

GRAIN YIELD STABILITY ESTIMATES OF LATE MATURITY MAIZE HYBRIDS

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With global climate change including unpredictable geographic and temporal weather patterns that lead to significant genotype × environment interaction (GEI) the maize performance assessment would need to be complemented with stability analysis. The objectives of this study were: i) estimation of parametric and non-parametric stability indices for grain yield of late maturity maize hybrids, ii) assessing correlations and grouping of stability indices for grain yield of late maturity maize hybrids. The eight maize hybrids of FAO 700 maturity group (ZP1-ZP7, and check Ch) were evaluated for grain yield in the multi-environment trial including five locations in Serbia during 2020. and 2021. year. Stability analyses included twenty parametric and non-parametric indices, Principal Component Analysis (PCA) and Pearson’s correlations between stability indices. The sum of ranks for tested late maturity maize hybrids were in the interval from 37 (ZP6) to 146 (ZP4). The average rank was in the range from 1.8 (ZP6) to 7.3 (ZP4). The interval of variation for standard deviation of average ranks for tested maize hybrids was from 1.3 (ZP4, Ch) to 2 (ZP2) indicating satisfying accordance of utilized parametric and non-parametric stability measures. The highest average grain yield across all tested environments was observed for ZP1, which was second most stable hybrid. The most stable late maturity maize hybrid tested over ten environments was proven to be ZP6 with sum of ranks and average rank of 37 and 1.8, respectively, with standard deviation of average rank 1.5. PCA biplot showed two groups of parametric and non-parametric

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stability estimates: I group-coefficient of variation (CV_i), Eberhart and Russel's regression coefficient (b_i), Perkins and Jinks's regression coefficient (B_i), GEI variance component ($\theta_{(i)}$), coefficient of determination (R_i^2); II group-Eberhart and Russel's deviation from regression ($S_{\bar{d}i}^2$), Wricke's ecovalence (W_i^2), Shukla's stability variance (σ_i^2), Perkins and Jink's deviation from regression (δ_i^2), superiority measure (P_i), the mean of the absolute rank differences of a genotype over all tested environments ($S_i^{(1)}$), the variance among the genotype ranks over all tested environments ($S_i^{(2)}$), the sum of the absolute deviations for each genotype relative to the mean of ranks $S_i^{(3)}$, the sum of squares of rank for each genotype relative to the mean of ranks ($S_i^{(6)}$), $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ - Thennarasu non-parametric stability estimates, mean variance component (θ_i), Kang's rank-sum (KR_i). Pearson's correlation bring along the redundant stability indices and one can choose to use W_i^2 or σ_i^2 , b_i or B_i , W_i^2 or θ_i , σ_i^2 or θ_i .

Keywords: *Zea mays* L., multi-environment trial, genotype \times environment interaction, univariate stability indices, correlations

INTRODUCTION

The underlying cause of differences among cultivars in relation to performance stability is the genotype \times environment interaction (GEI). GEI has three adverse effects in plant breeding: i) reducing the correlation between genotypic and phenotypic values and making the selection of superior and stable genotypes in a wide range of environments difficult; ii) as a component of a trait phenotypic variance, it decreases heritability, selection gain and hinders breeding for complex traits; iii) masking the potential benefits of exotic germplasm introgression (BRANKOVIĆ *et al.*, 2015). The stability indices complement the final maize hybrids performance evaluations in the multi-environment trials.

The late maturity hybrids can take more of the available heat units, which could be imperative when maize plants experience more heat events and an increase in evaporative demand due to climate change (BUHINIČEK *et al.*, 2021). The continuous process of breeding in Serbia implies the creation of maize hybrids with higher genetic yield potential, greater adaptability, resistance and tolerance to the most prevalent diseases and pests. Maize hybrids of late maturity groups are better adapted to better agro-ecological growing conditions in Serbia (ČAMDŽIJA *et al.*, 2012). Late to medium late maize hybrids were the most stable when tested in the multi-environment trial that included eight locations and two years of cropping (CREVAR *et al.*, 2011). Comparable shifting to late maturity hybrids is expected in Southeast Europe according to series of Agricultural Production Systems Simulator (APSIM) simulations especially when water regime (irrigation) is appropriately imposed (BUHINIČEK *et al.*, 2021).

Two different concepts of stability - biological and agronomic exists (SHOJAEI *et al.*, 2021). In the biological (static) concept, a stable genotype has the ability to maintain the same values of the examined traits in different environmental conditions. This concept can hardly be applied to quantitative traits, because they are under considerable environmental influence, but it can be useful for those traits that are less environment dependent for example resistance to disease or freezing. The agronomic (dynamic) concept assumes a predictable reaction of the genotype to the environmental conditions. According to this concept, a stable genotype does not deviate significantly from the average reaction of all genotypes to environmental conditions. For

the study of yield stability as well as other complex inherited quantitative traits, methods based on agronomic, i.e. dynamic concept of stability are recommended. Methods of stability estimation can be divided into multivariate and univariate, and the latter are further divided into parametric and non-parametric methods.

Two possible genetic mechanisms are proposed for underpinning stability: 1) the allelic sensitivity model, which suggests that the constitutive gene is regulated itself in direct response to the environment through the activation of different alleles in various environments; 2) the gene regulation model implies that one or more regulatory loci are under the direct influence of the environment and the constitutive gene is switched on or off by the regulatory gene (FASAHA *et al.*, 2015).

Along with creating a stable genotype, the aim of breeders is to create a widely adaptable genotype. The variation of factors of the external environment conditioned by the difference in locations is separated from the difference in climatic conditions (BUSTOS-KORTS *et al.*, 2018). Therefore, genotypes that can perform well in different locations are called adaptable genotypes. The second (climatic) variation is regarded as unpredictable, so the property of genotypes to maintain a constant yield in different climatic conditions is called stability.

