

STABILITY ANALYSIS OF TUBER YIELD USING UNBALANCED DATA FROM POTATO VARIETY TRIALS

Zlatko MIJIĆ¹, Vinko.KOZUMPLIK², Hrvoje ŠARČEVIĆ², Vladimir MEGLIĆ³,
Ivan VARNICA⁴, Tihomir ČUPIĆ⁵

¹ State Inspectorate, Sector of inspection in Agriculture, Beli Manastir, Croatia

² University of Zagreb, Faculty of Agriculture, Department of Plant Breeding, Genetics and Biometrics, Zagreb, Croatia

³ Agricultural Institute of Slovenia, Crop Science Department, Ljubljana, Slovenia

⁴ Croatian Agency for Agriculture and Food, Center for Seed and Seedling, Osijek, Croatia

⁵ Agricultural Institute Osijek, Department for Breeding and Genetic of Forage Crop, Osijek, Croatia

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Potatoes are grown in a wide region and in different environments unlike other crops, so it is known as one of the most spread world crops. In many agriculture areas around the world new genotypes are included in many multi-locational experiments at a large number of locations and years to determine the level and the stability of yields. However, there are a lot of problems with this traditional approach mostly due to the large number of genotypes that require consistent checking of every genotype at numerous locations and years. Multi-locational experiments require a lot of time and financial resources, and the possibility of error is greatly increased. In the present study we used the REML/BLUP

Corresponding author: Tihomir Čupić, Agricultural Institute Osijek, Department for Breeding and Genetic of Forage Crop, Južno predgrađe 17, Osijek, Croatia; Phone : ++ 385 31 515 543; E-mail: Tihomir.Cupic@poljinoh.hr

method to predict tuber yield in an unbalanced set consisting of 54 potato genotypes investigated over twelve years at three locations. The data were subjected to stability analysis using the AMMI model based on estimated values. The analysis of variance showed that the greatest effect can be attributed to the environment (E), then to their interaction (G×E) and least to the genotype. The first two multiplicative interaction components explained 85.4% of the interaction sum of squares. AMMI analysis enabled the identification of stable and productive genotypes as well as genotypes adapted to specific environments and clearly separated the three locations as mega-environments. The genotype selection index (GSI), due to its nature of combining the assessments of stability measure and yield rank, provided more useful information for selection and recommendation. The results of this study indicate the superiority of the prediction model in comparison with the traditional multi-location experiment methods allowing the creation of recommended list of potato varieties based on the analysis of unbalanced data sets.

Keywords: Potato, yield, unbalance data set, AMMI, Genotype Selection Index

INTRODUCTION

The Potato (*Solanum tuberosum* L.) is one of the most important vegetable crops in the world and the seventh most important food crop in Europe (FAOSTAT, 2018). Besides being used in direct feeding, most of the potato production are used by the processing industry to make chips, French fries, and other processed products. Despite the general trend of decline in the area under potatoes, worldwide production is growing due to an increase in average yields per hectare. The average potato yield on the world level increased substantially from 11.4 t ha⁻¹ in the 1962 to 20.1 t ha⁻¹ in 2017 (FAOSTAT, 2018). Yield of potatoes as other crops, is a very complex category which depends on many other characters and environmental conditions (FLIS *et al.*, 2014; MOMIROVIC *et al.*, 2016). Considerable variation in soil and climate results in significant variations in yield performance of the potato varieties, thus, genotype × environment (G×E) interaction is an important issue facing plant breeders and agronomists.

Evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (PIEPHO *et al.*, 2012). Measuring G×E helps to determine an optimum breeding strategy, to breed for specific or general adaptation, which depends on the expressions of stability under a limited or a wide range of environments (VOLTAS *et al.*, 2005; MOHAMMADI and AMRI, 2013). Determination of the performance and the stability of potato cultivars for yield are important so the breeders could give recommendation for the most suitable cultivars to the potato producers in a certain region (KOLECH *et al.*, 2015b). The conclusion about genetic materials in field experiments in order to classify those candidates to be released as cultivars is not an easy task. These conclusions must be based on true genotypic values. Experiments at different locations and in different years allow breeders to determine the value of G×E interaction for the evaluated and recommended genotypes (SILVA *et al.*, 2011; KOLECH *et al.*, 2015a; 2015b; TUCAK *et al.*, 2016). The G×E interaction is a major problem in the comparison of genotypes, because large number of genotypes and environments, which are involved in tests, give most often the unbalanced data sets. Therefore, there is a need to examine into the existing methodology for such data sets, which could be applicable for their improvement and balancing. In the "restricted maximum likelihood" (REML) and "best linear unbiased prediction" (BLUP) mixed models, variance components and random effect variances

