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Determining the Most Stable Potato Genotypes Using AMMI Yield Stability Analysis Method

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ABSTRACT

Genotype-environment interaction (GEI) is very important for breeders. It is considered a complicated issue in breeding programs to obtain stable and high-yielding genotypes to release new genotypes. This study was conducted to achieve a stable high-yielding genotype that is adaptive to climatic conditions of potato-producing regions in Iran. A total of 20 potato breeding lines along with five commercial varieties (Savalan, Agria, Caesar, Luta and Satina) were evaluated in a randomized complete block design with three replicates in the Agricultural Research and Natural Resources Stations of five location (Ardabil, Razavi Khorasan, Karaj, Isfahan and Hamadan) in Iran, for two years (2016 and 2017). Combined ANOVA of yield data for studied genotypes and environments indicates significant differences among potato genotypes, environments, and GE interaction was significant. Thus, the AMMI method and its parameters were used to analyze yield stability. The results indicated that only four interaction principal components were significant ($P<0.01$), which accounted for 81.2% of the GEI sum of squares. Based on type 1 parameters ($SIPC_1$, FA_1, Za_1, Dz_1, EV_1, and Da_1), genotypes G7, G10, G14, G20 and G24 were identified as to be stable. Moreover, according to the results of type 2, 3 and 4 parameters, genotypes G2, G6, G7, G14, G15 and G20, as well as cultivars Agria (G24) and Luta (G23), were found to be stable. Genotypes G6, G7, G14, G15, G20, and G24 were stable according to the ASV parameter, and genotypes G6 and G7 were stable based on the MASV parameter. Amongst the stable genotypes identified by the AMMI parameters, while genotype G6 was high-yielding, G14 and G24 (Agria) were moderate-yielding.

Keywords: AMMI Parameters, Potato Genotypes, Stability, Tuber Yield

1. Introduction

Potato (*Solanum tuberosum* L.) is the fourth staple food after wheat, rice, and corn in terms of nutrition and production importance (Fufa 2013). Given the growing rate of population and its consequences, such as hungrier people and more demand for food, the Food and Agricultural Organization (FAO) has introduced potato as a food security plant (Devauxet et al. 2014). Thus, the need for expanding potato production is globally felt to manage the increase in food demands and food security (Hassanabadi et al. 2013). Achievement to high-yield, adaptive, and stable genotypes is one of the main goals of potato breeders. However, Genotype-environment interaction (GEI) renders breeding programs difficult and complex (Kadhem & Baktash 2016). GEI is a genotype’s response to environmental changes (Crossa et al. 1991). It is important to understand the GEI structure and nature in breeding programs because a significant GEI can restrict efforts to select superior genotypes when introducing new varieties and cultivars in breeding programs (Shafii & Price 1998). Numerous statistical methods have been proposed to study GEI to determine stable genotypes (Sabaghnia et al. 2008). These methods can be divided into two categories-univariate and multivariate (Karimizadeh et al. 2012).

Among the multivariate methods, the additive main effect and multiplicative interaction (AMMI) model is more credible and widely used (Byarugaba et al. 2018). The AMMI model was first used by Gauch (1988) to analyze yield data. Then, Gauch and Zobel (1988) fully expanded and analyzed this model. In plant breeding, this method affects the accuracy of genotype yield estimation in multi-environment trials. Such an accurate estimation is obtained through evaluation and prediction via dissociating the data into modeling and validation data as well as comparing the values expected from the model with validation data (Safavi & Bahraminejad 2017). The AMMI is an integrated model of analysis of variance (ANOVA) and principal component analysis. This model first calculates the main effect of genotypes and environments using the ANOVA methods, and then, the genotype and environmental components of the interaction are computed for the matrix of deviation from incremental effect (Crossa et al.

1990). The first part of the AMMI model, the summable part, uses usual variance analysis, while the second part is multiplicative and utilizes the method of interaction principal component analysis to dissociate GEI into a range of 1to *n* principal components (Omrani et al. 2018). It is noteworthy to mention that in the AMMI method, the calculations are performed on the values of GEI, while the computation of principal components is performed on the differentials of main data from the total mean of entire data (Gauch 1988). The estimation accuracy of the AMMI method is similar to increasing the number of replicates. This method can be used to reduce replicates and related expenses, which, in turn, allows the use of more treatments to the experiment (Crossa et al. 1991).

Tarakanovas and Ruzgas (2006) introduced AMMI as an effective method to study GEI and stated that its bi-plots could determine the suitable varieties for cultivation in various environments as well as the varieties for cultivation in certain environmental conditions. The AMMI method is widely used to evaluate GEI and has been employed by various researchers for the selection of stable genotypes of potato (Byarugaba et al. 2018), sunflower (Khomari et al. 2016), oats (Safavi & Bahraminejad 2017), durum wheat (Karimizadeh et al. 2016), canola (Pourdad & Jamshid Moghaddam 2013) and lentil (Sabaghnia et al. 2008). Worku et al. (2018) used the multivariate method and index of the AMMI stability value and concluded that the clone CIP-396004.337 possessed the highest yield and stability. In a study conducted by Byarugaba et al. (2018) on 21 Dutch potato varieties from 2015 to 2016 in five regions, they utilized the multivariate methods, including the AMMI, and suggested eight varieties for the Uganda region.