The objectives of this study were to: i) estimate parametric and non-parametric stability indices for grain yield of late maturity maize hybrids; ii) assess correlations of stability indices for grain yield of late maturity maize hybrids and their grouping by principal component analysis.

MATERIALS AND METHODS

Plant material, field trials and experimental design

Seven maize hybrids (ZP1-ZP7) created at the Maize Research Institute „Zemun Polje“, together with widely grown commercial hybrid (Ch) used as a check, were tested at five locations in Serbia during two cropping seasons-2020 (20) year and 2021 (21) year as post-registration multi-environment trial. All of the examined hybrids belong to FAO 700 maturity group. The locations used for field trials were: Zemun Polje (ZPO) (44° 51' 41.72" N, 20° 20' 17.63" E, 80 m altitude), Kukujevcı (KU) (45° 4' 10.96" N, 19° 20' 26.59" E, 93 m altitude), Bačka Topola (BT) (45° 49' 0.62" N, 19° 38' 27.85" E, 102 m), Požarevac (PO) (44° 37' 16.79" N, 21° 11' 16.15" E, 81 m), and Rimski Šančevi (RS) (45° 19' 12" N, 19° 50' 3.98" E, 84 m). Haplic Chernozem (CHha) soil is at the ZPO, KU, BT, RS locations, whereas Dystric Fluvisol (FLdy) is at the PO (WRB, 2014). Standard agro-technical measures were applied at all test locations during both vegetation seasons. Integral protection against pests and weeds was successfully accomplished by a proper use of adequate pesticides.

The experimental design used in this study was Randomized Complete Block Design with two replicates. Planting density was 63.492 plants per hectare. Plot length was 5 m, with inter-row distance of 0.75 m. The elementary plot consisted of eight rows, while only measurements from four internal rows were used for statistical analysis. Sowing and harvesting were done mechanically, using Wintersteiger specialized trial equipment. The sowing dates were in the range from 9th April to 21st April in 2020 year, and in the range from 5th April to 7th May in 2021 year. The harvesting dates were in the range from 15th September to 7th October in 2020 year, and in the range from 20th September to 1st October in 2021 year.

Stability indices

The coefficient of variation (CV_i) (FRANCIS and KANNENBERG, 1978) as a stability statistic is considered together with mean yield when selecting most desirable genotypes.

$$CV_i = \frac{\sqrt{S_i^2}}{\bar{X}_i} \cdot 100$$

where S_i^2 is variance of the measured trait and \bar{X}_i is a mean value of the measured trait.

Regression coefficient (b_i) (EBERHART and RUSSELL, 1966) is the response of the genotype to the environmental index that is derived from the average performance of all genotypes in each environment. If b_i does not significantly differ from 1, then the genotype is generally adapted. A $b_i > 1$ is characteristic of genotypes with greater adaptability to high-yielding environments, and $b_i < 1$ is a characteristic of genotypes with greater adaptability to low-yielding environments.

$$b_i = 1 + \frac{\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j - \bar{x}_.) \cdot (\bar{x}_j - \bar{x}_.)}{\sum_j (\bar{x}_j - \bar{x}_.)^2}$$

Deviation from regression (S_{di}^2) (EBERHART and RUSSELL, 1966) is used simultaneous with b_i , and genotypes with an $S_{di}^2 = 0$ are most stable, while an $S_{di}^2 > 0$ indicates lower stability across all environments as the value increases.

$$S_{di}^2 = \frac{1}{E - 2} \cdot \left[\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_.) - (b_i - 1)^2 \cdot \sum (\bar{x}_j - \bar{x}_.)^2 \right]$$

where x_{ij} -yield of the i^{th} genotype in the j^{th} environment, \bar{x}_i -mean yield of the i^{th} genotype, \bar{x}_j -mean yield in the j^{th} environment, $\bar{x}_.$ -overall mean, E -number of environments.

Wricke's ecovalence (W_i^2) (WRICKE, 1962) measures the contribution of each genotype to the GEI sum of squares. The genotypes with low values have smaller deviations from the mean GEI across environments and are treated as more stable.

$$W_i^2 = \sum_i (x_{ij} - \bar{x}_i - \bar{x}_j - \bar{x}_.)^2$$

Shukla's stability variance (σ_i^2) (SHUKLA, 1972) of a genotype i across environments after the main effects of environmental means have been removed, represented with minimum values infer more stable genotype.

$$\sigma_i^2 = \frac{1}{(s-1) \cdot (t-1) \cdot (t-2)} \cdot [t \cdot (t-1) \cdot \sum_i (x_{ij} - \bar{x}_i - \bar{x}_j - \bar{x}_.)^2 - \sum_i \sum_j (x_{ij} - \bar{x}_i - \bar{x}_j - \bar{x}_.)^2]$$

where: s -number of environments; t -number of genotypes

The coefficient of determination (R_i^2) (PINTHUS, 1973) by use of common linear regression is a stability parameter and the genotypes having the values near to 1 are stable.

$$R_i^2 = \frac{b_i^2 \sum_j (\bar{x}_j - \bar{x}_.)^2}{\sum_j (x_{ij} - \bar{x}_i)^2}$$

where: b_i -regression coefficient, x_{ij} -yield of the i^{th} genotype in the j^{th} environment, \bar{x}_i -mean yield of the i^{th} genotype, \bar{x}_j -mean yield in the j^{th} environment, $\bar{x}_.$ -overall mean.

