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EVALUATION OF SUNFLOWER HYBRIDS IN MULTI-ENVIRONMENT TRIAL (MET)

Milan JOCKOVIĆ[*]*, Sandra CVEJIĆ, Siniša JOCIĆ, Ana MARJANOVIĆ-JEROMELA, Dragana MILADINOVIĆ, Bojan JOCKOVIĆ, Vladimir MIKLIČ, Velimir RADIĆ*

Institute of Field and Vegetable Crops, Maksima Gorkog 30, Novi Sad, SERBIA
**Corresponding author: jockovic@gmail.com*

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ABSTRACT

Sunflower has been proposed as a potential crop model for an adaptation to a changing environment and special attention should be paid to testing hybrids under different environments. Additive main effects and multiplicative interaction model (AMMI) supplemented with genotype main effects and genotype by environment interaction effects (GGE) were used for dissection of genotype by environment interaction and evaluation of hybrids and testing environments. The research included 24 sunflower hybrids grown across twelve environments. AMMI analysis identified four significant interaction principal components (IPC), while in GGE biplot the first two IPCs accounted together for 44.59%. Environmental factors contributed the largest proportion in the total variation of seed yield (67.40%), followed by interaction and genotypes. High yielding hybrids H1, H14 and H11 showed specific adaptation to environments E10 and E1, respectively. The average environment coordination (AEC) view of GGE biplot indicated H17 as the most desirable genotype regarding seed yield. From the results of this study it can be concluded that MET trials are important not just for evaluation of stability and choosing the most stable genotypes, but also the genotypes that will perform well in low yielding environments and be able to take advantage of the favourable environmental conditions.

Keywords*:* Environmental factors, seed yield, sunflower

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is one of the most important oil crops and preferable source of edible oil, worldwide. Besides its primary use in human consumption sunflower oil has a wide range of applications and can be used as a supplement in the chemical industry as well as in the pharmaceutical industry. Sunflower meal, a side product from oil extraction, is rich source of protein and it is efficiently utilized when blended with meal of soybean for use in the livestock feeding (Seiler and Jan, 2010). In accordance with the current forecasts scenarios of the increase in human population and climate change, it is assumed that current sunflower production is insufficient for the future needs (Radanović et al., 2018). Regarding this, sunflower has been proposed as a potential crop model for an adaptation to a changing environment and special attention should be paid to achieving high and stable yields under different conditions of cultivation. In the Balkan region, the sunflower is the most important oil crop, especially in Serbia and Romania. In the period 2012-2017 the average seed yield in Serbia was 2.63 t ha^{-1} harvested on 189217 ha with an average production of 497818 t and in Romania average, sunflower seed yield was 2.02 t ha^{-1} with harvested area of 1030138 ha and production of 2076742 t (FAO, 2019). The reasons why average seed yields are relatively low in both countries are that sunflower is mostly cultivated under natural conditions, without additional irrigation which effects production in years when drought stress appears.

Considering that sunflower is cultivated worldwide, one of the challengeable issues among plant breeders is genotype by environment interaction (GEI). Knowledge on the effect of environmental factors on growth and development of the crop could reduce the possibilities of significant yield loss and improve the selection of specific cultivars for growing in the target regions (Marjanović-Jeromela et al., 2011). Considering that genotype is fixed while the environment shows variation through years and locations finding the most productive hybrid for specific environmental conditions is possible via testing in different environments. This procedure is essential to maximize the productivity of sunflower hybrids across environments and to provide information about genotype effect (G), environment effect (E) and their interaction (GE). Genotype estimates across test locations, based on their discriminating ability, allows identification of mega-environments. Mega-environments represent subset of locations that are relatively homogenous with similar biotic and abiotic stresses and cropping system requirements (Yan and Rajcan, 2002).

