

STABILITY OF YIELD AND SEED COMPOSITION IN EARLY MATURING SOYBEAN GENOTYPES ASSESSED BY AMMI ANALYSIS

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Identification of stable sources for breeding for important agronomic traits is prerequisite for providing a continuous and long-term progress in breeding. In this study, thirty-one early-maturing genotypes from soybean collection of Maize Research Institute “Zemun Polje” were evaluated across four environments (two years and two locations) according to randomized complete block design with three replications. The aim of research was to examine the value of the interaction of genotype and environment for three important agronomic traits (seed yield, protein content and oil content) using an additive main effects and multiplicative interaction (AMMI) statistical model, and to identify stable sources for breeding for listed traits. The results of the research indicated that all traits were strongly influenced by environmental factors, while the influence of genotype and particularly interaction of genotype and environment was of less importance. AMMI analysis enabled identification of genotypes with above average value and high stability for seed yield (three genotypes), protein content (three genotypes) and oil content (two genotypes), which could be utilized as potential stable sources of variability in future soybean breeding programs.

Keywords: AMMI analysis, soybean, seed yield, seed composition

INTRODUCTION

Soybean (*Glycine max* [L.] Merr.) is a major protein and oilseed crop whose production takes place on over 120.4 million hectares in the world, while in the total world oilseeds production in 2019 soybean participated with 30.3% (FAOSTAT, 2020). In soybean, breeding for seed yield, environmental adaptation, or basic quality traits such as protein content or oil

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properties, are breeding targets of highest priority (MILADINOVIĆ *et al.*, 2015). Although advances made in breeding and improved management practices over past decades resulted in increased yield and enhanced seed composition, rate of gain is still not sufficient to reach global targets of doubling crop yields by 2050 to meet the needs of a growing population (RAY *et al.*, 2013). Furthermore, high demands of the modern processing industry as well as climate changes with increasingly frequent variation between growing regions and different seasons are setting new tasks for breeders – to develop new varieties with high and stable agronomic performance in different conditions.

Seed yield and seed protein and oil content are the most important soybean agronomic attributes. As a complex quantitative trait, seed yield and seed composition are determined by a number of genes with *minor* or *major* effect and are highly depending on environmental condition as well as genotype and environment ($G \times E$) interaction (ZHE *et al.*, 2010). Furthermore, the undesirable association between agronomic traits, i.e. negative correlation between seed yield and protein content, and positive between seed yield and oil content, as well as negative association of protein and oil content (YAN and RAJCAN, 2002; MILADINOVIĆ *et al.*, 2006; POPOVIĆ *et al.*, 2013), is one of the most difficult challenges for breeders. Regardless of the final breeding goal, majority of breeding programs show a tendency to use an elite genetic pool or commercial lines for creating new variability, while little attention is given to material stored in local collections. Although the world's soybean germplasm collections maintain a large number of genotypes, only 1% of the available variability is used in practical breeding programs (QIU *et al.*, 2011). Evaluation of accessions in collection and identification of stable sources for breeding for important agronomic traits is pre-requisite for providing a continuous and long term progress in breeding. Precise evaluation of genotypes is often hampered by the presence of an interaction i.e. the inability of the genotype to achieve the same performance in different environments (BAKER, 1988). Interaction is an aggravating factor in selection, since its presence in the total trait variation reduces the heritability of the trait, and thus the reliability of selection based on the main components (KELLY *et al.*, 1998; KANG, 2004). The interaction obscures the agronomic value of the introduced material (GIAUFRETT *et al.*, 2000), which has recently become increasingly important in soybean breeding, given the dramatic narrowing of the genetic basis due to breeding within elite lines (PERIĆ *et al.*, 2014). Plant introductions are in general poorly adapted, so for the successful integration of genes into elite soybean gene pool, it is necessary to determine the stability of the introduced sources (PALOMEQUE *et al.*, 2009). In order to provide a deeper understanding of $G \times E$ interaction for important agronomic traits in soybean, several models of stability analysis were conducted: GGE biplot (YAN and RAJCAN, 2002; ZHE *et al.*, 2010), additive main effects and multiplicative interaction - AMMI analysis (SUDARIĆ *et al.*, 2006a; LI *et al.*, 2020) and linear regression (KARASU *et al.*, 2009; BALEŠEVIĆ-TUBIĆ *et al.*, 2011), with AMMI and GGE models being the most commonly used to determine genotypes' response patterns across different environments. AMMI method gives the possibility of graphical representation of the interaction on the biplot, where the values of the main effects (genotypes, environments) are presented on the abscissa, and the values of the first interaction axis (IPC1) on the ordinate (CROSSA *et al.*, 1990). Using biplot methods, large number of genotypes can be evaluated for their performance, stability, and adaptation in individual environments and across environments (YAN and RAJCAN, 2003).