The linear sensitivity to change in environment measured by regression coefficient (B_i) (PERKINS and JINKS, 1968) is considered as stability estimate adjusted for location effects. Deviation from simple regression model (δ_i^2) (PERKINS and JINKS, 1968) is an additional measure of non-linear sensitivity to the environmental change and for each environment treated as a fixed effect rather than random effect. The GEI component of each genotype was considered as a linear function of the additive environmental component. The genotype is treated as stable when $B_i = 0$ and $\delta_i^2 = 0$.

$$B_i = \frac{\sum_j (GE)^2 \cdot (\bar{x}_j - \bar{x}_.)}{\sum_j (\bar{x}_j - \bar{x}_.)^2}$$

$$\delta_i^2 = \frac{1}{(n-2)} \cdot \sum_j (GE)^2 - \frac{B_i^2}{(n-2)} \cdot \sum_j (\bar{x}_j - \bar{x}_.)^2$$

where n is number of genotypes and $GE = x_{ij} - \bar{x}_i - \bar{x}_j - \bar{x}_.$

Superiority measure (P_i) (LIN and BINNS, 1988) is a stability parameter that uses the ranges of mean square of genotype and genotypes maximum response for each environment. A lower P_i value indicates a closer maximum response of a genotype, which implies the best and the most stable genotype.

$$P_i = \frac{n \cdot (\bar{X}_i - \bar{M})^2 + \sum_j (X_{ij} - \bar{X}_i - M_j + \bar{M})^2}{2n}$$

where X_{ij} is the yield of the i^{th} genotype in the j^{th} environment, M_j is the maximum response obtained among all the genotypes in the j^{th} environment, \bar{X}_i is the mean yield of the i^{th} genotype in the n environments, and \bar{M} is the mean of the maximum response in the n environments.

$S^{(1)}$ -the mean of the absolute rank differences of a genotype over all tested environments, $S^{(2)}$ -the variance among the genotype ranks over all tested environments, $S^{(3)}$ -the sum of the absolute deviations for each genotype relative to the mean of ranks, $S^{(6)}$ -the sum of squares of rank for each genotype relative to the mean of ranks (HÜHN, 1990; NASSAR and HÜHN, 1987) are non-parametric stability measures. The mean yield prior analysis is transformed into ranks for each genotype and environment, and the genotypes are considered stable if their ranks are similar across environments. The lowest value for each of these four statistics represents high stability of a genotype. The parameters $S^{(1)}$ and $S^{(2)}$ are

measurements of the stability alone and $S^{(3)}$ and $S^{(6)}$ combine yield and stability based on yield ranks of genotypes in each environment.

$$S_i^{(1)} = \frac{\sum_{j < j'} |r_{ij} - r_{ij'}|}{\binom{m}{2}} = \frac{2}{m \cdot (m-1)} \cdot \sum_{j=1}^{m-1} \sum_{j'=j+1}^m |r_{ij} - r_{ij'}|$$

$$S_i^{(2)} = \frac{1}{m-1} \sum_{j=1}^m (r_{ij} - \bar{r}_i)^2 \text{ and } \bar{r}_i = \frac{1}{m} \sum_{j=1}^m r_{ij}$$

$$S_i^{(3)} = \frac{\sum_{j=1}^m (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

$$S_i^{(6)} = \frac{\sum_{j=1}^m |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

where r_{ij} is the rank of the i^{th} genotype in the j^{th} environment, \bar{r}_i is the mean rank of the i^{th} genotype across all environments, and m is number of environments. The null hypothesis of no GEI effects implies "all genotypes are equally stable" with maximum stability. To test the null hypothesis that all genotypes have the same phenotypic stability one computes the statistic:

$$S^{(m)} = \sum_{i=1}^l Z_i^{(m)} = \sum_{i=1}^l \frac{[S_i^{(m)} - E\{S_i^{(m)}\}]^2}{\text{var}\{S_i^{(m)}\}}, m = 1, 2, \dots, l\text{-number of genotypes}$$

which under the null hypothesis may be approximated with χ^2 distribution with N degrees of freedom.

If one is interested in a specific variety or genotype, one may test the null hypothesis that the mean stability for the genotype is $E\{S_i^{(m)}\}$ by computing the statistic (HÜHN and NASSAR, 1989):

$$Z_i^{(m)} = \frac{[S_i^{(m)} - E\{S_i^{(m)}\}]^2}{\text{var}\{S_i^{(m)}\}}, m = 1, 2,$$

which under the null hypothesis is approximately χ^2 distributed with one degree of freedom. If the null hypothesis is rejected the genotype may be stable [i. e. $S_i^{(m)} < E\{S_i^{(m)}\}$] or unstable [i. e., $S_i^{(m)} > E\{S_i^{(m)}\}$].

$NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ (THENNARASU, 1995) are non-parametric stability estimates based on the ranks of adjusted means of the genotypes in each environment. The high stability is depicted with the low values of these measures.

$$NP_i^{(1)} = \frac{1}{m} \cdot \sum_{j=1}^m |r_{ij}^* - M_{di}^*|$$

$$NP_i^{(2)} = \frac{1}{m} \cdot \sum_{j=1}^m \frac{|r_{ij}^* - M_{di}^*|}{M_{di}^*}$$

$$NP_i^{(3)} = \frac{\sqrt{\frac{\sum (r_{ij}^* - \bar{r}_i^*)^2}{m}}}{\bar{r}_i^*}$$

$$NP_i^{(4)} = \frac{2}{m \cdot (m - 1)} \cdot \sum_{j=1}^{m-1} \sum_{j'=j+1}^m \frac{|r_{ij}^* - r_{ij'}^*|}{\bar{r}_i^*}$$

where r_{ij}^* is the rank of the i^{th} genotype in the j^{th} environment based on adjusted data, \bar{r}_i^* and M_{di}^* are mean and median ranks, respectively, for adjusted values, while \bar{r}_i and M_{di} are the mean and median ranks of i^{th} genotype in the j^{th} environment, respectively, for original values, and m is the number of environments. Adjusted phenotypic values ($X_{ij}^* = X_{ij} - \bar{X}_i + \bar{X}_.$) provides basis to determine r_{ij}^* (adjusted rank).