There are several statistical procedures that analyse yield trials in order to help researchers to make an appropriate agronomic conclusion but the most popular approach among researchers in last decade are Additive Main effects and Multiplicative Interaction (AMMI) and Genotype Main effects and Genotype by Environment interaction effects (GGE). Both of them are based on combination of analysis of variance (AOV) and singular value decomposition (SVD) statistics also known as principal component analysis (PCA). AMMI analysis efficiently separates main effects (genotype and environment) and their interaction (GE) as essential information required for most agricultural research purposes (Gauch, 2006). Although AMMI model is efficient, GGE biplot that combines sites regression analysis (SREG) and biplot technique is very useful to identify mega-environments using the "which-won-where" pattern (Yan et al., 2007). GGE biplot evaluate test locations in order to identify the best performing genotypes. Several previous studies investigated GE interaction in the sunflower seed yield (De La Vega and Chapman, 2001, 2006, 2010; Branković et al., 2012; Casadebaig et al., 2016; Mijić et al., 2017). Marinković et al. (2011) concluded that the variation of seed yield in sunflower was mainly caused by location, indicating the narrow adaptability, an i.e. adaptation of genotypes to a specific environment.

Bearing in mind, agro-climatic differences in regions where sunflower is grown, the knowledge on how GEI affect the performance of a given hybrid may aid in the selection of hybrids and their suitable environments for maximum yield. Based on the consideration, the objective of the current study was to evaluate the influence of different environments on seed yield productivity of sunflower hybrids and to determine the representative and discriminative ability of testing environments.

MATERIALS AND METHODS

Genetic material

The 24 hybrids were developed by crossing 12 CMS lines and 2 restorers, during 2012 season at the breeding nursery in Rimski šančevi of the Institute of Field and Vegetable Crops. Twelve cytoplasmic male sterile (CMS) lines were developed at the Institute of Field and Vegetable Crops, Novi Sad, Serbia during the period 2000-2010. CMS lines, developed from different gene pools, represents elite sunflower lines and were selected on the basis of high seed and oil yield, high-self-compatibility and high tolerance to diseases. Restorer lines used for creating experimental hybrids are parents of the best commercial hybrids with good combining abilities.

Experimental design

The research study was carried out at three locations in Serbia (Rimski šančevi, Šupljak and Novo Miloševo) and three locations in Romania (Teleorman, Valul lui Traian and Dalga) during 2013 and 2014 growing seasons. Genotype by environment interaction was evaluated using a combination of year and location as environments. The experiments were organized in a randomized complete block design (RCBD) with three replicates. In all environments, optimal agro-technical practices for sunflower were applied. The experimental units consisted of 4 rows with a length of 10 m. Plant spacing was 70 cm between rows and 25 cm between plants within a row. Harvest was done by combine Wintersteiger Nurserymaster Expert. Seed yield was recorded on plants from middle rows to avoid edge effect. Seed yield was expressed in kg ha^{-1} and adjusted to 11% moisture. Basic information of planting locations in Serbia and Romania is presented in Table 1, while in Table 2 are shown climatic data for environments in two growing seasons.

Table 1. Cite characteristics for sowing locations in Serbia and Romania

Basic data	**Serbia**			**Romania**		
	Rimski šančevi	**Subotica**	**Novo Miloševo**	**Teleorman**	**Valul lui Traian**	**Dalga**
Soil type	chernozem	sandy soil	humogley + salty soil	cambic chernozem +vertic pseudogley	vermic chernozem	chernozem + phreatic water
Climate	continental climate, with cold winters and hot, humid summers	continental climate, with cold winters and hot, humid summers	continental climate, with cold winters and hot, humid summers	wet, temperate continental climate	mixed climate between wet and warm continental and warm oceanic	wet, temperate continental climate
Coordinates	45°20´N 19°51´E	46°06´N 19°40´E	45°72´N 20°30´E	44°07´N 25°45´E	44°10´N 28°29´E	44°26´N 27°40´E

Table 2. Planting locations, environments and climatic data for 2013 and 2014 growing seasons