are directly predicted in the data set, not requiring independence of errors. These procedures allow higher modelling flexibility, becoming the standard procedure for some statistical analyses (RESENDE and DUARTE, 2007; PIEPHO and MÖHRING, 2007). In this context, the BLUP method could be adequately used to predict yield of genotypes in the environments where they are not examined (PIEPHO *et al.*, 2003, BUNTARAN *et al.*, 2019). Recently, REML/BLUP methods have been used to investigate the G×E interaction in different crops such as: wheat (YAN *et al.*, 2002; STUDNICKI *et al.*, 2015), maize (SO and EDWARDS, 2011; OLIVOTO *et al.*, 2017) soybean (YAN and RAJCAN, 2003), cowpea (SANTOS *et al.*, 2016), sorghum (ALMEIDA FILHO *et al.*, 2014; 2016) and sweet potatoes (TICONA-BENAVENTE and SILVA FILHO, 2015).

Different statistical methods, including parametric and non-parametric, have been used in estimating the genotype stability. Additive main effects and multiplicative interaction (AMMI) analysis is one of the most informative in comparison to other models in the stability interpretation (GUNJACA *et al.*, 2007; GAUCH *et al.*, 2008; MOHAMMADI and AMRI, 2013; MUTHONI *et al.*, 2014). AMMI is a combination of analysis of variance (ANOVA) and principal component analysis (PCA). The results obtained by AMMI analysis may be useful when making decisions in the examination pertaining to specific adaptability (drought, low temperatures, diseases, etc.) (ADEBOLA *et al.*, 2013; SA'DIYAH and HADI, 2016). In recent years this analysis has been developed into an important technique in the agricultural survey (BABIC *et al.*, 2010; RAK *et al.*, 2013; GIRIDHAR *et al.*, 2016; HADDAD *et al.*, 2016; MUSTAMU *et al.*, 2018).

Most previous studies on unbalanced data sets from multi-environment tests have been limited without practical solution of obtaining reliable recommendation of genotypes regarding wide and specific stability and other agronomical purposes. The objective of the present study was to assess the possibility of using unbalanced data set on the potato tuber yield in creating the recommended lists of high-yielding genotypes having wide and specific adaptability.

MATERIALS AND METHODS

Yield data from the Croatian official variety trials assessing value for cultivation and use (VCU) of potato were analyzed for the period from 2001 to 2012. In each of the 12 test years the trials were conducted at three locations, Seget Donji (43°31'N, 16°13' E, 5 m a.s.l., soil type Rhodic cambisol, pH (H₂O) 8.0, pH (KCl) 7.4, Humus 1.49%, P₂O₅ 26.2 mg 100g⁻¹, K₂O 22.0 mg 100g⁻¹, CaCO₃ 3.4%), Hercegovac (45°38'N, 16°59'E, 150 m a.s.l., soil type Stagnic gleysol, pH (H₂O) 5.77, pH (KCl) 4.38, Humus 1.81%, P₂O₅ 27.6 mg 100g⁻¹, K₂O 21.0 mg 100g⁻¹, CaCO₃ -%), and Osijek (45°31'N, 18°40'E, 94 m a.s.l., soil type Luvisol, pH (H₂O) 5.50, pH (KCl) 6.60, Humus 2.55%, P₂O₅ 26.4 mg 100g⁻¹, K₂O 29.7 mg 100g⁻¹, CaCO₃ 1.25%), giving in total 36 test environments (location-year combinations). The experimental layout in all trials was a randomized complete block design (RCBD) with four replications. Plots were 8 m long, with 4 rows with a 70 cm distance. In order to ensure uniform germination trials were machine-planted using tubers 30 to 55 mm in size. In all trials basic fertilization was implemented with 500 kg ha⁻¹ N:P:K (7:20:30) plus 100 kg ha⁻¹ Urea (46% N). Top dressing was implemented with 200 kg ha⁻¹ of KAN (27% N) in combination with mechanical destruction of weeds in the early phase of flowering.