To investigate the stability based on the AMMI model, various parameters have been proposed, such as Euclidean distance from the origin of significant Interaction Principal Component (IPC) axes (Da) (Annicchiarico 1997), distance of Interaction Principal Component (IPC) point with origin in space (Dz) (Zhang et al. 1998), absolute value of the relative contribution of IPCs to the interaction (Za) (Zali et al. 2012), stability statistic based on the first IPC axes in the fitted AMMI model (FA) (Raju 2002). Zobel (1994) introduced a parameter, i.e., averages of square eigenvector values (EV). Alternatively, another parameter, i.e., sums of the absolute value of the IPC scores (SIPC), was propounded by Sneller et al. (1997). Based on the two first Interaction Principal Component Analysis (IPCAs), AMMI stability value (ASV) (Purchase 1997) and modified AMMI stability value (MASV) (Zali et al. 2012) have been proposed.

The present study aims to identify and select stable high-yielding genotypes for potato-producing regions in Iran using the AMMI model and its parameters.

2. Material and Methods

2.1. Plant material and treatments

In this study, 20 potato genotypes (Table 1) and five standard varieties (Savalan, Agria, Caesar, Luta, and Satina) were evaluated in five locations (Ardabil, Razavi Khorasan, Karaj, Isfahan, and Hamadan) in Iran in two years (2016-2017). The climatic conditions and geographic location of the studied areas are presented in Table 2. The experimental design in all locations was randomized complete block with three replicates in both years. The chemical fertilizers, including ammonium phosphate, urea, and potassium sulfate whose dosages were calculated by the soil test, were incorporated into the soil (Table 3). All breeding lines and control varieties were cultivated in two six-meter-long rows with inter-row spacing of 75 cm and inter-plant spacing of 25 cm. Colorado beetles were controlled by applying 250 mL ha^{-1} Imidacloprid (Confidor). The plots were weeded in two stages within a 10- to 15-centimeter distance from the plants. The genotype yields were measured after the harvest.

Table 1-The list of the potato breeding lines and standard cultivars studied in this research

NO	*Line cod*	*Parents*		*NO*	*Line cod*	*Parents*		*NO*	*Standard cultivars*
		♀	♂			♀	♂		
G1	16	Luta	Caesar	G11	3	Luta	Caesar	G13	Caesar
G2	9	Luta	Caesar	G12	2	Luta	Caesar	G22	Satina
G3	15	Luta	Caesar	G14	21	Luta	Savalan	G23	Luta
G4	11	Luta	Caesar	G15	5	Luta	Savalan	G24	Agria
G5	13	Luta	Caesar	G16	1	Luta	Savalan	G25	Savalan
G6	5	Luta	Caesar	G17	2	Luta	Savalan		
G7	23	Luta	Caesar	G18	3	Luta	Savalan		
G8	56	Luta	Caesar	G19	16	Luta	Savalan		
G9	12	Luta	Caesar	G20	14	Luta	Savalan		
G10	4	Luta	Caesar	G21	13	Luta	Savalan		

Table 2- Climatic conditions and geographical position of studied regions

Location	*Latitude*	*Longitude*	*Altitude (m)*	*Temperature (^0C)*			*Precipitation (mm)*	*Relative humidity (%)*
				Average	*Minimum*	*Maximum*		
Ardabil	48° 18’E	38° 15’N	1351	9.90	4.10	15.80	277	68
Hamedan	48° 32’E	34° 48’N	1550	11.35	3.93	18.77	384	53
Karaj	51° 00’E	35° 48’N	1312	14.40	8.00	20.80	247	53
Razavi Khorasan	59° 23’E	35° 34’N	1600	14.10	7.10	21.10	225	55
Esfahan	51° 40’E	32° 37’N	1550	16.25	9.10	23.40	123	40

Table 3- Planting date and harvest of potato genotypes and Chemical fertilizers consumption in studied locations

Location	*Planting dates*	*Harvest dates*	*Chemical fertilizers*		
			Ammonium phosphate (kg ha^{-1})	*Urea (kg ha^{-1})*	*Potassium sulfate (kg ha^{-1})*
Ardabil	25-30 April	2-15 October	150	300	100
Hamedan	15-20 June	16-21 November	100	250	150
Karaj	25-30 June	19-21November	150	300	100
Razavi Khorasan	10-15 June	18-22 October	100	350	200
Esfahan	5-10 June	17-20 October	150	350	150

2.2. Statistical analysis

To determine the stability of the genotypes, the multivariate AMMI model whose statistical model is as follows was utilized:

$$Y_{IJ} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij} \tag{1}$$

Where; Y_{ij}, denotes the yield of *i*th genotype in *j*th environment; μ, is the grand mean; g_i and e_j , are the genotype and the environment deviations from the grand mean, respectively; λ_n , is the eigenvalue of the *n*th principal component axis; $\gamma_{in}$and δ_{jn} , are the eigenvectors of the genotype and environment for the axis *n*, respectively; and ρ_{ij} ,is the error term.