Objectives of this research were to evaluate agronomic traits performance and stability of early maturing soybean genotypes from Maize Research Institute “Zemun Polje” collection in individual environments and across environments, and to identify soybean genotypes that have high and stable performance in different environments using AMMI biplot.

MATERIALS AND METHODS

The plant material for this study encompassed thirty-one early-maturing (maturity group 0) genotypes from soybean collection of Maize Research Institute “Zemun Polje”, with different status in collection (domestic and introduced varieties, breeding lines and gene-bank accessions), originating from different parts of the world. The trials were conducted during two growing seasons (2011 and 2012), at locations Zemun Polje (44° 52' 00"N, 20° 19' 00" E) and Pančevo (44° 57' 35" N, 20° 41' 22" E) and arranged as randomized block design with 3 replications. The experimental plot size was 5 m², with each plot consisted of two rows per genotypes. The effect of competition between genotypes was eliminated by isolation rows sown in between. Crop density was 500000 plants ha⁻¹, as recommended for soybean varieties of maturity group 0. The soil type at Zemun Polje was carbonate-free chernozem, while in Pančevo experiment was set up on calcareous chernozem on the loess terrace. Sowing was done in mid-April in both years, and standard agricultural practices were applied during the growing seasons. At the R8 stage (full maturity), samples consisted of 30 plants per genotype were collected and used to measure seed yield per plant (g). After rows were harvested with small plot combine, seed samples were analyzed for protein and oil content (both expressed as a percentage on a dry matter basis) using grain analyzer Infraneo, Chopin Technologies®. The data were analyzed by a linear mixed model of classical analysis of variance with random effect of blocks within environment. Means were compared using Tukey's multiple comparison test. The basis for estimating the hypothetical parameters of the AMMI model was the matrix of genotype values in different environments (Z) from which the effects of genotype and environment are removed by double centering, thus obtaining a matrix of interaction values whose multidimensional and complex nature we want to approximate to a smaller number of dimensions.

$$\text{If } Z = \begin{bmatrix} g^{e_{11}} & g^{e_{12}} & \cdots & g^{e_{1e}} \\ g^{e_{21}} & g^{e_{22}} & \cdots & g^{e_{2e}} \\ \cdots & \cdots & \cdots & \cdots \\ g^{e_{g1}} & g^{e_{g2}} & \cdots & g^{e_{ge}} \end{bmatrix} \text{ with dimension } g \times e \text{ and rank } r = \min(g-1, e-1)$$

where each

$g \times e$ value is defined as $y_{ij} - \bar{y}_i - \bar{y}_j + \bar{y}_{..}$ (y_{ij} - value of i genotype in j environment; \bar{y}_i - effect of i genotype; \bar{y}_j - effect of j environment; $\bar{y}_{..}$ - grand mean), hypothetical parameters are estimated using the eigenvalue decomposition method (ECKART and YOUNG, 1936). Regardless of the number and statistical significance of individual AMMI models, i.e. the main components for graphical representation of $G \times E$ interaction results, the AMMI-1 display was applied (YAN and TINKER, 2006), bearing in mind all the advantages of the applied approach

(GAUCH and ZOBEL, 1996). The calculations were performed using R software (R CORE TEAM, 2015).

RESULTS AND DISCUSSION

Meteorological conditions

The years and locations of the experiment varied greatly regarding meteorological conditions (Table 1). In general, both years were dry, while 2012 appeared to be among the driest growing seasons in the history of meteorological observations. The sum of precipitation in June, July and August 2011 was three times higher than in 2012 at Zemun Polje, and almost four times higher than in 2012 at Pančevo. The average increase in monthly temperatures for listed months in 2012 compared to 2011 at Zemun Polje and Pančevo was by 2.2°C and 1.5°C, respectively. Environmental conditions in June, July and August are critical for yield formation (BOARD, 2002) and seed composition (VOLLMANN *et al.*, 2000a), since that period coincide with soybean reproductive stage (R3 – R8 - pod and grain formation and grain filling).

Table 1. Average monthly temperatures (*T*) and precipitations (*P*) in 2 locations during year 2011 and 2012 (*T_{av}*-average monthly *T*; *T_{6,7,8}*-average *T* in 6,7 and 8 month)