Location	**environment**	**Rain (mm)**	**Average monthly temperature**						**Mean**
			IV	**V**	**VI**	**VII**	**VIII**	**IX**	
Rimski šančevi	E1 2013	445	13	17	20	22	23	16	18.5
	E7 2014	644	13	16	21	22	21	17	18.3
Subotica	E2 2013	296	13	19	21	22	24	15	19.0
	E8 2014	563	13	16	21	23	21	17	18.5
Novo Miloševo	E3 2013	292	14	20	22	24	25	17	20.3
	E9 2014	425	13	16	20	22	21	17	18.2
Teleorman	E4 2013	314	14	19	22	23	24	17	19.8
	E10 2014	452	12	16	20	23	23	18	18.7
Valu lui Traian	E5 2013	102	13	19	24	23	24	19	20.3
	E11 2014	430	12	17	20	23	24	19	19.2
Dalga	E6 2013	253	14	20	23	24	25	18	20.7
	E12 2014	287	13	18	21	25	27	19	20.5

Statistical analysis

Additive main effect and multiplicative interaction (AMMI) method that combines the traditional ANOVA and principal component analysis (PCA) into a single analysis as proposed by Zobel et al. (1988) was used to analyze genotype effect (G), environment effect (E) and their interaction (GE).

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum \lambda_n \xi_{gn} \eta_{en} + \theta_{ge}$$

Where:

Y_{ge} – yield of genotype g in environment e

μ - grand mean

α_g – mean deviation of the genotype

β_e – mean deviation of the environment

λ_n – singular value for PCA axis n

ξ_{gn} – genotype eigenvector for PCA axis n

η_{en} – environment eigenvector for PCA axis n

θ_{ge} – residues, including experimental error

The AMMI biplot is constructed by plotting the scores of GE interactions that are placed on the ordinate (IPC1) and genotype and environmental means that are placed on the abscissa. In the biplot, genotype and environment main effects, genotype stability and adaptability to different environments are visualized. F-test was used to test the statistical significance of sources of variation.

For identification of the mega-environments using the „which-won-where“ pattern GGE biplot was constructed. The method was developed by Yan and Kang (2003) and allows an environment-centered matrix containing the GGE data to be subjected to singular value decomposition. The GGE biplot graphically displays G plus GE of the MET data in a way that facilitates visual variety evaluation and mega-environment identification (Yan, 2014).

Following equation is used to estimate each element in the matrix:

$$Y_{ij} = \mu + \beta_j + \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where:

Y_{ij} is the trait mean for genotype i in environment j

μ is the general mean

β_j represents the environment main effect

$\mu + \beta_j$ represents the mean yield across all genotypes in environment j

λ_1 and λ_2 are the singular values for the first and second PCs

ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2

η_{j1} and η_{j2} are eigenvectors of environment j for PC1 and PC2

ε_{ij} is the residual associated with genotype i in environment j

RESULTS AND DISCUSSION

Investigation of developed promising genotypes in different environments is one of the most challengeable tasks for plant breeders. Reliable estimation of the extent to which genotype by environment interaction (GEI) affects a trait of interest is an important determinant for the evaluation and selection of genotypes, especially for target regions. In order to obtain reliable information about GEI effect, it is necessary to organize a multi-environment trial. Multi-environment trial should include environments that have different agro-climatic characteristics in order to obtain a more reliable estimation of tested genotypes.

Like previously stated by Kaya (2014), sunflower is one of the most important oil crops that can be grown in many parts of the world because of ability to be cultivated in generally dry and rained conditions. As it can be seen from the climatic table in the study yearly variations are caused mainly by precipitation (Table 2). The exception is only locality Dalga wherein both years climatic conditions were relatively constant with precipitation lower than 300 mm. It is evident that precipitation was higher in 2014 growing season in all environments. Higher amounts of rainfall had an influence on disease pressure and percent of fertilization during the flowering time which resulted in lower yields in almost all environments during 2014 growing season. Supporting results of the current paper, Del Gatto et al. (2015) reported that during 3 year period sunflower hybrids tested in Northern Italy had higher yields in a year with less precipitation. When comparing environments, precipitation ranged between 102 mm (E5) and 644 mm (E7). The average temperature during the vegetation period varied between 18.17 ºC (E9) and 20.67 ºC (E6). Higher amounts of rainfall have contributed to lower average temperatures in all environments during 2014 growing season. Also, differences in soil type on each location indicated the presence of diverse environmental conditions. Considering environmental factors, the influence of soil type can be minimized by doing analysis and adding an adequate amount of nutrients across locations, but climatic factors during the year, distribution of rainfall and sum of temperatures are not repeatable. In a previous study Romay et al. (2010) highlighted the significance of climatic conditions on seed yield in maize.