Several statistics of the AMMI model were employed to investigate the stability of the genotypes. Various parameters, including EV (Zobel 1994), SIPC (Sneller et al. 1997), Da (Annicchiarico 1997), Za (Zali et al. 2012), and FA (Raju 2002) were also calculated. Furthermore, the first tow IPCA was used for computing ASV (Purchase 1997) and MASV (Zali et al. 2012).

$$Zai = \sum_{n=1}^{N} |\gamma_{in} \partial_n| \tag{2}$$

$$DZi = \sqrt{\sum_{n=1}^{N} \gamma_{in}^2} \tag{3}$$

$$MASV = \sqrt{\sum_{K=1}^{N-1} (SSIPC_n/SSIPC_{n+1})\,(IPCn)^2 + (IPCn+1)^2} \tag{4}$$

$$ASV = \sqrt{(\mathrm{SSIP1/SSIP2})\,(\mathrm{IPC1})^2 + (\mathrm{IPC2})^2} \tag{5}$$

$$Dai = \sqrt{\sum_{\mathrm{n=1}}^{\mathrm{N}} (\lambda_{\mathrm{n}} \gamma_{\mathrm{in}})^2} \tag{6}$$

$$EV = \sum_{\mathrm{n=1}}^{\mathrm{N}} \gamma_{\mathrm{in}}^2 / \mathrm{n} \tag{7}$$

$$SIPC = \sum_{\mathrm{n=1}}^{\mathrm{N}} \lambda_{\mathrm{n}}^{0.5}\, \gamma_{\mathrm{in}} \tag{8}$$

$$FA = \sum_{n=1}^{N} \lambda_n^2 \gamma_{in}^2 \tag{9}$$

To draw the bi-plot, Minitab 16 software was used, and the entire analyses and calculations of the AMMI model were carried out with of Genstat Release 12.0.

3. Results and Discussion

The results of the combined analysis of variance of yield data showed that the effects of environment (each location and year was considered as different environment), genotype, and their interactions were significant ($P<0.01$; Table 4). The effect of genotype, environment, and GEI accounted for 7.2%, 35.5%, and 42.3% of the total sums of squares, respectively. The mean squares of $IPCA_1$ and $IPCA_2$ were found to be significant ($P<0.01$) and cumulatively captured 57.7% of GEI (Table 4) as $IPCA_1$ and $IPCA_2$ components accounted for 34% and 23.7% of GEI sum of the squares, respectively. The $IPCA_3$ and $IPCA_4$ explained 13.1% and 10.4% of the GEI variations, respectively. In total, the first four components accounted for 81.2% of the GEI variation. Thus, the remaining components of the model cover only 18.2% of the sum squares of GEI.

Table 4- Combined analysis of yield data of potato genotypes (lines and standard cultivars)

Source	*df*	*SS*	*MS*	*Proportion*	*Noise*
Environments	9	27981	68.51^{**}	0.355a	0.007^{c}
Genotypes	24	5676	10.33^{**}	0.072a	0.097^{c}
Genotype × Environment	216	33347	154.4^{**}	0.423a	0.148^{c}
IPCA 1	32	11334	354.2^{**}	0.340b	–
IPCA 2	30	7893	263.1^{**}	0.237b	–
IPCA 3	28	4390	156.8^{**}	0.131b	–
IPCA 4	26	3477	133.7^{**}	0.104b	–
Residuals	100	6252	62.5	–	0.423^{d}
Error	480	10984	22.9	–	–
Total	749	78896	105.3	–	–

* and **, significant at 0.05 and 0.01 respectively; IPCA , Interaction Principal Component Analysis; [a], Calculated by dividing on sum of (GEN, ENV, and GEN×ENV) SS; [b], Calculated by dividing on ENV×GEN interaction SS; [c], Calculated by [(df×MS Error)/SS]; [d], The portion of residual SS from total GEN×ENV was calculated as SSE/(ENV×GEN SS)

To better understand the AMMI model, a bi-plot (Figure 1) was drawn. Genotypes G5, G9, G12, G15, G16, G17, G18, G21, and G23 (cv. Luta) and environments E2, E9 and E5 were found to have higher IPCA1 and, hence, the highest interactions. In Figure 1, the vertical line in the mid-section of the bi-plot indicates the grand mean value of the two experimental years. The genotypes and environments on the right had higher yields than mean. As the bi-plot illustrates, genotypes G1, G3, G5, G6, G8, G9, G17, G19, and G25 (cv. Savalan) possessed the highest mean yield. Among the environments, E1, E2, and E9 had the highest yield, while E3 had the lowest (Table 5).