Month	Zemun Polje				Pančevo			
	2011. T (°C)	P (mm/m ²)	2012. T (°C)	P (mm/m ²)	2011. T (°C)	P (mm/m ²)	2012. T (°C)	P (mm/m ²)
4.	14.6	14.9	13.0	56.2	14.0	9.3	13.8	86.0
5.	17.3	89.6	17.9	58.5	17.7	113.2	18.4	99.8
6.	22.3	26.2	24.4	14.8	24.8	93.1	24.3	9.6
7.	24.1	44.0	27.1	19.8	22.9	67.0	26.7	37.1
8.	24.7	66.0	26.2	4.8	24.1	18.7	25.4	1.5
9.	23.2	32.4	22.3	20.7	21.8	29.1	21.1	28.5
Vegetation period	<i>T_{av}</i> =21.1	Σ =273.10	<i>T_{av}</i> =21.82	Σ =174.8	<i>T_{av}</i> =20.9	Σ =330.4	<i>T_{av}</i> =21.6	Σ =262.5
	<i>T_{6,7,8}</i> =23.7	$\Sigma_{6,7,8}$ = 136.2	<i>T_{6,7,8}</i> =25.9	$\Sigma_{6,7,8}$ =39.4	<i>T_{6,7,8}</i> =23.9	$\Sigma_{6,7,8}$ = 178.8	<i>T_{6,7,8}</i> =25.5	$\Sigma_{6,7,8}$ =48.2

Seed yield

The analysis of variance of mixed model indicated high statistical significance ($p < 0.01$) for the effects of genotype, environment and their interaction for seed yield per plant (Table 2). The most important source of variation was environment, followed by genotype, while the smallest part of the variation was attributed to the effect of the G \times E interaction. The predominant influence of environment on yield variation was expected given the meteorological conditions during 2011 (moderate drought) and 2012 (extreme drought), and was in accordance with results of numerous studies on soybean yield variation (YAN and RAJCAN, 2002; MILADINOVIĆ *et al.*, 2006). Similar to findings presented by SUDARIĆ *et al.* (2006a) and LI *et al.* (2020), although significant, G \times E interaction was generally of less importance than effects of genotypes and environments.

Genotypes tested at Zemun Polje in both years achieved an average grain yield above the group mean; while genotypes tested at Pančevo achieved a yield below the group mean (Table 3). The seed yield reduction in 2012 due to extreme drought was clearly observed at both locations.

Table 2. F-test values from ANOVA of the mixed model for seed yield per plant

Source of variation	F-test values
Genotype (G)	22.6**
Environment (E)	629.1**
G x E	4.8**

** highly significant at $P < 0.01$ level

Table 3. Average seed yield per plant of 31 soybean genotypes at Zemun Polje (ZP) and Pančevo (PA) during years 2011 and 2012 and significance of differences based on Tukey's test

Genotype	Seed yield per plant (g)				Mean
	Environment ZP 2011	ZP 2012	PA 2011	PA 2012	
FS 2 78	18.27	16.35	12.33	8.43	13.84 ^{efg}
Afrodita	18.81	14.87	14.61	9.88	14.54 ^{cde}
Apache	16.81	14.98	9.21	7.49	12.12 ^{klmo}
Atlas	13.87	14.36	10.73	6.18	11.28 ^{opq}
Aura	14.73	13.72	13.69	7.91	12.51 ^{ijklm}
BlackTokio	16.11	15.69	11.29	10.72	13.45 ^{hij}
Chandor	18.85	14.97	13.19	10.72	14.43 ^{dif}
Dawson	16.95	15.28	11.94	5.84	12.50 ^{ijklm}
Lucija	16.54	15.50	13.40	11.22	14.17 ^{df}
F01-484	18.08	15.41	11.52	6.81	13.01 ^{ghk}
Julijana	14.58	13.57	12.55	13.95	13.66 ^{efh}
Bačka	14.21	14.59	12.11	9.81	12.68 ^{hkn}
Issik	17.00	13.04	10.64	6.36	11.76 ^{mnp}
K-1	16.07	12.79	10.94	7.00	11.70 ^{mnp}
K 2 2	21.27	18.84	17.54	18.07	18.93 ^a
Kanadska 1	13.48	12.94	9.28	6.69	10.59 ^{qr}
L 1128	15.95	13.58	11.93	10.16	12.90 ^{ghk}
KWS Ilona	18.26	13.37	12.83	7.15	12.90 ^{ghk}
Vita	14.47	13.59	11.85	9.77	12.42 ^{klm}
Lambert	13.62	12.57	10.42	7.54	11.04 ^{pqr}
Lanka	21.95	15.22	13.98	11.84	15.75 ^b
OACEclipse	16.55	12.81	10.77	7.70	12.01 ^{kmp}
L 7/88	20.97	16.51	13.37	11.21	15.51 ^{bc}
PI 301	17.04	15.60	17.75	9.42	15.02 ^{bd}
PRW 80	16.33	14.78	12.65	10.31	13.52 ^{ghi}
Turska 1	16.71	13.49	12.32	9.25	12.94 ^{ghk}
Turska 2	13.79	7.84	11.20	8.06	10.22 ^r
Am 3	17.78	11.52	11.78	9.10	12.55 ^{ijklm}
ZPS 015	16.15	15.63	13.71	9.80	13.82 ^{efg}
Kolubara	13.72	13.08	11.13	8.44	11.60 ^{mq}
Mean	16.67 ^a	14.24 ^b	12.31 ^c	9.21 ^d	13.11