AMMI analysis provides us valuable information and estimation of genotype performance, significant for the development of high yielding genotypes in specific environment (Hristov et al., 2010). In crop production, yield stability is considered the most important socioeconomic category, especially in extreme environmental conditions (Ceccareli, 1994; Piepho, 1998). Because of that, it is fundamental to grow stable cultivars with good seed and oil yields in diverse agro-ecological conditions (Moghaddam and Pourdad, 2011). AMMI analysis of variance gives a clear insight into differences between hybrids and environments observed in this study (Table 3). AMMI analysis of variance showed that in the total variation of the experiment additive effects, genotype (G) and environment (E), as well as their interaction (GEI) was statistically significant (Table 3). Regarding additive effects, G and E accounted together for 74.95%, while their interaction accounted for 25.05%, in treatment sum of squares. Environmental factors contributed the largest proportion in the total variance of the experiment which is in agreement with the earlier statement that in multi-environment trials the main portion of the variability in yield is caused by the environment (Yan, 2001; Mohammadi and Amri, 2013; Oliveira et al., 2014). AMMI analysis partitioned GE interaction into four principal components which accounted together for 69.97%. The first principal component (IPC1), which is caused by the effect of genotype and environment, explained the largest part (28.45%) of the total variability in interaction, for seed yield.

Table 3. AMMI analysis of variance

Source	degrees of freedom	Sum of squares	Mean squares	F-value	Variation explained (%)
Treatments	287	443162348	1544120	7.68**	100
Genotypes (G)	23	33442470	1454020	7.23**	7.55
Environments (E)	11	298688824	27153529	58.21**	67.40
Interaction (GEI)	253	111031054	438858	2.18**	25.05
IPC1	33	31584715	957113	4.76**	28.45
IPC2	31	19587622	631859	3.14**	17.64
IPC3	29	16531522	570052	2.83**	14.89
IPC4	27	9983343	369753	1.84**	8.99
Residuals	133	33343852	250706	1.25	30.03

* $P<0.05$; ** $P<0.01$

Observing the overall average productivity of tested sunflower hybrids across 12 environments seed yield varied from 3452 kg ha^{-1} for hybrid H10 to 4263 kg ha^{-1} recorded for hybrid H17 (Table 4). Also, hybrids H1, H14 and H11 were distinguished from others in terms of productivity by higher average yield than the overall mean. Environment E4 was the highest yielding environment with an average seed yield of 5044 kg ha^{-1}, while the lowest yielding environment was E9 (2565 kg ha^{-1}). Besides E4, environments E8, E1, E7, E3 and E10 recorded higher average yields than the overall average and can be classified as high yielding environments, while environments E2, E5, E6, E11 and E12 can be considered as low yielding environments compared to the overall average.

Table 4. AMMI average values of sunflower seed yield (kg ha^{-1}) across environments