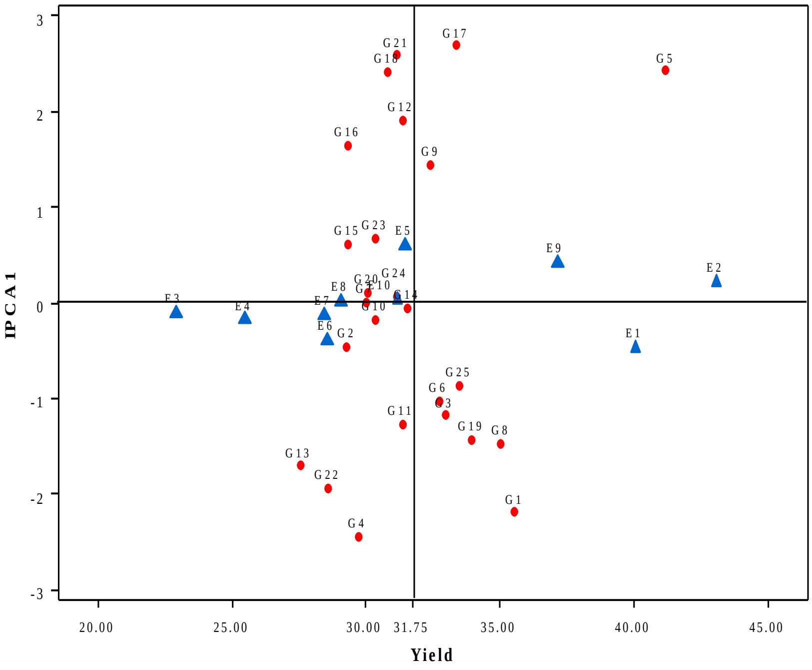

Figure 1- The bi-plot of mean yield and first principle component for potato genotypes and 10 environments

Table 5- The mean yield and interaction principle components (IPCAs) of yield for all environments

Environment	*Environment Code*	*Yield (t ha^{-1})*	*IPCA1*	*IPCA2*	*IPCA3*
Ardabil (2016)	E1	40.07	-3.677	-0.086	-2.61
Hamedan (2016)	E2	43.05	1.701	-5.278	0.761
Karaj (2016)	E3	22.88	-0.909	1.762	4.107
Isfahan (2016)	E4	25.45	-1.411	1.296	-0.272
Razavi Khorasan (2016)	E5	31.44	4.626	3.144	-1.497
Ardabil (2017)	E6	28.55	-3.05	-1.11	-1.027
Hamedan (2017)	E7	28.44	-0.98	2.385	-0.266
Karaj (2017)	E8	29.05	0.133	-0.795	-0.526
Isfahan (2017)	E9	37.12	3.23	-1.024	-1.509
Razavi Khorasan (2017)	E10	31.16	0.337	-0.301	2.833

To evaluate the stability of the genotypes and environments and to associate the genotypes to the various environments, another bi-plot was utilized (Figure 2). Figure 2 illustrates the bi-plot using IPCA1 and IPCA2 for studied genotypes and environments. Accordingly, stable genotypes can be introduced and various environments can be classified. The genotypes and environments in the center of the bi-plot, i.e., environments E3, E4, E7, E8, and E10 along with genotypes G7, G14, G20 and G24 (cv. Agria) had the minimum genotype × environment interaction. So, they were superior to the other genotypes and environments in terms of not having GEI. The genotypes adjacent to an environment were specifically adaptive to the related environment and the genotypes near the component axes were found to have more general adaptation. Therefore, genotypes G14 and G24 (cv. Agria) were specifically adapted to environments E10; genotypes G15 and G23 (cv. Luta) were specifically adapted to environment E5; and genotypes G7 and G20 were specifically adapted to environments E1, E3, and E6 (Figure 2). On the other hand, genotypes G6, G7, G10, G14, G16, G20, G21, G24 (cv. Agria), and G13 (cv. Caesar) exhibited general adaptation because they were closer to the axes of the principal components of the interactions (Figure 2). Since 57.5 percent of the variance – i.e. more than half of the entire variance – was captured by the first and second principal components, it was better to use the results of the AMMI model's statistics to determine stability.

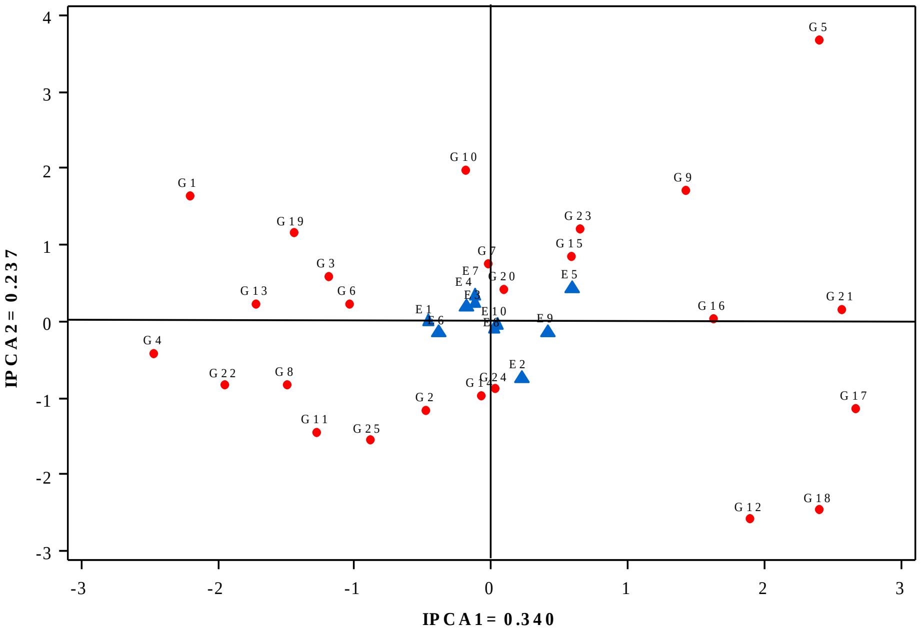

Figure 2- The bi-plot of the first two principal axis scores of potato breeding lines, standard cultivars, and environments