Four fungicide applications were performed in each year and at each trial location to control diseases. The yields of potato tubers were measured at two middle rows.

Each year a different number of breeding lines together with three control varieties Jaerla (medium early), Agria (medium late) and Désirée (medium late) have been included in the trials.

Breeding lines were tested for three years until 2009 and for two years afterwards. Thus, with four replications, the total number of yield observations was 144 for the three control varieties and 36 or 24 for breeding lines tested for three and two years, respectively. Fifty-four genotypes including three control varieties and 51 breeding lines, which were subsequently released as varieties based on their VCU performances, were considered for statistical analysis.

REML/BLUP method was used to predict the average yield of genotypes in the environments they were not tested. For estimating the variance components algorithm implemented in software GenStat 8 (GenStat, Committee 2005) was used. Initially, the analysis of variance was done for each environment separately according to RCBD. After checking the genetic variability between genotypes and the homogeneity of variances between environments by Bartlett's test, a joint analysis of variance for genotypes over 36 environments (3 locations \times 12 years) was performed. The environments were considered as random effects while the genotypes were treated as fixed variables. Analysis of variance was performed using the statistical package SAS release 9.4 (SAS Institute, 2013). In the model equation:

$$Y_{ijk} = m + g_k + e_j + ge_{jk} + r_{ij} + \epsilon_{ijk}$$

Y_{ijk} is defined as the observation of genotype k in environment j and replication i ; m is the overall mean; e_j is the environmental effect (e) in environment j (for $j=1, \dots, E$); r_{ij} is the effect of replication i (for $i=1, \dots, R$) in environment j ; g_k is the effect of genotype k (for $k=$ number of lines); ge_{jk} is the interaction effect of environment j and genotype k ; ϵ_{ijk} is the interaction effect of environment j , replication i and genotype k . The factors e and r were defined as random and g was defined as fixed effect.

After detecting a significant $G \times E$ interaction, adaptability and stability of potato genotypes were estimated by the AMMI method using CropStat 7.2 software (CROPSTAT, 2009). The AMMI model does not make provision for a quantitative stability measure, and as such a measure is essential in order to quantify and rank genotypes in terms of yield stability. Genotype selection index (GSI), was used by taking into consideration the AMMI stability value and mean yield for yield stability (FARSHADFAR, 2008). GSI was calculated for the i th genotype as:

$$GSI_i = RASV_i + RY_i;$$

where $RASV_i$ is the rank of the AMMI stability value and RY_i is the rank of the mean tuber yield of the i th genotype across environments.

RESULTS AND DISCUSSION

Test environments

A description of the 36 test environments including sowing and harvesting dates, weather variables and mean tuber yield of potato genotypes are shown in table 1. The sowing over 12 experimental years at Seget Donji started in average one month earlier and harvesting finished two months earlier than at Hercegovac and Osijek, resulting in one month shorter growing season at Seget Donji as compared to other two locations. The range of mean daily temperatures over 12 growing seasons varied between 16.4 and 19.6°C for Seget Donji, between 16.9 and 19.0°C for Hercegovac and between 15.5 and 20.2°C for Osijek, with similar overall means across years. Differences among locations for amounts of pre-season, season and total precipitations were more pronounced than differences in mean temperatures, but large across-year variation of amount of precipitation was also observed within each location. The lowest mean tuber yield was observed at Seget Donji (30.36 t ha⁻¹) and the highest at Osijek (38.37 t ha⁻¹). Substantial variation of tuber yield was observed across year's at all three locations, with the

yields of best performing years being almost three times higher than the yields of lowest ranking years.