Genotype	2013									2014									2013 / 2014 Avg.
	Serbia				Romania				2013	Serbia				Romania				2014	
	E1	E2	E3	Mean	E4	E5	E6	Mean	Mean	E7	E8	E9	Mean	E10	E11	E12	Mean	Mean	
H1	4762	3802	4254	4273	5178	4083	3948	4403	4338	4605	4497	3084	4062	4432	3791	3658	3960	4011	4175
H2	3991	4201	4221	4138	5686	3717	4187	4530	4334	4357	4793	2395	3848	3790	3699	3832	3774	3811	4073
H3	4339	3996	4071	4135	4732	3779	3711	4074	4105	4001	4089	2234	3441	4039	3676	3672	3796	3619	3862
H4	3932	3373	3633	3646	5060	3319	3710	4030	3838	4513	4437	2676	3875	3546	3917	3135	3533	3704	3771
H5	4725	3689	4723	4379	5153	4069	3996	4406	4393	4212	4548	2852	3871	3913	3287	3592	3597	3734	4063
H6	3914	3759	4150	3941	5500	3582	3952	4345	4143	4129	4603	2377	3703	3565	3187	3499	3417	3560	3851
H7	4386	3661	4318	4122	4541	3697	3655	3964	4043	3846	4086	2258	3397	3597	3477	3428	3501	3449	3746
H8	4347	3524	4385	4085	4692	3640	3740	4024	4055	3979	4271	2414	3555	3407	3511	3330	3416	3486	3770
H9	4290	4016	3805	4037	4707	3821	3533	4020	4029	3859	3842	2133	3278	4401	3317	3694	3804	3541	3785
H10	3602	3726	3642	3657	4511	3137	3469	3706	3682	3670	3921	1635	3075	3206	3612	3289	3369	3222	3452
H11	4653	3355	4404	4137	5293	3914	3969	4392	4265	4627	4695	3262	4195	3912	3539	3327	3593	3894	4079
H12	4028	3021	3932	3660	5420	3444	3781	4215	3938	4491	4647	3001	4046	3462	3186	2971	3206	3626	3782
H13	5282	3255	4530	4356	4145	4099	3601	3948	4152	4377	4055	3209	3880	4120	3959	3264	3781	3831	3991
H14	4733	3786	3825	4115	4709	3920	3713	4114	4115	4674	4185	2985	3948	4547	4323	3565	4145	4047	4080
H15	4004	3848	3679	3844	4990	3549	3674	4071	3958	4176	4180	2290	3549	3987	3658	3512	3719	3634	3796
H16	4167	3970	4237	4125	4911	3664	3842	4139	4132	3971	4298	2156	3475	3644	3637	3632	3638	3557	3844
H17	4869	3663	4138	4223	5253	4100	3973	4442	4333	4929	4605	3435	4323	4573	4044	3571	4063	4193	4263
H18	4345	3597	3801	3914	5391	3948	3647	4329	4122	4219	4204	2805	3743	4632	2699	3494	3608	3676	3899
H19	4348	3281	4439	4023	4985	3723	3719	4142	4083	3921	4333	2599	3618	3502	2829	3216	3182	3400	3741
H20	3711	3511	4249	3824	5364	3436	3783	4194	4009	3658	4428	2050	3379	3161	2507	3297	2988	3184	3596
H21	4737	3600	4275	4204	4905	4139	3603	4216	4210	3936	4020	2716	3557	4509	2695	3540	3581	3569	3890
H22	4569	3658	4437	4221	5343	4048	3902	4431	4326	4193	4471	2841	3835	4171	2937	3572	3560	3698	4012
H23	4157	3177	3998	3777	5153	3650	3568	4124	3951	3977	4221	2647	3615	3810	2542	3128	3160	3388	3669
H24	3467	3997	3934	3799	5444	3498	3665	4202	4001	3303	4117	1514	2978	3654	2114	3632	3133	3056	3528
Average	4307	3645	4128	4027	5044	3749	3764	4186	4107	4151	4314	2565	3677	3899	3339	3452	3563	3620	3863
CV(%)	16%	16%	13%		9%	11%	5%			18%	9%	27%		15%	23%	11%			21%
LSD (0.05)	994.1	937.8	757.8		413.1	257.3	229.1			1103	596.3	799		637.5	1022	356.9			368.3

For a clearer explanation of the main effects and their interaction biplot is constructed for evaluation of stability and adaptability (Figure 1). Average values of the main effects (Gx and Ex) were entered on the abscissa, while IPC1 values (IPCg and IPCe) were plotted on the ordinate. Values plotted on abscissa control the wide sense adaptability, while IPCA values (ordinate) control the narrow sense adaptability (Gauch and Zobel, 1997). Reliable estimation of genotype productivity is essential in order for identifying genotypes capable for the highest productivity in specific environments, i.e. genotypes for target environments. Earlier studies emphasize the importance of GEI for creating genotypes adopted to target areas and implementing AMMI model in order to increase accuracy (Fox et al., 1997; Marjanović-Jeromela et al., 2008; Gauch, 2013).