Mean variance component (θ_i) (PLAISTED and PETERSON, 1959) represents variance component of GEI for interactions between each of the possible pairs of genotypes. The mean of the estimate for all combinations with a common genotype is a measure of stability. The genotypes with lower values for the θ_i are estimated as more stable.

$$\theta_i = \frac{p}{2 \cdot (p - 1) \cdot (q - 1)} \cdot \sum_{j=1}^q (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_.)^2 + \frac{SSGE}{2 \cdot (p - 2) \cdot (q - 1)}$$

where $SSGE = \sum \sum (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_.)^2$ is the GEI sum square, and p and q are the numbers of genotypes and environments, respectively.

GEI variance component ($\theta_{(i)}$) (PLAISTED, 1960) is a modified measure of stability parameter after i^{th} genotype is deleted and GEI variance from this subset is the stability index for i^{th} genotype. The genotypes with higher values for the $\theta_{(i)}$ are considered more stable.

$$\theta_{(i)} = \frac{-p}{(p-1) \cdot (p-2) \cdot (q-1)} \cdot \sum_{j=1}^q (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_.)^2 + \frac{SSGE}{(p-2) \cdot (q-1)}$$

Kang's rank-sum (KR_i) (KANG, 1988) uses both yield and σ_i^2 as selection criteria. The genotype with the highest yield and lower σ_i^2 are assigned a rank of one. The ranks of yield and

stability variance are added for each genotype and the genotypes with the lowest rank-sum are the most desirable.

Statistical analyses

Environment represented year \times test location combination. The stability indices were calculated using Stabilitysoft program (POUR-ABOUGHADAREH *et al.*, 2019) and GEA-R software version 4.1 (PACHECO *et al.*, 2015). The Pearson's coefficients of correlation between stability parameters were calculated using IBM SPSS program (IBM CORP., 2022). Principal component analysis (PCA) biplot showing grouping of stability indices was constructed using program RStudio (RSTUDIO TEAM, 2020).

RESULTS AND DISCUSSION

Variability of grain yield of evaluated late maturity maize hybrids over ten environments and descriptive statistical parameters are given in Table 1.

Table 1. Mean grain yield ($t\ ha^{-1}$) and variation of late maturity maize hybrids in each environment and across ten environments

Hybrid	Environment										Mean yield ($t\ ha^{-1}$)	σ	Rank
	ZPO20	ZPO21	KU20	KU21	BT20	BT21	PO20	PO21	RS20	RS21			
ZP1	14.182	10.327	14.733	10.167	12.975	6.553	16.001	10.669	13.744	10.338	11.969	2.840	1
ZP2	14.468	10.002	12.841	10.011	12.261	6.369	15.289	8.892	14.345	9.833	11.431	2.867	4
ZP3	13.915	8.422	13.877	10.399	12.396	7.525	14.273	10.348	14.037	8.495	11.369	2.647	5
ZP4	14.390	10.106	12.429	10.440	10.981	6.407	12.012	8.103	14.972	9.619	10.946	2.642	7
ZP5	13.889	9.786	13.002	9.417	11.018	7.810	13.914	10.378	10.927	9.347	10.949	2.058	6
ZP6	14.131	9.901	13.728	10.135	11.881	6.487	15.237	9.162	13.993	10.273	11.493	2.764	3
ZP7	13.056	10.500	13.724	10.569	11.214	6.123	14.291	8.170	13.057	8.177	10.888	2.725	8
Ch	14.009	10.948	14.586	11.299	13.525	5.985	14.624	9.745	13.421	9.491	11.763	2.800	2
Mean	14.005	9.999	13.615	10.305	12.031	6.657	14.455	9.433	13.562	9.447	11.351		
σ	0.436	0.738	0.817	0.536	0.936	0.655	1.198	1.006	1.211	0.773			
Min	13.056	8.422	12.429	9.417	10.981	5.985	12.012	8.103	10.927	8.177			
Max	14.468	10.948	14.733	11.299	13.525	7.810	16.001	10.669	14.972	10.338			

σ -standard deviation ZPO-Zemun Polje; KU-Kukujevci; BT-Bačka Topola; PO-Požarevac; RS-Rimski Šančevi; 20-2020 year; 21-2021 year

The mean grain yield of late maturity hybrids varied from 10.888 $t\ ha^{-1}$ (ZP7) to 11.969 $t\ ha^{-1}$ (ZP1). The highest average grain yield across all tested environments was observed for ZP1 (11.969 $t\ ha^{-1}$) with standard deviation 2.840. The highest value of standard deviation for hybrid's grain yield was observed for ZP2 (2.867 $t\ ha^{-1}$) and the lowest value for ZP5 (2.058 $t\ ha^{-1}$). The mean grain yield of hybrids per environment varied in the range from 6.657 $t\ ha^{-1}$ (BT21)

to 14.455 t ha⁻¹ (PO20). The highest value of standard deviation for grain yield per each of ten environments was shown for RS20 (1.211 t ha⁻¹) and the lowest value was for ZPO20 (0.436 t ha⁻¹). The interval of variation for mean grain yield across hybrids was 1.081 t ha⁻¹ and for mean grain yield across environments 7.798 t ha⁻¹ inferring greater environmental impact and the need to perform stability analysis. The average mean yield per environment was 13.534 t ha⁻¹ and 9.168 t ha⁻¹ and for 2021 vegetation season, respectively, corroborating the influence of variable climatic factors that led to the grain yield variation.

Tukey (HSD) test of statistical significance of difference in the mean grain yield between tested late maturity maize hybrids is shown in Table 2.

Table 2. Tukey (HSD) test of statistical significance of difference in the mean grain yield between tested late maturity maize hybrids

Genotype	ZP1	ZP2	ZP3	ZP4	ZP5	ZP6	ZP7	Ch
ZP1	-	0.538	0.600	1.023*	1.020*	0.476	1.081*	0.205
ZP2		-	0.063	0.485	0.482	-0.062	0.543	-0.332
ZP3			-	0.423	0.420	-0.124	0.481	-0.395
ZP4				-	-0.003	-0.547	0.058	-0.818*
ZP5					-	-0.544	0.061	-0.814*
ZP6						-	0.605	-0.271
ZP7							-	-0.875*
Ch								-

* The mean difference is significant at the 0.05 level.