A moderate negative correlation ($r = -0.54$ to $r = -0.62$) between mean yield of potato tuber and mean daily temperature over growing season was observed for all three experimental locations (Table 2). On the other hand, correlations of tuber yield with amount of precipitation were low or negligible except in the case of total precipitation at Seget Donji, which was in moderate positive correlation ($r = 0.59$) with tuber yield. Similarly, number of rainy days during growing season was in moderate positive correlation only at Seget Donji, which is not surprising having in mind that this location was much dryer over the 12-year period than other two locations.

Table 1. General information about vegetation at three locations from 2001 to 2012

Year	Env. Code	Planting date	Harvesting date	Average Temp (°C)	Precipitation (mm)			Yield±SE
					PS	GS	Total	
Seget Donji (Se)								
2001	Se01	16.03.	15.06.	16.9	380	245	625	24.73±2.27
2002	Se02	08.03.	03.07.	17.5	452	188	640	23.22±1.98
2003	Se03	06.03.	01.07.	17.9	473	77	550	21.17±1.97
2004	Se04	18.03.	05.07.	16.4	576	334	910	59.53±1.95
2005	Se05	16.03.	30.06.	17.1	711	253	964	30.46±2.26
2006	Se06	16.03.	06.07.	16.4	611	250	861	41.62±1.89
2007	Se07	06.03.	05.07.	18.3	243	302	545	20.39±2.33
2008	Se08	26.02.	02.07.	17.1	303	422	725	31.67±2.77
2009	Se09	10.03.	09.07.	17.1	717	436	1153	37.39±3.41
2010	Se10	03.03.	13.07.	18.5	720	287	1007	30.28±2.04
2011	Se11	09.03.	12.07.	19.1	525	239	764	23.96±1.97
2012	Se12	06.03.	10.07.	19.6	266	201	467	25.17±2.90
Mean				17.7	498.1	269.5	767.6	30.80
Hercegovac (He)								
2001	He01	11.04.	21.09.	16.9	222	578	800	57.44±1.98
2002	He02	28.03.	04.09.	18.1	262	529	791	31.74±1.98
2003	He03	02.04.	28.08.	19.6	231	181	412	23.67±1.98
2004	He04	02.04.	29.08.	16.9	300	442	742	44.43±2.46
2005	He05	08.04.	05.09.	16.9	401	460	861	34.68±2.26
2006	He06	18.04.	05.09.	17.1	363	410	773	35.45±1.89
2007	He07	03.04.	28.08.	19.0	318	294	612	33.76±2.33
2008	He08	07.04.	28.08.	18.1	315	376	691	44.79±2.55
2009	He09	07.04.	01.09.	18.7	304	253	557	37.26±3.41
2010	He10	21.04.	28.08.	18.5	482	583	1065	23.89±2.04
2011	He11	31.03.	01.09.	18.3	215	279	494	39.57±1.97
2012	He12	05.04.	28.08.	19.0	181	319	500	42.19±2.90
Mean				18.1	299.5	392	691.5	37.41

Year	Env. Code	Planting date	Harvesting date	Average Temp (°C)	Precipitation (mm)			Yield±SE (t/ha)
					PS	GS	Year	
Osijek (Os)								
2001	Os01	03.04.	28.08.	18.3	280	455	735	35.28±2.27
2002	Os02	26.03.	26.08.	16.7	177	379	556	59.62±1.98
2003	Os03	03.04.	02.09.	20.2	151	194	345	20.74±1.98
2004	Os04	26.03.	22.09.	15.5	212	479	691	42.83±2.55
2005	Os05	06.04.	02.09.	17.7	312	624	936	46.03±2.26
2006	Os06	04.04.	17.08.	17.8	246	391	637	37.85±1.89
2007	Os07	05.04.	08.09.	18.9	212	182	394	30.40±2.33
2008	Os08	04.04.	26.08.	19.4	270	307	577	47.32±2.54
2009	Os09	08.04.	10.09.	19.6	200	205	405	39.75±3.40
2010	Os10	09.04.	11.08.	18.9	333	537	870	33.03±2.04
2011	Os11	05.04.	31.08.	19.1	208	229	437	42.89±1.97
2012	Os12	04.04.	22.08.	20.1	156	258	414	38.07±2.90
Mean				18.5	229.8	353.3	583.1	39.48