This study calculated other parameters of the AMMI method including $SIPC_1$, FA_1, Za_1, Dz_1, EV_1, and Da_1 (type 1, using the first IPCA); $SIPC_2$, FA_2, Za_2, Dz_2, EV_2, and Da_2 (type 2, based on the first and second IPCA); $SIPC_3$, FA_3, Za_3, Dz_3, EV_3, and Da_3 (type 3, using three principal components); and $SIPC_4$, FA_4, Za_4, Dz_4, EV_4, and Da_4 (type 4, based on the four components) (Tables 6, 7, and 8). Also, MASV and ASV were calculated based on the first two and four principal components and their sum of squares, respectively (Tables 6, 7, and 8).

Table 6- The SIPC and FA parameters of the AMMI model for tuber yields of 25 genotypes tested in 10 environments

Genotypes	*MTY*	*SIPC1*	*SIPC2*	*SIPC3*	*SIPC4*	STD_{SIPC}	FA_1	FA_2	FA_3	FA_4	STD_{FA}	*MASV*
G1	35.57	2.203	3.829	5.066	6.122	1.686	298.313	433.886	492.426	530.393	101.70	4.352
G2	29.30	0.47	1.652	1.807	2.449	0.825	13.601	85.230	86.145	100.167	39.06	2.166
G3	32.99	1.192	1.765	3.299	3.871	1.260	87.286	104.125	194.136	205.266	60.60	2.934
G4	29.71	2.462	2.892	3.201	3.814	0.569	372.493	381.965	385.624	398.401	10.72	3.133
G5	41.21	2.407	6.081	6.335	7.589	2.230	356.071	1048.471	1050.932	1104.501	356.89	6.914
G6	32.73	1.035	1.243	1.249	1.43	0.161	65.827	68.040	68.042	69.155	1.40	1.301
G7	30.01	0.016	0.768	1.399	2.017	0.857	0.015	29.022	44.248	57.270	24.62	1.693
G8	35.05	1.49	2.335	3.108	4.835	1.425	136.385	173.019	195.886	297.424	69.00	3.085
G9	32.44	1.427	3.139	4.593	6.495	2.153	125.142	275.428	356.250	479.412	148.55	4.419
G10	30.39	0.188	2.158	2.678	4.154	1.639	2.176	201.146	211.473	285.652	121.28	3.701
G11	31.36	1.278	2.739	4.891	5.685	2.011	100.377	209.869	387.106	408.541	147.34	4.407
G12	31.37	1.897	4.497	5.87	8.087	2.591	221.253	567.939	640.067	807.411	246.60	5.767
G13	27.55	1.717	1.932	2.915	3.504	0.840	181.196	183.563	220.562	232.384	25.93	2.626
G14	31.58	0.071	1.052	2.759	3.494	1.563	0.306	49.687	161.172	179.570	86.65	3.135
G15	29.35	0.596	1.434	1.762	3.676	1.302	21.822	57.838	61.949	186.627	72.00	2.526
G16	29.32	1.631	1.645	2.758	3.47	0.900	163.450	163.461	210.879	228.127	33.12	2.670
G17	33.38	2.673	3.819	5.798	6.568	1.787	439.307	506.661	656.524	676.716	115.42	4.836
G18	30.84	2.399	4.884	5.929	7.335	2.083	353.755	670.552	712.351	779.661	188.97	5.476
G19	33.96	1.443	2.582	2.897	4.443	1.237	127.907	194.422	198.228	279.612	62.10	3.039
G20	30.10	0.094	0.502	2.308	2.722	1.302	0.544	9.092	133.877	139.719	76.32	2.833
G21	31.18	2.572	2.708	3.277	4.864	1.051	406.450	407.400	419.787	505.526	47.55	3.578
G22	28.61	1.944	2.796	4.237	5.311	1.497	232.361	269.618	349.071	388.306	71.45	3.648
G23	30.37	0.659	1.862	2.728	2.734	0.981	26.657	100.915	129.600	129.601	48.61	2.524
G24	31.14	0.031	0.933	2.943	4.192	1.889	0.060	41.830	196.413	249.486	119.84	3.602
G25	33.52	0.886	2.462	4.336	4.593	1.738	48.241	175.582	309.945	312.189	126.19	4.011
Mean yield	31.75											

MTY, Mean Tuber Yield (t ha^{-1}); STD, Standard Deviation

Table 7- The Za and Dz parameters of the AMMI model for tuber yields of 25 genotypes tested in 10 environments