The values of genotypes marked with the same letters did not differ at significance level 0.05

The differences in the average yield values of genotypes examined in the same year at different locations were greater than the differences found in genotypes tested at the same location in different years. Our results are not in accordance with studies of other authors who reported higher influence of year as compared to location impact (SUDARIĆ *et al.*, 2006a; ZHE *et al.*, 2010). Predominant influence of location in total variation of seed yield could be explained

by possible influence of soil type in terms of fertility and physical properties (VOLLMANN *et al.*, 2000b), presence of weed competition (VOLLMANN *et al.*, 2010) as well as tillage system and crop rotation applied (UGRENOVIĆ, 2013).

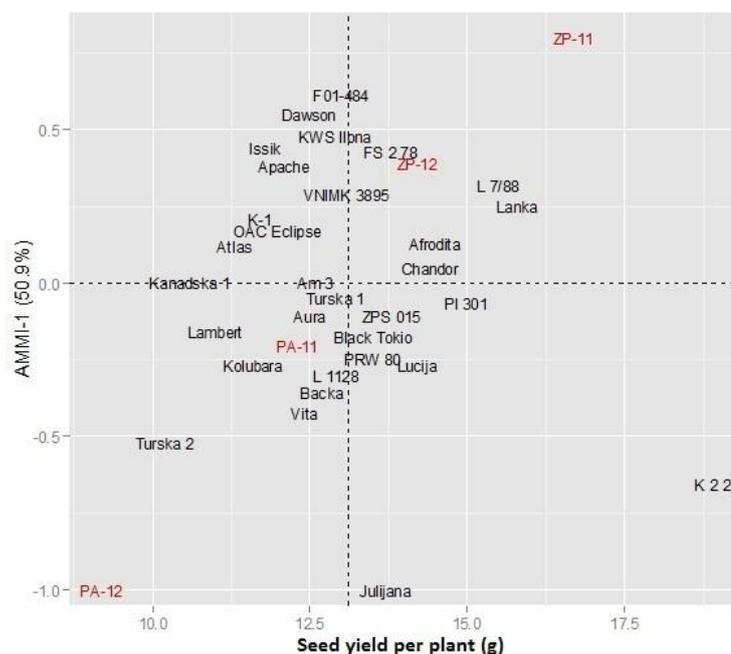


Figure 1. AMMI-1 biplot for seed yield of 31 soybean genotypes across 4 environments (ZP-Zemun Polje, PA-Pančevo, 11 i 12 –years of experiment)

Graphical representation of the interaction for grain yield of soybean genotypes using AMMI-1 biplot shows that the first main component explains 50.9% of the sum of the $G \times E$ interaction (Figure 1). The four environments differed greatly in both the main effects and the interaction value. Genotypes tested at Zemun Polje during 2012 and at Pančevo in 2011 showed the greatest stability, while genotypes tested at Zemun Polje in 2011 and at Pančevo in 2012 expressed high value of the interaction component.

The differences in the main effects of genotypes were relatively small, as indicated by lower degree of dispersion of genotypes on the biplot and grouping of majority of genotypes around the group mean. On the other hand, there was a large difference between genotypes in their interaction values, depicting different reactions of genotypes to changes in environmental conditions. The genotypes with scores close to zero, positioned around the stability line (Kanadska 1, Atlas, Am 3, Turkey 1, Aura, ZPS 015, Afrodita, Chandor and PI 301) contributed the least to the variation in grain yield through environments. Among them, from the breeding

aspect, the most important are those with a yield above the average (domestic variety Afrodita, and introduced genotypes Chandor and PI 301) which showed a less sensitivity to changes in environmental conditions. The last two listed confirmed the results of research on soybean yield stability conducted by SUDARIĆ *et al.* (2006b) who found that introduced materials could have a breeding potential similar to domestic ones. Although genotypes L 7/88 and Lanka stood out as a high yielding, low stability limits their use in breeding for grain yield. Genotype with highest yield in the group (K 2 2) was at the same time among the most unstable genotypes, confirming findings of numerous authors (KELLY *et al.*, 1998; KANG, 2004) that genotypes with extreme value of quantitative trait often express high interaction value.