PS (Pre-season) ; GS (Growing season); Total= PS +GS

Table 2. Correlation between mean yield of potato tuber and weather parameters for three experimental locations over the twelve year period

Location	Temperature (°C) ^a		Precipitation (mm)			No. of RD ^d		
		*	PS ^b	GS ^c	Total			
Seget Donji	-0.62	*	0.45	0.48	0.59	*	0.69	**
Hercegovac	-0.54	*	-0.45	0.23	-0.05		0.28	
Osijek	-0.54	*	0.08	0.31	0.26		0.38	

^a mean daily temperature over growing season; ^b PS (Pre-season); ^c GS (Growing season); ^d RD-rainy days over growing season; *, ** correlation coefficient significant at P<0.05 and P<0.01, respectively

Analysis of variance

The combined analysis of variance for potato tuber yield across environments revealed highly significant (P<0.01) effects of genotype (G), environment (E) and G×E interaction (Table 3). Environment had the largest effect, explaining 78.9% of the total sum of squares, whereas G and G×E interaction accounted for 9.3% and 10.9% of the total sum of squares, respectively. The high values of sum of squares due to environment suggest a great variability of agro ecological conditions in the conducted trials. On the other hand relatively low effect of the genotype could be explained by the fact that only elite genotypes, which were subsequently released as varieties, were included in the analysis. This is in accordance with the results of FLIS *et al.* (2014), who studied tuber yield of 22 potato cultivars grown in six environments and found that the E, G, and G×E sources of variation accounted for 72%, 8% and 16% of the total sums of squares, respectively. Similarly, in the study of MULEMA *et al.* (2008), who analyzed tuber yield of 12 potato genotypes across 12 environments, the E, G, and G×E sources of variation explained 54,

11 and 25% of the total sum of squares, respectively. Relatively low contribution of genetic variance to the total variance was also reported for yield of other crop species (FRIESEN *et al.*, 2016; ZORIĆ *et al.*, 2017). On the other hand, FLIS *et al.*, (2014), in a study analyzing tuber yield of potato genotypes from three series of regional trials in Europe (Poland, Hungary and Spain), reported a higher contribution of location (58%) to the total sum of squares. However, relatively high contribution of G in the study of FLIS *et al.*, (2014) was accompanied by low contribution of G×E source of variation to the total sums of squares (6%).

Table 3. AMMI analysis of variance for tuber yield (t/ha) of 54 potato genotypes over 36 environments including the first two interaction principal component axes (IPCA)

Source of variation	df	SS	MS	% SS	p
Total	7775	942717	121		-
Treatment	1943	933605	480	99.1	0.00
Genotype (G)	53	87332	1648	9.3	0.00
Environment (E)	35	743445	21241	78.9	0.00
GE interaction	1855	102828	55	10.9	0.00
IPCA1	87	53989	621		0.00
IPCA2	85	33836	398		0.00
Residuals	1683	15003	9		
Error	5724	9112	1.592	0.9	-

AMMI Model

AMMI analysis revealed that the first two Interaction Principal Components (IPCA 1 and IPCA 2) were significant ($P < 0.01$) explaining 52.5% and 32.9% of the interaction sum of squares, respectively. Therefore, most of the information could be graphically displayed in an AMMI1 biplot (Figure 1a), which shows genotype and environment means on the abscissa and the corresponding IPCA1 values on the ordinate. Genotypes with IPCA1 scores near zero had little interaction across environments and, likewise, locations with IPCA1 scores near zero had little interaction across genotypes and low discrimination among genotypes. Genotypes with low IPCA1 scores can be considered stable with wide adaptation to test environments (CARBONELL *et al.*, 2004). On the other hand, genotypes with high values of IPCA1 scores weather positive or negative have high interaction effects across environments showing specific adaptation to environments with the IPCA1 values of the same sign.

Mean tuber yield in 54 potato genotypes varied from 26.11 t ha⁻¹ (G10) to 44.56 t ha⁻¹ (E6). On the other hand much higher variation of tuber yield was observed among environments with SE07 (19.32 t ha⁻¹) being the lowest yielding and SE04 (56.83 t ha⁻¹) the highest yielding environment. A wide variation of mean tuber yield was also observed among years within the three test locations, which clustered into three distinct groups separated from each other along the IPCA1 axis. Most within the location Seged Donji (SE), except SE04, were low yielding. On the contrary environments within the location Osijek (OS) were predominantly high yielding, whereas within the location Hercegovac (HE) a uniform dispersion of environments from low to high yielding was observed.