The statistically significant ($P > 0.05$) differences in the mean grain yield across all ten test environments were shown for following maize hybrids pairs: ZP1-ZP4, ZP1-ZP5, ZP1-ZP7, ZP4-Ch, ZP5-Ch, and ZP7-Ch.

Evaluations and ranking of the late maturity maize hybrids based on 11 different parametric (CV_i , b_i , S_{di}^2 , W_i^2 , σ_i^2 , R_i^2 , B_i , δ_i^2 , P_i , θ_i , $\theta_{(i)}$) and 9 different non-parametric ($S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, KR_i) estimates of stability are presented in Table 3 and Table 4, respectively.

As different parametric and non-parametric measures of stability encompass different approaches and aspects of assessment by using variances, regression, GEI sum of squares, mean squares of genotypes, absolute rank differences, variance of ranks, sum of squares of rank, ranks of adjusted means of the genotypes, yield and variance simultaneously, the outcomes of stability analysis aren't uniform for each stability estimate. It is then valid to rank stability estimates for each tested hybrid and calculate sum of ranks and average rank for each hybrid. The sum of ranks for tested late maturity maize hybrids were in the interval 37 (ZP6)-146 (ZP4) (Table 4). The average rank was in the range from 1.8 (ZP6)-7.3 (ZP4) (Table 4). The interval of variation for standard deviation of average ranks for maize hybrids was from 1.3 (ZP4, Ch) to 2 (ZP2) indicating satisfying accordance of utilized parametric and non-parametric stability measures (Table 4). According to the results of stability analysis the most stable late maturity maize hybrid tested over ten environments was proven to be ZP6 with sum of ranks and average rank of 37 and 1.8, respectively, with standard deviation of 1.5 (Table 4).

Table 3. Stability measures of parametric and non-parametric statistics for grain yield of late maturity maize hybrids grown in ten environments.

Genotype	CV_i (%)	b_i	S_{dt}^2	W_i^2	σ_i^2	R_i^2	B_i	δ_i^2	P_i	$S_i^{(1)}$	$Z_i^{(1)}$	$S_i^{(2)}$	$Z_i^{(2)}$	$S_i^{(3)}$	$Z_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	θ_i	KR_i	
ZP1	23.73	1.08	0.40	3.23	0.37	0.96	0.08	0.35	0.26	1.80	3.46	2.50	2.79	3.46	2.00	2.00	2.00	0.46	0.34	0.28	0.70	0.59	4
ZP2	25.08	1.10	0.31	2.72	0.29	0.97	0.10	0.27	0.71	2.64	0.00	4.90	0.05	9.38	4.04	1.80	0.422	0.43	0.56	0.71	0.56	6	
ZP3	23.29	0.99	0.78	5.46	0.70	0.91	-0.02	0.68	0.48	2.38	0.31	4.28	0.35	8.56	4.00	1.80	0.31	0.49	0.53	0.65	0.73	11	
ZP4	24.14	0.94	1.52	10.87	1.50	0.83	-0.06	1.33	1.91	3.18	1.55	7.43	1.76	17.15	5.95	2.40	0.60	0.73	0.82	0.54	1.07	15	
ZP5	18.79	0.74	0.85	10.10	1.39	0.84	-0.26	0.74	1.82	2.51	0.07	5.88	0.15	17.07	5.68	2.00	1.30	0.75	0.81	0.55	1.02	13	
ZP6	24.05	1.07	0.17	1.47	0.11	0.98	0.07	0.15	0.59	1.44	7.08	1.57	5.00	3.00	2.04	0.90	0.22	0.29	0.31	0.74	0.48	4	
ZP7	25.03	1.03	0.50	3.53	0.41	0.95	0.03	0.43	1.47	2.51	0.07	4.90	0.05	13.36	5.33	2.20	0.88	0.77	0.76	0.69	0.61	12	
Ch	23.80	1.06	0.54	3.96	0.48	0.95	0.06	0.47	0.47	2.82	0.20	5.79	0.11	9.83	3.70	2.30	0.42	0.46	0.53	0.68	0.64	7	
											$\sum Z_i^1 = 12.74$		$\sum Z_i^2 = 10.26$										

CV_i -coefficient of variation; b_i -Eberhart and Russel's regression coefficient; S_{dt}^2 -Eberhart and Russel's deviation from regression; W_i^2 -Wricke's covalence; σ_i^2 -Shukla's stability variance; R_i^2 -coefficient of determination; B_i -Perkins and Jinks's regression coefficient; δ_i^2 -Perkins and Jink's deviation from regression; P_i -superiority measure; $S_i^{(1)}$ -the mean of the absolute rank differences of a genotype over all tested environments; $S_i^{(2)}$ -the variance among the genotype ranks over all tested environments; $S_i^{(3)}$ -the sum of the absolute deviations for each genotype relative to the mean of ranks; $S_i^{(6)}$ -the sum of squares of rank for each genotype relative to the mean of ranks; $NP_i^{(1)}, NP_i^{(2)}, NP_i^{(3)}, NP_i^{(4)}$ -Thennarasu non-parametric stability estimates; θ_i -mean variance component; KR_i -Kang's rank-sum.

Table 4. Ranking¹ late maturity maize hybrids grown in ten environments on the basis of stability estimates.