Protein content

Analysis of variance of the mixed model for protein content in soybean genotypes revealed high statistical significance ($p < 0.01$) for the effects of genotype, environment and their interaction (Table 4). Environment proved to be the most important source of variation, while less variation was attributed to the effects of genotype and $G \times E$ interaction. Superior magnitude of environment, being responsible for most of the variation occurred was confirmed in other studies (VOLLMANN *et al.*, 2000a; SUDARIĆ *et al.*, 2006a) and could be result of unfavorable climatic conditions in the years of testing. Although protein content is a genetically determined trait and is considered a varietal characteristic, a significant portion of variability is attributed to environmental factors (HURBURGH, 2000; POPOVIĆ *et al.*, 2013), primarily temperature and moisture supply (GIBSON and MULLEN, 1996; PERIĆ *et al.*, 2013) and soil nitrogen supply (VOLLMANN *et al.*, 2000; PERIĆ *et al.*, 2009).

Table 4. F-test values from ANOVA of the mixed model for seed protein content

Source of variation	F-test values
Genotype (G)	51.9**
Environment (E)	239.4**
G x E	9.2**

** highly significant at $P < 0.01$ level

The average protein content of genotypes tested at Zemun Polje was higher than the group mean in both years, while no significant difference was found in average protein content at this location between two years (Table 5). The lack of significant difference in genotypes' response to environmental changes was not expected given that the years of experiment were very contrasting in terms of meteorological conditions, but could be explained by the relatively small interaction value of genotypes tested at Zemun Polje. Genotypes tested at Pančevo during 2012 achieved significantly higher protein content than in 2011, although 2012 was less favourable compared to 2011. MATOŠA KOČAR *et al.* (2017) examined elite soybean lines in the region of eastern Croatia and found significantly higher protein content in 2012 as compared to 2011. POPOVIĆ *et al.* (2016) reported higher protein synthesis in years with lower precipitation during growing season. VOLLMANN *et al.* (2000a) determined the highest protein content in short-season soybean varieties in moderately dry years with high temperatures during grain filling. The increase in protein concentration under unfavourable conditions does not result from

their increased synthesis, but from differences in the concentration of other components whose synthesis is not equally inhibited (ROTUNDO and WESTGATE, 2009).

Table 5. Seed protein content of 31 soybean genotypes at Zemun Polje (ZP) and Pančevo (PA) during years 2011 and 2012 and significance of differences based on Tukey's test

Genotype	Environment				Mean
	ZP 2011	ZP 2012	PA 2011	PA 2012	
FS 2 78	39.96	41.16	37.76	40.67	39.89 ^c
Afrodita	39.38	38.25	35.29	38.47	37.85 ^{lm}
Apache	39.81	41.90	37.53	38.58	39.45 ^{df}
Atlas	38.81	40.76	37.38	37.32	38.57 ^{ij}
Aura	40.55	40.87	39.00	42.17	40.65 ^b
BlackTokio	37.50	38.43	36.20	37.23	37.34 ^{nop}
Chandor	39.19	39.42	37.43	39.10	38.78 ^{gi}
Dawson	37.95	38.78	36.39	37.19	37.58 ^{mo}
Lucija	38.73	40.15	38.22	38.11	38.80 ^{gi}
F01-484	37.91	38.09	36.35	36.66	37.25 ^{op}
Julijana	35.77	36.63	36.40	39.40	37.05 ^p
Bačka	37.51	38.03	36.64	39.54	37.93 ^{km}
Issik	39.87	40.16	39.66	37.51	39.30 ^{df}
K-1	42.02	41.21	40.31	41.63	41.29 ^a
K 2 2	36.41	36.45	35.40	38.02	36.57 ^q
Kanadska 1	40.08	40.42	38.57	39.47	39.64 ^{cd}
L 1128	38.66	38.50	37.27	37.87	38.08 ^{kl}
KWS Ilona	39.08	38.46	37.86	37.81	38.30 ^{jk}
Vita	38.07	38.49	37.30	37.74	37.90 ^{lm}
Lambert	40.53	39.52	38.98	37.45	39.12 ^{fgh}
Lanka	39.27	38.92	38.70	40.11	39.25 ^{df}
OACEclipse	38.79	38.15	37.57	40.72	38.81 ^{gi}
L 7/88	39.84	40.30	38.70	38.35	39.30 ^{df}
PI 301	38.70	37.54	36.64	37.84	37.68 ^{lmn}
PRW 80	40.25	38.77	38.44	40.68	39.53 ^{cde}
VNIMK3895	40.21	39.20	38.38	40.50	39.57 ^{cd}
Turska 1	39.57	38.97	37.37	39.11	38.76 ^{gi}
Turska 2	39.16	39.14	37.49	39.13	38.73 ^{hi}
Am 3	40.09	38.05	37.02	39.16	38.58 ^{ij}
ZPS 015	40.37	41.27	36.54	38.43	39.15 ^{efg}
Kolubara	39.05	39.37	37.43	39.12	38.74 ^{hi}
Mean	39.13 ^a	39.20 ^a	37.56 ^b	38.87 ^a	38.69

The values of genotypes marked with the same letters did not differ at significance level 0.05

The AMMI-1 model explained the 61.5% variation of the sum of the squares of the $G \times E$ interaction for the protein content (Figure 2). Three environments (ZP-11, ZP-12 and PA-12) differed less in their main effects, so genotypes tested in the mentioned environments had an average value of protein content close to the group mean, while the genotypes tested at Pančevo in 2011 had an below-average value of protein content. The highest $G \times E$ interaction value was observed in genotypes tested in Pančevo during 2012, while the genotypes tested in Zemun Polje showed somewhat greater stability during both experimental years.