Genotypes A14, C5, C6, C14, D2, D3, E4, G2, G5, G10 and H3 had high values of IPCA1 scores ($> \pm 1.8$) and can be considered unstable showing specific adaptation to certain environments. Among them G5 is high yielding and extremely unstable, whereas C5, C6 and G10 are low yielding and unstable. Based on the AMMI1 model genotypes E6, A14, F2 and B17 can be considered as high yielding with specific adaptation to certain environments. The most stable genotypes by the AMMI1 model were E2, G13, C11, F5, G6.

For a more secure separation of specifically adaptable genotypes, it is more appropriate to use the AMMI2 model, which differentiates the environmental vectors by two IPCA axes (Figure 1b). By AMMI2 biplot analysis the G×E relationship can be expressed in terms of interaction patterns derived in biplot. A biplot is generated by using genotypic and environmental scores of the first two AMMI components in which both genotypes and environments are displayed simultaneously. Biplot displays interactions while the main effects are pushed to the origin, meaning that the genotypes with vector points away from the origin contribute significantly more interaction than those end point vector genotypes close to the origin, indicating that they are more stable. Genotypes A14, B16, B17, C5, C6, C15, G2, G5 and G10 with endpoints far from the origin show far more significant interactions than other genotypes. Genotype C15 was isolated as unstable because it was not like other genotypes coincided with the directions of the environmental vectors that had a similar pattern of interaction.

Other genotypes such as C5, C6, G2, G10, A14 as well as B17, B16 and G5 can easily be identified as specifically adaptable in certain environments because their vector direction coincides with the environment direction. Genotypes with the smallest G×E interaction and being the closest to the origin are considered to be the most stable.

In the study, genotypes E3, G7, G13 and H2 had the least interactions and can be considered stable, but when the results from both AMMI models are linked, these genotypes can be defined as medium yielded and stable in all environments. If we reduce the criterion of the distance from the reference point, we will extract the A12, E2 and G3 genotypes that have achieved high and stable yields throughout the environment.

Mega environments

According to the AMMI2 model (Figure 1b), it is evident that the three locations clearly separated and concentrated on completely opposite sides of the biplot. Therefore, we can consider them as mega-environments (ME), which YAN and RAJČAN (2003) defined as a group of locations that consistently share the same best varieties. The five best yielding genotypes in each of the three mega-environments, corresponding to the three locations, are shown in table 4. As can be seen from the table, although some of the best performing genotypes appeared in two mega-environments none of them were shared among all three mega-environments. YAN *et al.*, (2007) reported that the AMMI2 model cannot clearly distinguish the mega environments. Contrary to that GAUCH *et al.* (2008); GAUCH (2013); HONGYU *et al.* (2014) stated that the AMMI2 model can clearly separate the mega-environments, which is also confirmed in the present study, where a consistent interaction pattern between years and genotypes within locations were observed.