Genotypes	*MTY*	Za_1	Za_2	Za_3	Za_4	STD_{Za}	Dz_1	Dz_2	Dz_3	Dz_4	STD_{Dz}	*ASV*
G1	35.57	0.096	0.149	0.176	0.195	0.043	0.281	0.361	0.413	0.451	0.073	3.100
G2	29.30	0.020	0.060	0.063	0.074	0.023	0.060	0.176	0.177	0.209	0.065	1.309
G3	32.99	0.052	0.071	0.103	0.114	0.029	0.152	0.172	0.302	0.317	0.086	1.539
G4	29.71	0.107	0.121	0.128	0.139	0.013	0.314	0.320	0.324	0.340	0.011	2.981
G5	41.21	0.104	0.226	0.231	0.254	0.067	0.307	0.598	0.599	0.637	0.153	4.671
G6	32.73	0.045	0.052	0.052	0.055	0.004	0.132	0.135	0.135	0.139	0.003	1.258
G7	30.01	0.001	0.026	0.039	0.050	0.021	0.002	0.105	0.146	0.181	0.077	0.752
G8	35.05	0.065	0.093	0.109	0.140	0.031	0.190	0.224	0.256	0.391	0.088	1.975
G9	32.44	0.062	0.119	0.150	0.183	0.052	0.182	0.300	0.381	0.502	0.135	2.420
G10	30.39	0.008	0.073	0.084	0.111	0.044	0.024	0.276	0.289	0.384	0.154	1.983
G11	31.36	0.055	0.104	0.150	0.164	0.049	0.163	0.261	0.435	0.456	0.141	2.117
G12	31.37	0.082	0.168	0.198	0.237	0.066	0.242	0.436	0.490	0.620	0.157	3.454
G13	27.55	0.074	0.082	0.103	0.113	0.018	0.219	0.221	0.272	0.290	0.036	2.069
G14	31.58	0.003	0.036	0.072	0.085	0.037	0.009	0.137	0.308	0.333	0.153	0.985
G15	29.35	0.026	0.054	0.061	0.095	0.028	0.076	0.140	0.149	0.360	0.124	1.101
G16	29.32	0.071	0.071	0.095	0.108	0.018	0.208	0.208	0.275	0.301	0.047	1.954
G17	33.38	0.116	0.154	0.196	0.210	0.043	0.341	0.377	0.494	0.512	0.085	3.402
G18	30.84	0.104	0.186	0.209	0.234	0.056	0.306	0.463	0.493	0.548	0.104	3.800
G19	33.96	0.063	0.100	0.107	0.135	0.030	0.184	0.243	0.248	0.363	0.075	2.071
G20	30.10	0.004	0.018	0.056	0.064	0.029	0.012	0.058	0.298	0.306	0.155	0.423
G21	31.18	0.112	0.116	0.128	0.156	0.020	0.328	0.329	0.341	0.436	0.052	3.085
G22	28.61	0.084	0.113	0.143	0.162	0.034	0.248	0.275	0.360	0.405	0.073	2.480
G23	30.37	0.029	0.068	0.087	0.087	0.028	0.084	0.188	0.234	0.234	0.071	1.439
G24	31.14	0.001	0.031	0.074	0.096	0.043	0.004	0.126	0.349	0.409	0.190	0.903
G25	33.52	0.038	0.091	0.131	0.135	0.045	0.113	0.247	0.391	0.394	0.134	1.900

Table 8- The EV and Da parameters of the AMMI model for tuber yields of 25 genotypes tested in 10 environments

