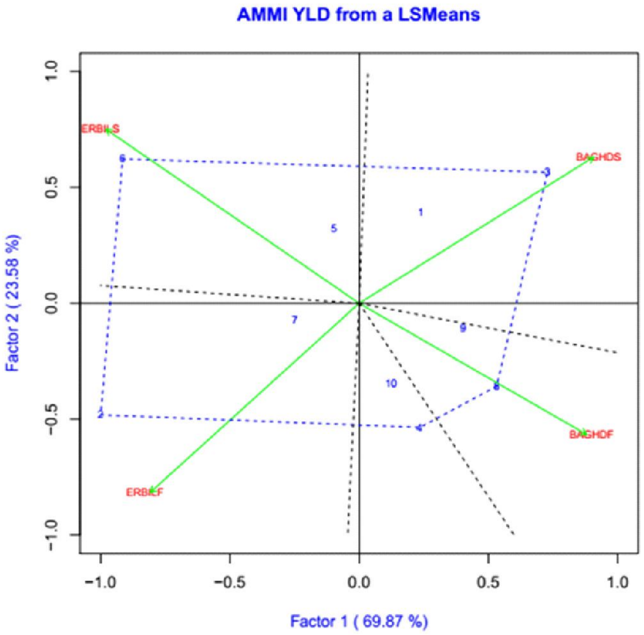

Fig. 2 : Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for potato genotypes.

yield. The AMMI biplot provides a visual expression of the relationships between the first interaction principal component axis (IPCA1) and means of genotypes and environments (fig. 1) with the biplot accounting for up to 93.45% of the total sum of squares. Genotype, environment and PCA 1 respectively accounted for 98.44%, 0.244% and 69.87% of the total sum of squares. Genotypes3, 8, 1 and 5 were the highest yielding but most unstable genotypes. Genotypes 3, 6 and 2 were the low yield unstable genotypes.

The IPCA 1 versus IPCA 2 biplot (i.e. AMMI 2 biplot) (fig. 2) explain the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Osiru *et al*., 2009).

A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific environmental conditions. However, for the AMMI 2 model, IPCA2 scores was considered in interpreting GEI that captured 12.6% of the interaction sum of squares as suggested by Gauch and Zobel (1996). A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). Furthermore, when IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot (fig. 2), the more stable they are.

References

Almehemdi, A. F., Z. M. Abdulrazaq and Y. S. Sekhi (2017). Evaluation of some caraway cultivars performance using ternary plot and AMMI biplot technique. *Iraqi J. Desert. Study*, **7 (1)** : 84-91.

Al-Rawi, O. H., M. D. Y. El-Jubouri, S. H. Cheyed and A. F. Amehemdi (2018). Assessment of multi-cultivars of caraway using ternary plot under arid zone circumstances.

Asfaw, A., F. Alemayehu, F. Gurmu and M. Atnaf (2009). AMMI and SREG GGEbiplot analysis for matching varieties onto soybean production environments in Ethiopia. *Scientific Research and Essay*, **4** : 1322-1330.

Badoni, A. and J. S. Chauhan (2010). Potato seed production of cultivar Kufri Himalini, *In vitro*. *Stem cell*, **1** : 1-6.

Crossa, J. (1990). Statistical analysis of multi-location trials. *Adv. Agron.*, **44** : 55-85.

Eberhart, S. A. and W. A. Russell (1966). Stability parameters for comparing varieties. *Crop Sci*., **6** : 36-40.

FAO (2008). Workshop on opportunities and challenges for promotion andsustainable production and protection of the potato crop in Vietnam andelsewhere in Asia 25-28.

Finlay, K. W. and G. N. Wilkinson (1963). The analysis of adaptation in a plant breedingprogram. *Aust. J. Agric. Res*., **14** : 742-754.

Gauch, G. (1992). Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs. Elsevier Science Publishers, Amsterdam, TheNetherlands.

Gauch, H. G. (2006). Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.*, **46** : 1488-1500.

Gauch, H. G. and R. W. Zobel (1988). Predictive and postdictive success of statistical analysis of yield trials. Theor. Appl. Genet. 76: 1-10.http://www.potato2008.org/en/potato/economy.html

Martin, J. and A. Alberts (2004). A comparison of statistical methods to describe genotype × environment interaction and yield stability in multi- locationmaize trials. Faculty of Agriculture, Department of Plant Sciences (Plant Breeding) at the University of the Free State.

Osiru, M. O., O. M. Olanya, E. Adipala, R. Kapinga and B. Lemaga (2009). Yield stability analysis of Ipomoea batatus L. cultivars in diverse environments. *Aust J Crop Sci.*, **3(4)** : 213-220.

Pourdad, S. S. and R. Mohammadi (2008). Use of stability parameters for comparing safflower genotypes in multienvironment trials. *Asian J. Plant. Sci.*, **7** : 100-104.

Purchase, J. L. (1997). Parametric stability to describe G x E interactions and yieldstability in winter wheat. PhD Thesis, department of agronomy, faculty of Agric.Univ. of Orange Free State, Bloemfontein, South Africa.

Gollob, H. F. (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, **33** : 73-115.

Sadeghi, S. M., H. Samizadeh, E. Amiri and M. Ashouri (2011). Additive main effectsand multiplicative interactions (AMMI) analysis of dry leaf yield in tobaccohybrids across environments. *Afr J of Biotechnology,* **10**: 4358-4364.

Singh, R. K. and B. D. Chaudhary (1977). *Biometrical methods in quantitative genetic analysis*. Kalyani publishers, New Delhi, India.

Thillainathan, M. and G. C. J. Fernandez (2002). A novel approach to plant genotypicclassification in multi-site evaluation. *Hort. Sci.*, **37** : 793-798.

Vargas, M. V. and J. Crossa (2000). *The AMMI analysis and graphing the biplot*. CIMMYT, INT., Mexico.

Yan, W., M. S. Kang, B. Ma, S. Wood and P. L. Cornelius (2007). GGE biplotvs AMMI analysis of genotype-by-environment data. *Crop Sci.*, **47**: 643-655.

Zobel, R. W., M. S. Wright and H. G. Gauch (1988). Statistical analysis of a yield trial. *Agron. J.*, **80** : 388-393.