As presented in Figure 1 genotypes and environments positioned around abscissa showed the low effect of interaction, i.e. demonstrated wide adaptability. Left and right position of genotypes and environments in relation to the vertical line, which represents overall mean, demonstrated lower and higher average performance. Among twelve environments, Valu lui Traian in 2013 (E5) demonstrated the highest stability for production because of the lowest IPC1 value. In contrast, Teleorman E4, Subotica (E8) and Rimski šančevi (E1) were high yielding environments but also demonstrated the highest interaction values and are defined as unstable environments considering seed yield. Unfavorable environments, distinguished with lower average yields and high level of interaction, were E9 and E11. Regarding sunflower hybrids genotype H5 was distinguished from other hybrids with the lowest interaction value and high seed yield and is considered more resilient to differences in environmental conditions. Bearing in mind that random nature of the year-dependent factors which causes yearly variations makes environmental factors generally unpredictable, for stable and profitable sunflower production focus should be on hybrids with high genetic yield potential, wide adaptability and yield stability.

Observing genotype position on AMMI biplot it can be seen that hybrids H24 and H13 were differentiated by the highest values of GE interaction and these are the most unstable hybrids identified. Furthermore, the position of hybrids on biplot indicates positive interaction with certain environments as hybrids positioned above abscissa had positive interaction with environments E2, E3, E4, E6, E8 and E12 and vice versa. Genotypes positioned bellow abscissa had positive interaction with environments E1, E5, E7, E9, E10 and E11. Results of AMMI biplot also indicated that the highest yielding hybrids had a specific adaptation to certain environments. For instance, hybrid H17 showed high interaction values and a specific adaptation to high yielding environments E1 and E7. High yielding hybrids H1, H14 and H11 showed specific adaptation to environments E10 and E1, respectively. These genotypes also performed very good in low yielding environments E9 and E11. Furthermore, hybrid H2 showed specific adaptation and achieved the highest yields in environments with low precipitation such as E2, E4, E6 and E12. In accordance with the study, several previous studies evaluated adaptability and stability of genotypes and concluded that high yielding genotypes have specific adaptability in certain environments (da Silveira et al., 2013; Temesgen et al., 2014; Nowosad et al., 2016).

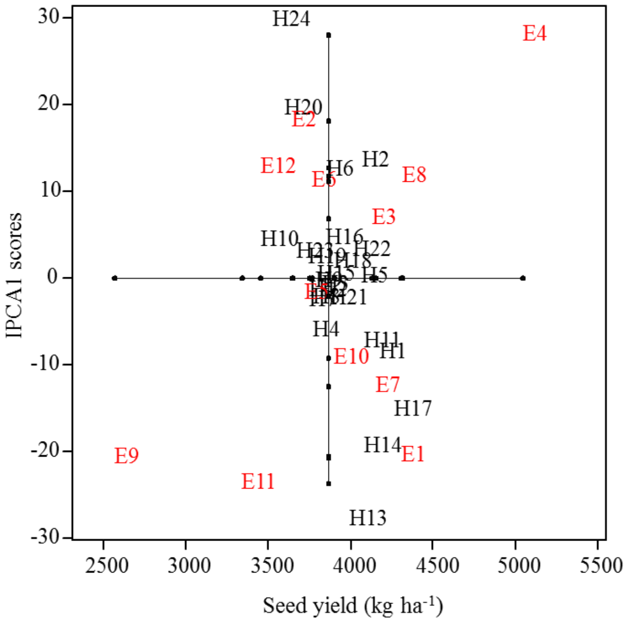

Figure 1. AMMI biplot for GEI based on IPC1 scores

Identification of “ideal” testing environment is important in plant breeding in order to rationalize resources and confine genotype testing to sites which will give informative data thereby facilitating a rapid response to the selection. Mega-environments allow identification of the most discriminative and representative environments that are considered “ideal” for the evaluation of general and specific adaptation of tested genotypes. Favorable test environments are characterized with high IPC1 values and low IPC2 (interaction) values (Hassani et al., 2018).