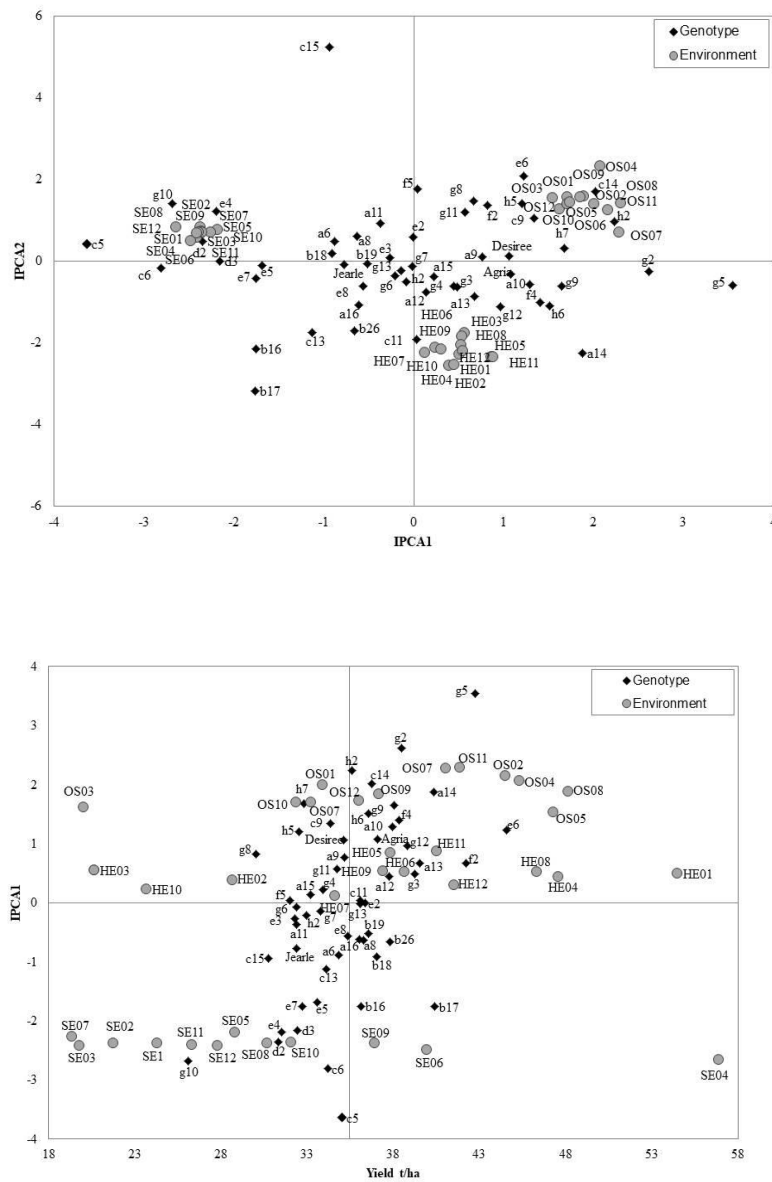


Figure 1. AMMI biplot of 54 genotypes of potato a) for primary component (IPCA1) and Yield; b) for primary and secondary components (IPCA1 , IPCA2) .

Table 4. The five highest yielded potato genotypes in three mega-environments

Mega locations	Mean	Score	1st	2nd	3th	4th	5th
OS	38.37	1.90	E6(12)	G5(12)	F2(12)	C14(9)	G2(12)
HE	37.62	0.49	B17 (12)	A14(12)	G5(12)	A13(7)	G12(8)
SE	30.36	-2.39	C5(12)	E6(12)	B17(10)	F2(12)	C6(12)

* The number in parenthesis indicates how many times a particular genotype was among the five highest yielding at a particular location

GSI model

In order to distinguish stable high yielding genotypes from a group of specifically adapted genotypes, we used Genotype Selection Index (GSI), which combines the estimated stability measure with yield data (FARSHADFAR, 2008) and gives more useful information for selection and recommendation (OLIVEIRA *et al.*, 2014; GIRIDHAR *et al.*, 2016). Based on GSI values (Table 5) the seven best ranking genotypes (G3 > A13 > A12 > G13 > E2 > B19 > F2) with index values < 30 can be considered as the most stable high yielding genotypes suitable for growing in all environments.

Table 5. Genotype Selection Index (GSI) for 54 potato genotypes

Gen.	GSI	Gen.	GSI	Gen.	GSI	Gen.	GSI	Gen.	GSI	Gen.	GSI
G3	18	G12	35	A9	43	E3	51	Jaerla	63	G8	79
A13	23	Agria	38	F4	43	G6	51	B16	64	E7	81
A12	24	E8	39	H2	44	B17	53	C9	65	C5	84
G13	25	G7	39	G4	47	G11	53	C13	69	C6	84
E2	27	E6	41	G9	49	H6	53	H3	70	D3	85
B19	28	A10	42	A14	51	G5	55	F5	73	E4	95
F2	28	A15	42	A6	51	G2	57	H5	74	D2	98
A8	35	B26	42	C11	51	A11	58	E5	75	C15	104
B18	35	A16	43	Désirée	51	C14	60	H7	77	G10	105