Genotype	CV_e	b_i	S_{di}^2	W_i^2	σ_i^2	R_i^2	B_i	δ_i^2	P_i	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	θ_i	KR	Sum of ranks	Average rank	Standard deviation	
ZP1	3	6	3	3	3	3	6	3	1	2	2	2	1	4	5	2	1	3	3	1	57	2.8	1.5
ZP2	8	7	2	2	2	2	7	2	5	6	4	4	5	2	4	3	5	2	2	3	77	3.8	2.0
ZP3	2	1	6	6	6	6	1	6	3	3	3	3	4	2	2	5	3	6	6	5	79	4.0	1.8
ZP4	6	4	8	8	8	8	4	8	8	8	8	8	8	8	6	6	8	8	8	8	146	7.3	1.3
ZP5	1	8	7	7	7	7	8	7	7	4	7	7	7	4	8	7	7	7	7	7	131	6.6	1.7
ZP6	5	5	1	1	1	1	5	1	4	1	1	1	2	1	1	1	2	1	1	1	37	1.8	1.5
ZP7	7	2	4	4	4	4	2	4	6	4	4	6	6	6	7	8	6	4	4	6	98	4.9	1.6
Ch	4	3	5	5	5	5	3	5	2	7	6	5	3	7	3	4	4	5	5	4	90	4.5	1.3

¹The lower ranks mean greater stability; CV_e -coefficient of variation; b_i -Eberhart and Russel's regression coefficient; S_{di}^2 -Eberhart and Russel's deviation from regression; W_i^2 -Wricke's co-variability; σ_i^2 -Shukla's stability variance; R_i^2 -coefficient of determination; B_i -Perkins and Jinks's regression coefficient; δ_i^2 -Perkins and Jinks's deviation from regression; P_i -superiority measure; $S_i^{(1)}$ -the mean of the absolute rank differences of a genotype over all tested environments; $S_i^{(2)}$ -the variance among the genotype ranks over all tested environments; $S_i^{(3)}$ -the sum of the absolute deviations for each genotype relative to the mean of ranks; $S_i^{(6)}$ -the sum of squares of rank for each genotype relative to the mean of ranks; $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ -Theil's non-parametric stability estimates; θ_i -mean variance component; KR -Kang's rank-sum.

The most unstable late maturity maize hybrid tested over ten environments was ZP4 with sum of ranks and average rank of 146 and 7.3, respectively, with standard deviation of 1.3 (Table 4).

The Principal Component Analysis (PCA) of stability measures for grain yield of late maturity maize hybrids across 10 environments with components PC1 and PC2 explained 87.05% of total variance and outcome is graphically displayed in Figure 1.

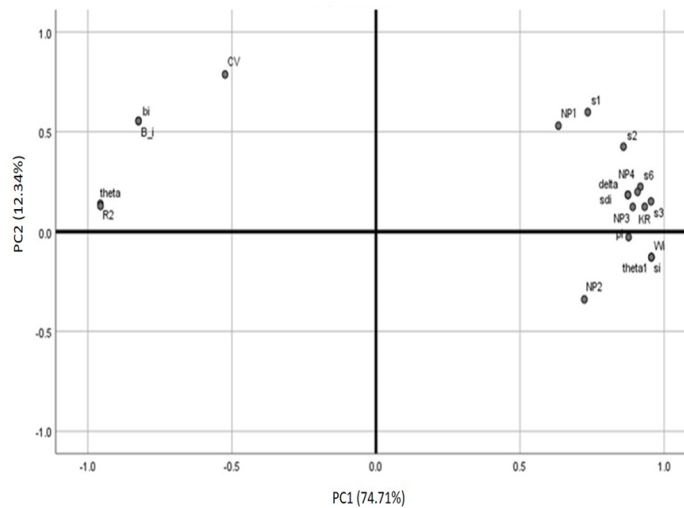


Figure 1. PCA biplot showing grouping of stability measures. CV-coefficient of variation; bi-Eberhart and Russel's regression coefficient; sdi-Eberhart and Russel's deviation from regression; Wi-Wricke's ecovalence; si-Shukla's stability variance; R2-coefficient of determination; B_i-Perkins and Jink's regression coefficient; delta-Perkins and Jink's deviation from regression; pi-superiority measure; s1-the mean of the absolute rank differences of a genotype over all tested environments; s2-the variance among the genotype ranks over all tested environments; s3-the sum of the absolute deviations for each genotype relative to the mean of ranks; s6-the sum of squares of rank for each genotype relative to the mean of ranks; NP1, NP2, NP3, NP4-Thennarasu non-parametric stability estimates; theta1-mean variance component; theta-GEI variance component; KR-Kang's rank-sum.

On the PCA biplot is evident the existence two groups of stability estimates: I group- CV_i , b_i , B_i , $\theta_{(i)}$, R_i^2 ; II group- S_{di}^2 , W_i^2 , σ_i^2 , δ_i^2 , P_i , $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, θ_i , KR_i .

The values of Pearson's coefficients of correlation between twenty stability estimates for grain yield of late maturity maize hybrids grown in ten environments are shown in Table 5.

Table 5. Pearson's coefficients of correlation between stability estimates for grain yield of late maturity maize hybrids grown in ten environments.