The which-won-where polygon of GGE biplot is helping in the visualization of representativeness and discriminative ability of environments by comparison of the distance between genotypes and environments (Figure 2). Polygon is created by drawing the lines between the furthest hybrids in the biplot. The lines which start from the coordinate origin are perpendicular to the sides of the polygon dividing the polygon into sectors in which different mega-environments can be detected (Yan and Tinker, 2006). Environments sharing a single sector have the same hybrid as the best and they may be considered as a mega-environment (Stojaković et al., 2015). The equality line divided the test environments into four mega-environments for sunflower seed yield, as environments that share a single sector have the same hybrid as the best one and they are considered as a mega-environment. The first mega-environment was identified as E2, while the second mega-environment consisted of E1, E5, E10, E11 and E12. As the third mega-environment group of three environments E3, E7 and E9 were identified. Environments E4, E6 and E8 were identified as the fourth mega-environment. Although "which-won-where" model formed four mega-environments it can be seen that there is no logical grouping pattern, meaning that the most of locations in different years of testing showed positive and negative PC1 scores which made a group change depending on the year. Regarding this, Yan (2014) defined that GEI which is dominated by GLY (genotype x location x year) interaction cannot divide target regions into mega-environments as the target environment represents single but complex mega-environment and for proper evaluation of genotype productivity multi-year and multi-location trials are necessary. Which means that it is not sufficient to run trials in a single, ''ideal'' location, because such a location does not exist, but rather in a number of locations in order to cover as many environments as possible.

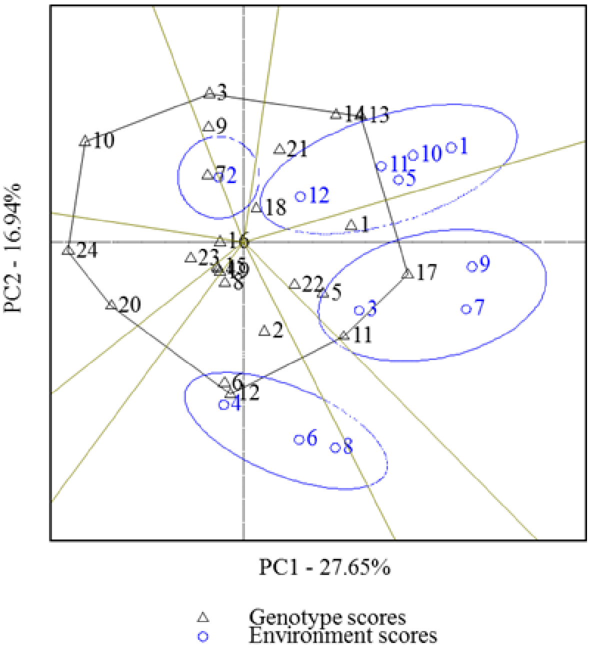

Figure 2. Which-won-where polygon view of the GGE biplot of genotypes and environments

Representativeness of test environments is presented by concentric circles that help in visualizing the distance between each environment and average environment (Figure 3). The average environment presents the average performance of the target environment and it is presented by the centre of the concentric circles (Yan and Kang, 2003; Jandong et al., 2011).

Bearing in mind that the environment that is closest to the center of the concentric circles is the most representative the present study has shown that E7 and E9 are the most representative. Also, in GGE biplot the concentric circles helps to identify an ideal genotype for a trait of interest. The center of concentric circles represents the position of an "ideal" genotype. It equals the longest vector of the genotypes that had above average mean yields and by a zero projection onto the perpendicular line. The ideal genotype is considered one which at the same time has high average yield and high stability. The average environment coordination (AEC) view of GGE biplot indicated that H17 was the closest to the "ideal" genotype and was accordingly identified as the most desirable genotype with respect to seed yield. In terms of "ideal" genotype, although such genotype may not exist in reality, it can be used as a reference for genotype evaluation (Solonechnyi et al., 2015).