Genotypes varied greatly regarding the main effects and interaction component. A large number of genotypes with average protein content (introduced lines Turska 1, Turska 2, Chandor and domestic variety Kolubara) expressed little contribution to the interaction in the environments in which they were examined. Genotypes of high stability (FS 2 78 and Kanadska

1) achieved above average protein content, while genotype that synthesized the highest percentage of seed protein (K-1) showed a very high stability of the trait. These three genotypes are representing a valuable source of germplasm for breeding for improved chemical composition of soybean seed and confirming the fact that introduced lines might present stable sources of germplasm for future breeding programs, as well. Aura had high protein content but due to low stability, breeding potential of this variety is limited. Similar to findings of SUDARIĆ *et al.*, (2006a) and PERIĆ *et al.*, (2020), the greatest response to changes in environmental conditions was expressed by the genotypes of the lowest protein content in the grain, while the genotypes with the average value of the trait were mainly the most stable.

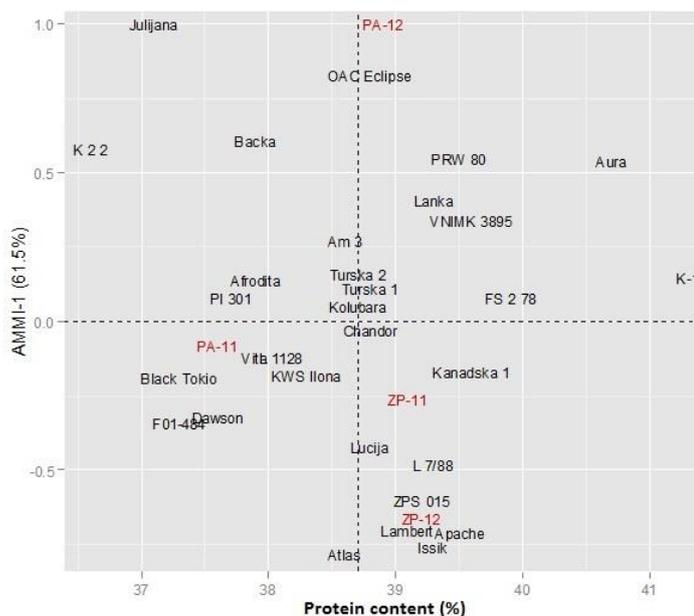


Figure 2. AMMI-1 biplot for seed protein content of 31 soybean genotypes across 4 environments (ZP-Zemun Polje, PA-Pančevo, 11 i 12 –years of experiment)

Oil content

Analysis of the variance of the mixed model for oil content in soybean genotypes indicates high statistical significance ($p < 0.01$) of the effects of genotypes, environment and their interaction (Table 6). Environmental influence was predominant over influence of genotype and interaction $G \times E$. Although oil content is a genetically determined trait and is considered a varietal characteristic, only 50% of the total variation in seed composition is the result of genotype (BRUMM and HURBURGH, 2002), while the rest of the variability is attributed to environmental factors, primarily temperature and humidity, as well as the interaction of genetic

and agroecological factors (VOLLMANN *et al.*, 2000a; NASCIMENTO *et al.*, 2010; LAKIĆ *et al.*, 2019; POPOVIĆ *et al.*, 2013; 2020).

Table 6. F-test values from ANOVA of the mixed model for seed oil content

Source of variation	F-test values
Genotype (G)	46.9**
Environment (E)	116.9**
G x E	6.6**

** highly significant at $P < 0.01$ level

Table 7. Seed oil content of 31 soybean genotypes at Zemun Polje (ZP) and Pančevo (PA) during years 2011 and 2012 and significance of differences based on Tukey's test