*The data are sorted from stable to unstable

CONCLUSION

The present study demonstrated that the REML/BLUP method is a suitable procedure for estimating the mean tuber yield in the unbalanced dataset consisting of 54 potato genotypes examined over twelve years at three locations. The combined ANOVA revealed that tuber yield was significantly affected by the major effects of environment, genotype and their interaction

Further partitioning of the interaction term by AMMI analysis showed that the first two interaction principal components (IPCA 1 and IPCA 2) explained as much as 85.4% of the interaction sum of squares. It is demonstrated that the AMMI model provides agronomically meaningful insights into the data structure and satisfy the goal to identify high-yielding genotypes. In addition, the AMMI2 model was successful in separating specifically adapted genotypes from stable ones and was able to clearly separate the mega-environments

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ANALIZA STABILNOSTI PRINOSA GOMOLJA KORIŠĆENJEM NEBALANSIRANIH PODATAKA O ISPITIVANJIMA SORTI KROMPIRA

Zlatko MIJIĆ¹, Vinko.KOZUMPLIK², Hrvoje ŠARČEVIĆ², Vladimir MEGLIĆ³, Ivan VARNICA⁴, Tihomir ČUPIĆ⁵

Državni inspektorat, Sektor za poljoprivredu, Beli Manastir, Hrvatska

² Agronomski fakultet sveučilišta u Zagrebu, Odjela za oplemenjivanje bilja, genetiku i biometriku, Zagreb, Hrvatska

³ Kmetiljski institut, Odjel za ratarstvo, Ljubljana, Slovenija

⁴ Hrvatska agencija za poljoprivredu i hranu, Centar za Sjemenarstvo, Osijek, Hrvatska

⁵ Poljoprivredni institute Osijek, Odjel za oplemenjivanje o genetiku Krmnog bilja, Osijek, Hrvatska

Izvod

Krompir se uzgaja u širokom regionu i u različitim sredinama, za razliku od drugih useva, pa je poznat kao jedan od najrasprostranjenijih svjetskih useva. U mnogim poljoprivrednim oblastima širom sveta novi genotipovi su uključeni u mnoge multilokacijske eksperimente na velikom broju lokacija i godina kako bi se odredila visina i stabilnost prinosa. Međutim, postoji mnogo problema sa ovim tradicionalnim pristupom, uglavnom zbog velikog broja genotipova koji zahtevaju stalno istraživanje svakog genotipa na mnogo lokacija i godina. Multilokacijski eksperimenti zahtijevaju mnogo vremena i finansijskih resursa, a mogućnost greške se uveliko povećava. Upotreba REML/BLUP metode daje dovoljno podataka za pouzdanu prognozu prinosa novih genotipova uzimajući u obzir da je baza podataka koja se sastoji od 54 genotipova krompira istraživana dvanaest godina. Podaci su podvrgnuti AMMI modelu koji je zasnovan na procijenjenim vrednostima za određivanje stabilnosti genotipova u skupu neuravnoteženih podataka. Rezultati su pokazali relativno stabilnu efikasnost prinosa za većinu genotipova u zavisnosti od životne sredine (lokacija-godina), i ukazali na dobru procenu. ANOVA je pokazala da se najveći efekti mogu pripisati okolini (E), njihovoj interakciji (G×E) i najmanjoj genotipu. Prve dve ose multiplikativne interakcije bile su 85,4% od sume kvadrata. Rezultati interakcija glavnih komponenti pokazali su veliku varijabilnost okruženja u odnosu na prinose i jasno razlikovali lokacije. AMMI analiza je omogućila identifikaciju stabilnih i produktivnih genotipova (G3 i A12) kao i genotipova za specifična okruženja. Indeks selekcije genotipa, zbog svoje prirode kombinovanja procene mere stabilnosti i ranga prinosa, pružio je više korisnih informacija za izbor i preporuku. Rezultati ove studije ukazuju na superiornost modela predviđanja u poređenju sa tradicionalnim metodama eksperimenta sa više lokacija i korišćenjem dobijenih vrednosti u kreiranju preporučenih lista sorti krompira.

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