	CV_i (%)	b_i	S_{di}^2	W_i^2	σ_i^2	R_i^2	B_i	δ_i^2	P_i	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(4)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	θ_i	
b_i	0.891**																		
S_{di}^2	-0.261	-0.587																	
W_i^2	-0.594	-0.840**	0.919**																
σ_i^2	-0.594	-0.840**	0.919**	1.000**															
R_i^2	0.593	0.849**	-0.923**	-0.997**	-0.997**														
B_i	0.891**	1.000**	-0.587	-0.840**	-0.840**	0.849**													
δ_i^2	-0.261	-0.587	1.000**	0.919**	0.919**	-0.923**	-0.587												
P_i	-0.372	-0.721	0.688	0.783	0.783	-0.788*	-0.721*	0.688											
$S_i^{(1)}$	0.000	-0.298	0.703	0.624	0.624	-0.607	-0.298	0.703	0.549										
$S_i^{(2)}$	-0.189	-0.491	0.780*	0.762*	0.762*	-0.748*	-0.491	0.780*	0.690	0.974**									
$S_i^{(3)}$	-0.390	-0.719*	0.755*	0.833*	0.833*	-0.831*	-0.719*	0.755*	0.902**	0.815*	0.910**								
$S_i^{(4)}$	-0.289	-0.653	0.728*	0.771*	0.771*	-0.777*	-0.653	0.728*	0.883**	0.813*	0.883**	0.983**							
$NP_i^{(1)}$	-0.035	-0.230	0.605	0.535	0.535	-0.511	-0.230	0.605	0.410	0.813*	0.796*	0.659	0.632						
$NP_i^{(2)}$	-0.684	-0.800*	0.337	0.609	0.609	-0.602	-0.800*	0.337	0.765*	0.324	0.483	0.748*	0.698	0.431					
$NP_i^{(3)}$	-0.339	-0.678	0.669	0.733*	0.733*	-0.744*	-0.678	0.669	0.901**	0.671	0.771*	0.941**	0.951**	0.646	0.810*				
$NP_i^{(4)}$	-0.307	-0.661	0.689	0.752*	0.752*	-0.756*	-0.661	0.689	0.899**	0.793*	0.873**	0.986**	0.996**	0.616	0.732*	0.958**			
$\theta_{\square\square}$	0.594	0.840**	-0.919**	-1.000**	-1.000**	0.997**	0.840**	-0.919**	-0.783*	-0.624	-0.762*	-0.833*	-0.772*	-0.535	-0.609	-0.733*	-0.752*		
θ_i	-0.594	-0.840**	0.919**	1.000**	1.000**	-0.997**	-0.840**	0.919**	0.783*	0.624	0.762*	0.833*	0.771*	0.535	0.609	0.733*	0.752*	-1.000**	
KR_i	-0.336	-0.708*	0.844**	0.842**	0.842**	-0.864**	-0.708*	0.844**	0.847**	0.701	0.792*	0.913**	0.936**	0.578	0.618	0.925**	0.917**	-0.842**	0.842**

**-correlation is significant at the 0.01 level, *-correlation is significant at the 0.05 level.

CV_i -coefficient of variation; b_i -Eberhart and Russel's regression coefficient; S_{di}^2 -Eberhart and Russel's deviation from regression; W_i^2 -Wricke's ecovalence; σ_i^2 -Shukla's stability variance; R_i^2 -coefficient of determination; B_i -Perkins and Jinks's regression coefficient; δ_i^2 -Perkins and Jink's deviation from regression; P_i -superiority measure; $S_i^{(1)}$ -the mean of the absolute rank differences of a genotype over all tested environments; $S_i^{(2)}$ -the variance among the genotype ranks over all tested environments; $S_i^{(3)}$ -the sum of the absolute deviations for each genotype relative to the mean of ranks; $S_i^{(4)}$ -the sum of squares of rank for each genotype relative to the mean of ranks; $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ -Themarasu non-parametric stability estimates; θ_i -mean variance component; $\theta_{\square\square}$ -GEI variance component; KR_i -Kang's rank-sum.

A highly significant ($P < 0.01$) absolute value of Pearson's coefficient of correlation of +1 indicating a perfect linear relationship was observed between σ_i^2 and W_i^2 , b_i and B_i , W_i^2 and θ_i , σ_i^2 and θ_i . A highly significant ($P < 0.01$) absolute value of Pearson's coefficient of correlation of -1 indicating a perfect linear relationship was observed between W_i^2 and $\theta_{(i)}$, σ_i^2 and $\theta_{(i)}$, θ_i and $\theta_{(i)}$. It would be redundant to use them all in the stability analysis studies so one can choose to use W_i^2 or σ_i^2 , b_i or B_i , W_i^2 or θ_i , σ_i^2 or θ_i .

Also, a positive, very strong ($r > 0.900$), and statistically highly significant correlation ($P < 0.01$) was detected between following stability estimates pairs: $NP_i^{(2)}$ and P_i , $S_i^{(2)}$ and P_i , $S_i^{(2)}$ and $S_i^{(3)}$, KR_i and $S_i^{(3)}$, KR_i and $NP_i^{(3)}$, W_i^2 and S_{di}^2 , σ_i^2 and S_{di}^2 , δ_i^2 and W_i^2 , δ_i^2 and σ_i^2 , δ_i^2 and θ_i , S_{di}^2 and θ_i , KR_i and $NP_i^{(3)}$, KR_i and $S_i^{(6)}$, $NP_i^{(3)}$ and $S_i^{(3)}$, $NP_i^{(3)}$ and $S_i^{(6)}$, $NP_i^{(4)}$ and $NP_i^{(3)}$, $S_i^{(2)}$ and $S_i^{(1)}$, $S_i^{(6)}$ and $S_i^{(3)}$, $NP_i^{(4)}$ and $S_i^{(3)}$, $NP_i^{(4)}$ and $S_i^{(6)}$, $\theta_{(i)}$ and R_i^2 . A negative, very strong ($r < -0.900$), and statistically highly significant correlation ($P < 0.01$) was shown for following stability estimates pairs: $\theta_{(i)}$ and δ_i^2 , S_{di}^2 and $\theta_{(i)}$, δ_i^2 and R_i^2 , R_i^2 and S_{di}^2 , R_i^2 and W_i^2 , R_i^2 and σ_i^2 , R_i^2 and θ_i .

Without adaptation approximately 53% of the cultivation areas would require hybrid renewal before 2050 under RCP 4.5 and RCP 8.5 emission scenarios (ZHANG *et al.*, 2021). The yield loss would be 2.3% in 2030s under RCP 4.5 for late maturing maize hybrids but tripled (7.1%) for early maturing hybrids (ZHANG *et al.*, 2021). The late maturing hybrids did not consistently suffer from greater yield losses under the climate change suggesting that other traits may be at work such as heat and drought resistance, grain filling rate and light use efficiency according to XIAO *et al.* (2020). In France CAUBEL *et al.* (2018) concluded that whatever the planting date, higher temperatures in the future will be favorable for late maturity maize varieties in the northern part of the country.