Genotype	Seed oil content (%)				Mean
	Environment				
	ZP 2011	ZP 2012	PA 2011	PA 2012	
FS 2 78	21.22	20.10	22.18	19.77	20.82 ^{jk}
Afrodita	21.42	20.37	22.71	20.42	21.23 ^{dg}
Apache	21.09	19.71	22.56	20.98	21.09 ^{efgh}
Atlas	21.52	19.83	22.85	22.06	21.57 ^{bc}
Aura	19.35	18.94	19.90	18.04	19.06 ^o
BlackTokio	20.60	20.03	21.40	19.77	20.45 ^m
Chandor	20.57	19.36	21.42	20.27	20.40 ^m
Dawson	21.28	19.87	22.33	20.92	21.10 ^{efg}
Lucija	21.34	19.79	21.60	20.61	20.84 ^{hjk}
F01-484	22.42	20.77	22.71	21.53	21.86 ^a
Julijana	22.39	21.46	22.57	21.34	21.94 ^a
Bačka	21.62	20.75	22.13	20.58	21.27 ^{df}
Issik	21.23	19.95	21.76	21.90	21.21 ^{dg}
K-1	20.24	19.11	20.84	19.04	19.81 ⁿ
K 2 2	21.80	20.63	22.20	19.47	21.02 ^{fghij}
Kanadska 1	21.18	19.85	21.04	20.32	20.60 ^{km}
L 1128	21.58	20.54	22.42	20.87	21.35 ^{cd}
KWS Ilona	21.85	21.22	22.28	21.79	21.79 ^{ab}
Vita	21.40	20.20	21.17	20.45	20.81 ^{jk}
Lambert	21.06	20.60	21.66	21.53	21.21 ^{dg}
Lanka	20.90	20.12	21.57	19.52	20.53 ^{lm}
OACEclipse	22.14	20.71	22.99	19.59	21.36 ^{cd}
L 7/88	21.47	20.17	21.45	20.85	21.98 ^{ghij}
PI 301	20.81	20.15	21.22	19.98	20.54 ^{lm}
PRW 80	21.69	20.81	22.29	20.12	21.23 ^{dg}
VNIMK3895	19.59	19.98	20.33	18.95	19.71 ⁿ
Turska 1	21.32	20.62	22.48	20.77	21.30 ^{de}
Turska 2	21.60	20.43	22.58	20.43	21.26 ^{df}
Am 3	21.03	20.35	22.39	20.45	21.05 ^{efgj}
ZPS 015	20.37	19.80	22.23	20.70	20.77 ^{ikl}
Kolubara	21.46	20.52	22.00	20.60	21.14 ^{dg}
Mean	21.21 ^b	20.22 ^c	21.91 ^a	20.44 ^c	20.94

The values of genotypes marked with the same letters did not differ at significance level 0.05

Average oil content of genotypes tested at both locations was higher than the group mean during 2011, and lower in 2012, respectively (Table 7). The differences in the average oil

content of genotypes tested at the same location in different years were greater than the differences found in genotypes tested in the same year at different locations. The same trend was noted by SUDAR *et al.* (2003), confirming findings of SUDARIĆ *et al.* (2006a) who pointed out that in the total variation of oil content caused by environmental factors, the effect of the year was many times greater than the effect of location.

The highest average oil content was synthesized during 2011, whereas Pančevo achieved a significantly higher average oil content compared to Zemun Polje. Water deficit and extremely high temperatures in 2012 led to decrease in oil content at both locations. The results of our study were in agreement with findings of VOLLMANN *et al.* (2000a), who noted that the formation of enhanced oil content was promoted by high amounts of rainfall during the seed filling period. On the other hand, MATOŠA KOČAR *et al.* (2018) reported increase in average amounts of oil in hot and dry conditions, while BALEŠEVIĆ-TUBIĆ *et al.* (2011) determined significantly higher average oil content in the unfavorable years. DORNBOS and MULLEN (1992) found that in conditions of water deficit, the oil content decreases linearly with increasing temperature, with the decrease up to 12% in conditions of extreme drought. Moisture deficiency accompanied by high temperatures during the seed filling stage shortens the period of seed filling and reduces the oil content by up to 20% (ROTUNDO and WESTGATE, 2009).