Genotypes	*MTY*	*EV_1*	*EV_2*	*EV_3*	*EV_4*	*STD_{EV}*	*Da_1*	*Da_2*	*Da_3*	*Da_4*	*STD_{Da}*	*ASV*
G1	35.57	0.079	0.065	0.057	0.051	0.012	17.272	20.830	22.191	23.030	2.540	3.100
G2	29.30	0.004	0.015	0.010	0.011	0.005	3.688	9.232	9.281	10.008	2.931	1.309
G3	32.99	0.023	0.015	0.030	0.025	0.006	9.343	10.204	13.933	14.327	2.545	1.539
G4	29.71	0.099	0.051	0.035	0.029	0.032	19.300	19.544	19.637	19.960	0.273	2.981
G5	41.21	0.094	0.179	0.120	0.101	0.038	18.870	32.380	32.418	33.234	6.915	4.671
G6	32.73	0.017	0.009	0.006	0.005	0.006	8.113	8.249	8.249	8.316	0.085	1.258
G7	30.01	0.000	0.006	0.007	0.008	0.004	0.123	5.387	6.652	7.568	3.329	0.752
G8	35.05	0.036	0.025	0.022	0.038	0.008	11.678	13.154	13.996	17.246	2.355	1.975
G9	32.44	0.033	0.045	0.048	0.063	0.012	11.187	16.596	18.875	21.895	4.523	2.420
G10	30.39	0.001	0.038	0.028	0.037	0.017	1.475	14.183	14.542	16.901	6.972	1.983
G11	31.36	0.027	0.034	0.063	0.052	0.017	10.019	14.487	19.675	20.212	4.805	2.117
G12	31.37	0.059	0.095	0.080	0.096	0.018	14.875	23.831	25.300	28.415	5.810	3.454
G13	27.55	0.048	0.024	0.025	0.021	0.012	13.461	13.549	14.851	15.244	0.906	2.069
G14	31.58	0.000	0.009	0.032	0.028	0.015	0.553	7.049	12.695	13.400	5.968	0.985
G15	29.35	0.006	0.010	0.007	0.032	0.013	4.671	7.605	7.871	13.661	3.763	1.101
G16	29.32	0.043	0.022	0.025	0.023	0.010	12.785	12.785	14.522	15.104	1.195	1.954
G17	33.38	0.116	0.071	0.081	0.065	0.023	20.960	22.509	25.623	26.014	2.446	3.402
G18	30.84	0.094	0.107	0.081	0.075	0.014	18.808	25.895	26.690	27.922	4.099	3.800
G19	33.96	0.034	0.030	0.021	0.033	0.006	11.310	13.944	14.079	16.722	2.210	2.071
G20	30.10	0.000	0.002	0.030	0.023	0.015	0.738	3.015	11.571	11.820	5.746	0.423
G21	31.18	0.108	0.054	0.039	0.048	0.031	20.161	20.184	20.489	22.484	1.113	3.085
G22	28.61	0.062	0.038	0.043	0.041	0.011	15.243	16.420	18.683	19.705	2.043	2.480
G23	30.37	0.007	0.018	0.018	0.014	0.005	5.163	10.046	11.384	11.384	2.956	1.439
G24	31.14	0.000	0.008	0.041	0.042	0.022	0.246	6.468	14.015	15.795	7.172	0.903
G25	33.52	0.013	0.031	0.051	0.039	0.016	6.946	13.251	17.605	17.669	5.057	1.900

Based on type 1 parameters, genotypes G7, G10, G14, G20, and G24 (cv. Agria) were found to be the most stable ones due to their lowest values. According to type 2 parameters, genotypes G6, G7, G14, G15, G20, and G24 (cv. Agria) were selected as the most stable genotypes. Genotypes G2, G6, G7, G14, G15, G20, and G23 (cv. Luta) were the stable ones based on the type 3 parameters. Genotypes G2, G6, G7, G20, and G23 (cv. Luta) accounted for the lowest values based on the type 4 parameters. The standard deviation was computed for all parameters. Genotypes G2, G7, G6, and G23 (cv. 'Luta') showed the lowest standard deviation of the EV parameter. Cultivar Caesar and genotypes G4, G6, and G16 obtained the lowest value of the standard deviation of D and Za parameters. The standard deviation value of the parameter SIPC for genotypes G2, G4, G6, and G13 (cv. Caesar) and Da for genotypes G4, G6, G13 (cv. Caesar), and G21 were the lowest. Genotypes G4, G6, G7, and G13 (cv. Caesar) acquired the lowest value of standard deviation in terms of the FA criterion.

Since genotypes G6, G7, G14, G15, G20, and G24 (cv. Agria) had the lowest values of ASV parameter, they were considered as the stable genotypes. On the other hand, genotypes G5, G12, G17, and G18 had the highest values of this parameter. Thus, they were selected as the unstable ones (Table 7 and 8). Based on the MASV parameter, genotypes G6, and G7 were selected as the stable genotypes. However, genotypes G5, G10, G12, G17, and G18 were found to be unstable.

GEI was found to be significant in the present study and was six times greater than genotype main effect. This reflects its complexity and high effect on tuber yield in various environments. The large magnitude of GEI causes more dissimilarity in the genetic systems that control the physiological processes that are conferring yield stability in different environments (Karimizadeh et al. 2016, 2019).

Additionally, the significance of GEI is indicative of the genotypes' evaluation in several environments to identify the general and specific adaptation. Thus, considering the significance of GEI, the AMMI method and its parameters were utilized to select the stable genotype. GEI stability is in biological or agricultural forms (Tollenaar & Lee 2002). Breeders tend to use agricultural and dynamic concept of stability instead of its static concept. According to this concept, there is a predictable response in relation to the environmental factors, and the yield of genotypes is likely to be improved through enhancing the environmental conditions. The genotype yield matches the estimated or predicted levels in all environments (Tollenaar & Lee 2002). Sabbaghniya et al. (2008, 2013) expressed that the AMMI method and its parameters were useful for investigating static stability. Zali et al. (2012) investigated the AMMI parameters and classified them into two groups. While the first group included EV, MASV, DZ, SIPC, and FA, the second group consisted of ZA, ASV, and Da. They stated that both of the groups were closely associated with the mean yield. Karimizadeh et al. (2016) stated that ASV features agricultural concepts of stability.

According to the parameters of type I ($SIPC_1$, FA_1, Za_1, Dz_1, EV_1, and Da_1), genotypes G7, G10, G14, G20, and G24 were stable although their yields were below the grand mean (Table 9). Hence, they cannot be considered as the ideal breeding lines. These breeding lines possess the Type I stability, which is equivalent to the biological stability (Lin et al. 1986). The tuber yields of genotypes G14 and G24 were nearly equal to the grand mean. Thus, these breeding lines can be used in breeding programs where the qualitative characteristics are of interest.