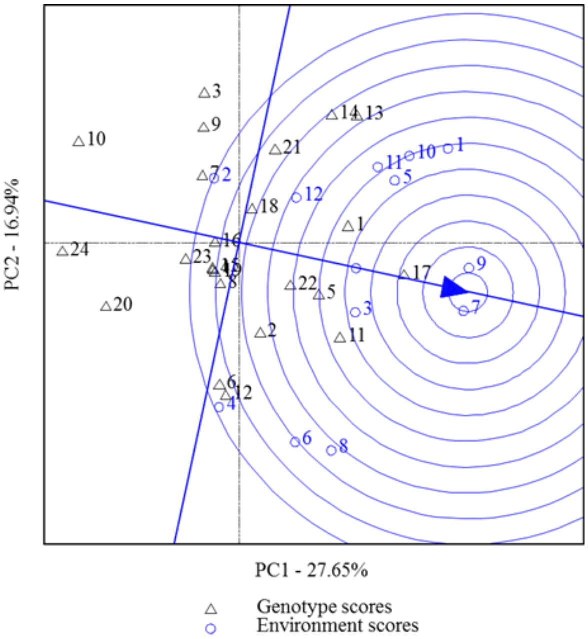

Figure 3. Genotype ranking within environments and representativeness of test environments

The discriminative ability of test environments is presented in Figure 4 and it is based on the length of the vectors formed by each environment which presents standard deviation of genotype within each environment. Environments with short vectors have low discriminating power and they are not informative as genotypes react similarly in it. Hence, environments E2, E12 and E3 had low discriminating power, while environments E1, E7, E8 and E9 were the most discriminative.

Combining the results presented in Figures 3 and 4 environments E7 and E9 can be identified as the most "ideal" as they are both the most representative and discriminative. Furthermore, results are indicating that there is no logical grouping pattern regarding the representative and discriminative ability of test environments. The same locations in different years had a different position in relation to the center of concentric circles and the position and length of the vectors in relation to the ''ideal'' location, which indicates no repeatable pattern.

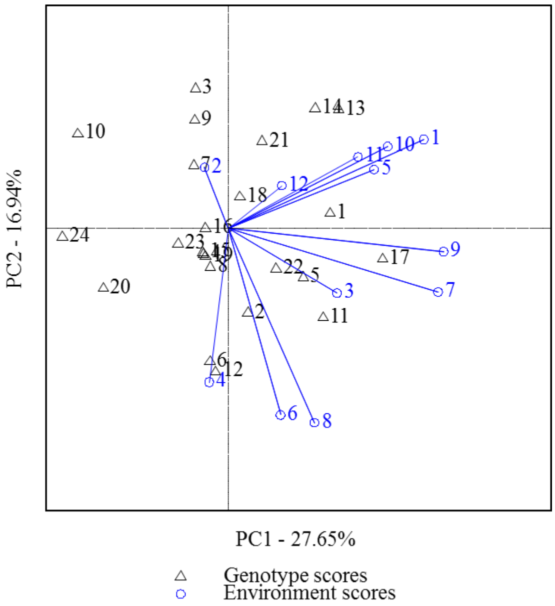

Figure 4. GGE biplot vector view indicating discriminative abilities of tested environments

CONCLUSIONS

Combining the AMMI and GGE is very useful for obtaining reliable information about adaptability and stability of genotypes, as well as discriminating ability and representativeness of test environments. Variation in productivity of sunflower hybrids was significantly affected by differences in environment, followed by genotype by environment interaction and diversity in genotypes. Bearing in mind that "ideal" genotype in general is considered to have high and stable seed yield across different environments, specific adaptation to certain environments (i.e. high positive interaction values) is also desirable as ability of genotype to fully utilize favorable environmental conditions. The highest yielding hybrids H17, H1, H14 and H11 showed specific adaptation to favorable environments. Althought AMMI analysis showed that hybrid H17 expressed high interaction values, average environment coordination view of GGE biplot indicated that H17 was the most desirable sunflower hybrid as it was closest to the "ideal". Hybrid H5 was differentiated from other hybrids with the highest stability accompanied by high seed yield and is considered more resilient to differences in environmental conditions. Graphical visualization of GGE biplot demonstrated that four mega-environments were formed. Analysing representativeness and discriminating ability of the test environments this study identified environments E7 and E9 as the most "ideal". From the results of this study it can be concluded that MET trials are important not just for evaluation of stability and choosing the most stable genotypes, but also the genotypes that will perform well in low yielding environments and be able to take advantage of the favorable environmental conditions.

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