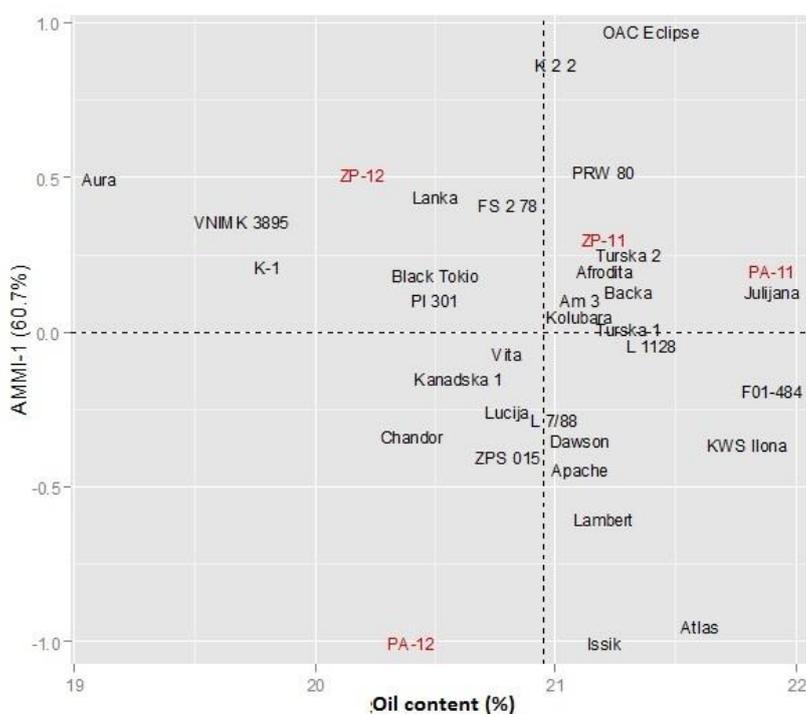


Figure 3. AMMI-1 biplot for seed oil content of 31 soybean genotypes across 4 environments (ZP-Zemun Polje, PA-Pančevo, 11 i 12 –years of experiment)

Most of the variation (60.7%) of interaction $G \times E$ for seed oil content was explained by the first interaction axis of the AMMI-1 biplot (Figure 3). Four environments displayed considerable variation both in the main and interaction effects. Genotypes tested at Pančevo during 2011, in addition to the highest oil content, also expressed the lowest value of interaction, i.e. high stability, while genotypes examined during 2012 at both locations showed the most variable response to changes in agroecological conditions, and were considered unstable.

The dispersion of genotypes on the biplot indicates large differences between them, both in terms of mean values and in response to changes in environmental conditions. Beside a few genotypes of extremely unstable reaction (OAC Eclipse, K 2 2, Issik, Atlas), maturity group 0 is characterized by the presence of a large number of genotypes with above average oil content and stable reaction to environmental changes (introduced lines Am 3, Turska 1 and L 1128 and domestic varieties Kolubara, Afrodita and Bačka) which might present a valuable breeding sources. Variety Julijana, originating from Croatia, achieved the highest oil content and due to a very high stability is considered a promising initial material for breeding for improved seed oil content. Furthermore, Romanian line F01-484 stood out for its very high oil content and stability on satisfactory level. AMMI-1 analysis pointed out that among genotypes of stable and above average oil content those developed in the region of Southeast Europe were predominated.

CONCLUSIONS

According to the results of our study, AMMI-1 analysis proved to be an effective method for understanding the $G \times E$ interaction and enabled the identification of soybean genotypes of high value and satisfactory trait stability. For all examined traits, predominant influence of environment on total variation was determined, while interaction $G \times E$ was of less importance. Among 31 soybean genotypes from the maturity group 0, both domestic and introduced genotypes were identified as potential sources for improvement in breeding for important agronomic traits. From the breeding aspect, the most important varieties of maturity group 0 were Afrodita, Chandor and PI 301, characterized by high and stable yield, while the genotypes of high protein content with satisfactory stability were K-1, Kanadska 1 and FS 2 78. Varieties Juliana and F- 01 484 had the highest oil content and low interaction value, representing a promising starting material for breeding for increased seed oil content.

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**STABILNOST PRINOSA I HEMIJSKOG SASTAVA ZRNA RANOSTASNIH
GENOTIPOVA SOJE PROCENJENA AMMI ANALIZOM**

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Izvod

Identifikacija stabilnih izvora za oplemenjivanje na važne agronomske osobine preduslov je za kontinuirani i dugoročni napredak u oplemenjivanju. U ovom istraživanju, trideset jedan ranostasni genotip iz kolekcije soje Instituta za kukuruz „Zemun Polje“ testiran je u četiri sredine (dve godine i dve lokacije) prema potpuno slučajnom blok dizajnu u tri ponavljanja. Cilj istraživanja bio je da se ispita vrednost interakcije genotipa i okoline za tri važne agronomske osobine (prinos semena, sadržaj proteina i sadržaj ulja) pomoću statističkog modela aditivnih glavnih efekata i višestruke interakcije (AMMI), te da se identifikuju stabilni izvori za oplemenjivanje na navedene osobine. Rezultati istraživanja ukazali su da su sve osobine bile pod jakim uticajem faktora spoljašnje sredine, dok su uticaj genotipa, a posebno interakcija genotipa i spoljašnje sredine bili od manjeg značaja. AMMI analiza omogućila je identifikaciju genotipova iznadprosečne vrednosti i visoke stabilnosti za prinos semena (tri genotipa), sadržaj proteina (tri genotipa) i sadržaj ulja (dva genotipa), koji bi se mogli iskoristiti kao potencijalni stabilni izvori varijabilnosti u budućim programima oplemenjivanja soje.

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