Table 9- The two-way table of the environment and genotype means

Genotypes	Ardabil (2016) E1	Hamedan (2016) E2	Karaj (2016) E3	Isfahan (2016) E4	Razavi Khorasan (2016) E5	Ardabil (2017) E6	Hamedan (2017) E7	Karaj (2017) E8	Isfahan (2017) E9	Razavi Khorasan (2017) E10	Genotype mean
G1	54.273	49.443	20.373	34.853	18.957	42.180	30.587	30.217	42.700	32.067	35.565
G2	43.323	31.847	19.957	23.593	33.557	25.893	24.567	26.770	29.217	34.310	29.303
G3	36.193	48.187	31.613	23.593	27.297	42.513	30.347	29.130	28.520	32.533	32.993
G4	46.540	36.440	22.503	29.490	20.800	33.457	30.910	27.853	24.147	24.933	29.707
G5	44.067	80.960	24.167	27.883	43.257	31.633	28.653	39.750	53.830	37.863	41.206
G6	39.930	44.390	27.117	28.957	27.180	37.430	30.790	31.130	35.047	25.277	32.725
G7	42.043	45.053	17.693	18.767	30.910	29.430	23.877	29.350	34.120	28.897	30.014
G8	52.570	41.210	20.497	39.143	33.027	28.487	34.543	37.463	27.957	35.617	35.051
G9	33.290	58.830	21.290	19.570	36.180	25.230	23.413	32.823	32.563	41.200	32.439
G10	40.507	46.863	19.187	19.300	22.373	35.060	18.452	28.670	44.650	28.833	30.390
G11	52.443	33.923	19.317	26.813	36.543	33.983	32.653	24.180	31.440	22.350	31.365
G12	29.223	38.780	29.383	25.203	51.907	18.770	33.457	25.797	27.660	33.533	31.371
Caesar	42.250	34.670	25.297	18.763	17.667	30.917	21.300	23.463	29.050	32.166	27.554
G14	47.343	33.040	19.000	22.520	34.537	27.023	30.233	32.870	41.903	27.333	31.580
G15	34.470	40.987	17.567	22.520	23.783	24.873	23.653	30.130	46.573	28.917	29.347
G16	30.090	41.560	19.740	21.447	34.073	21.340	22.350	20.070	41.837	40.660	29.317
G17	39.247	41.340	16.830	25.470	55.800	23.877	23.990	32.533	45.747	28.967	33.380
G18	27.510	31.890	20.000	27.347	46.803	21.550	36.680	22.960	49.123	24.500	30.836
G19	50.857	55.210	22.950	32.707	25.407	30.170	33.100	29.997	30.540	28.700	33.964
G20	38.413	42.930	10.973	20.373	29.667	31.743	34.793	28.260	39.717	24.100	30.097
G21	25.517	44.480	23.997	22.520	36.130	18.936	25.567	33.460	51.040	30.100	31.175
Satina	36.947	27.895	22.667	24.667	16.820	31.607	30.790	26.500	27.920	40.267	28.608
Luta	35.080	48.540	21.333	23.325	26.913	22.323	21.653	32.153	37.860	34.500	30.368
Agria	36.043	38.233	33.133	26.770	26.667	21.337	31.123	21.930	39.750	36.383	31.137
Savalan	43.690	39.517	45.530	30.543	29.723	23.903	33.440	28.743	35.010	25.100	33.520
Env. mean	40.074	43.049	22.885	25.445	31.439	28.547	28.437	29.048	37.117	31.164	31.720

According to the bi-plot, genotypes G6, G7, G10, G13 (cv. Caesar), G14, G16, G20, G21, and G24 (cv. Agria) had general adaptation in the entire studied regions. Among the all stable genotypes in the study, genotype G6 produced higher yield than average yield of all genotypes tested. In addition, G14 and G24 (cv. Agria) had tuber yield near to mean tuber yield of all genotypes. The availability of cultivars that are highly adaptive to a vast range of regions is one of the important goals of the breeding programs (Mohebodini et al. 2006). Hassanpanah et al. (2018) investigated 11 genotypes in five regions and selected genotypes 397031-16, 397045-13, and 397009-8 for their yield stability and dry matter as well as the other qualitative and quantitative traits. In another study using multivariate methods and qualitative characteristics, Hassanpanah et al. (2016) selected clones 1 and 2 as the stable clones with high tuber yield and for uses as chips, French fries, and roasting.

4. Conclusions

Yield-stable G6 performed high tuber yield with 32.73 t/ha, and the other two yield-stable genotypes G14 and G24 (cv. Agria) produced moderate tuber yield with 31.58 t/ha and 31.14 t/ha, respectively. In conclusion, potato breeding lines G6 and G14 could be considered as candidate for registration in Iran. In addition, Agria might be proposed as a suitable variety for regions such as Ardebil, Hamadan, Razavi Khorasan, Isfahan, and Karaj.

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