Significant $G \times E$ interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (quantitative or absolute differences between genotypes) or variations in the comparative ranking of the genotypes (qualitative or rank changes) (FASAHAHAT *et al.*, 2015). When genotypic performance in different environments is extremely different, GEI becomes major challenge to selection and genetic improvement (CAUBEL *et al.*, 2018; FASAHAHAT *et al.*, 2015). The plenty of studies evaluated genotypes stability on the base of univariate parametric and non-parametric methods in maize (BRANKOVIĆ-RADOJČIĆ, *et al.*, 2022; KATSENIOS *et al.*, 2021; MITROVIĆ *et al.*, 2018; BUJAK *et al.*, 2014; CREVAR *et al.*, 2011) and in other field crops also (CUBUKCU *et al.*, 2021; AFZAL *et al.*, 2021; AHMADI *et al.*, 2015).

LIU *et al.* (2010) showed PCA biplot revealing the grouping of univariate stability parameters for maize genotypes tested over 25 locations and among them $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ and $S_i^{(6)}$ were in the same group, $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ in the second group, and $NP_i^{(1)}$ and KR_i in the third, what is not consistent with our research, with all of the above parameters grouped in one group. The same author found the statistically significant very strong correlation ($P < 0.01$) between $S_i^{(2)}$ and $S_i^{(2)}$ (0.99), $NP_i^{(3)}$ and $NP_i^{(4)}$ (0.99), $NP_i^{(2)}$ and $NP_i^{(4)}$ (0.99), and medium strong between $NP_i^{(4)}$ and KR_i (0.79), similar as in our study.

OHUNAKIN *et al.* (2021) assessed correlations among univariate stability measures for grain yield of tropical maize hybrids infected with Northern leaf blight in Nigeria and showed

statistically significant very strong correlation ($P < 0.01$) between W_i^2 and σ_i^2 , θ_i and σ_i^2 , θ_i and W_i^2 , (+1.00), θ_i and $\theta_{(i)}$, W_i^2 and $\theta_{(i)}$, σ_i^2 and $\theta_{(i)}$, (-0.97), S_{di}^2 and σ_i^2 , S_{di}^2 and W_i^2 (0.90). The almost exact values ($P < 0.01$) as in our study for stability measures correlations were found in Shojaei *et al.* [80] for W_i^2 and σ_i^2 (0.99), b_i and W_i^2 , b_i and σ_i^2 , (-0.85) and in MITROVIĆ *et al.* (2018) and BRANKOVIĆ-RADOJČIĆ *et al.* (2022) for $S_i^{(1)}$ and $S_i^{(2)}$, and $S_i^{(3)}$ and $S_i^{(6)}$ pairs.

CONCLUSION

The most stable late maturity maize hybrid tested over ten environments was shown to be ZP6 with sum of ranks and average rank of 37 and 1.8, respectively, with standard deviation of average rank of 1.5. The highest average grain yield across all tested environments was observed for ZP1 which was second most stable hybrid with sum of ranks and average rank of 57 and 2.8, respectively, with standard deviation of average rank of 1.5. PCA biplot has two groups of parametric and non-parametric stability estimates: I group- CV_i , b_i , B_i , $\theta_{(i)}$, R_i^2 ; II group- S_{di}^2 , W_i^2 , σ_i^2 , δ_i^2 , P_i , $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, θ_i , KR_i . Pearson's correlation bring along the redundant stability indices and one can choose to use W_i^2 or σ_i^2 , b_i or B_i , W_i^2 or θ_i , σ_i^2 or θ_i .

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ANALIZA STABILNOSTI PRINOSA ZRNA HIBRIDA KUKURUZA KASNE GRUPE ZRENJA IZ SRBIJE

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Izvod

Ciljevi ovog istraživanja su: i) ocena parametrijskih i neparametrijskih pokazatelja stabilnosti prinosa zrna hibrida kukuruza kasne grupe zrenja, ii) utvrđivanje korelacija između pokazatelja stabilnosti i njihovog grupisanja. Osam hibrida FAO 700 grupe zrenja (ZP1-ZP7, kontrola (Ch)) su testirani za prinos zrna tokom višelokacijskog ogleada u Srbiji sa pet lokaliteta i dve godine. Suma rangova za testirane hibride kukuruza je bila u intervalu od 37 (ZP6) do 146 (ZP4). Na osnovu analize stabilnosti utvrđeno je da je najstabilniji hibrid ZP6 sa sumom rangova 37, prosečnim rangom 1,8, i standardnom devijacijom prosečnog ranga po sredinama od 1,5, a da je najprinosniji ZP1 koji je bio drugi po stabilnosti. Analiza glavnih komponenti je pokazala postojanje dve grupe pokazatelja stabilnosti: I grupa-koeficijent varijacije (CV_i), koeficijent regresije po Eberhart i Russel (b_i), koeficijent regresije po Perkins i Jinks (B_i), komponenta varijanse interakcije ($\theta_{(i)}$), koeficijent determinacije (R_i^2), II grupa- devijacija od regresije po Eberhart i Russel (S_{di}^2), ekovalenca po Wricke (W_i^2), varijansa stabilnosti po Shukla (σ_i^2), devijacija od regresije po Perkins i Jinks (δ_i^2), indeks superiornosti (R_i), prosečna razlika ranga genotipa po sredinama ($S_i^{(1)}$), varijansa ranga genotipa po sredinama ($S_i^{(2)}$), suma odstupanja ranga svakog genotipa u odnosu na prosečni rang ($S_i^{(3)}$), suma kvadrata ranga za svaki genotip u odnosu na prosečni rang ($S_i^{(6)}$), $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$ -neparametrijski pokazatelji stabilnosti po Thenararu, komponenta prosečne varijanse (θ_i), suma rangova po Kang (KR_i). Pearson-ova korelaciona analiza je ukazala da je korišćenje svih pokazatelja stabilnosti suvišno i da se može izabrati jedan od dva: W_i^2 ili σ_i^2 , b_i ili B_i , W_i^2 ili θ_i , σ_i^2 ili θ_i .

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