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Assessment of Genotype × Environment Interactions for Black Soybean Yield using Ammi and GGE Biplot

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***Abstract* – Soybean production in Indonesia is facing challenges of diverse growing environments, leading to genotype and environment interaction (GEI). Ten soybean genotypes, consisting of eight promising lines and two check cultivars (Detam 1 and Mallika) were evaluated at 16 locations in 2011. The aim of this study was to evaluate the GEI using AMMI and GGE biplot analysis for black soybean yield in order to identify stable genotypes. The results indicate a significant effect of genotype, environment, and GEI with respect to yield. The average yield of ten black soybean genotypes was 2.59 t/ha. The yield of promising lines ranged from 2.51 to 2.88 t/ha. Genotype W9837 x Cikuray-66 has the highest yield (2.88 t/ha) among all genotypes and check cultivars. AMMI model showed that the first three were significant, which explained 37.66%, 18.19%, and 17.63% of the interaction sum of squares, respectively. The partitioning of the G + GE sum of squares through GGE biplot showed that PC1, PC2, PC3, and PC4 are significant components that explain 45.19%, 3.94%, 13.50%, and 12.78% of G + GE sum of squares, respectively. Genotypes W9837 × Cikuray-66 was stable according to both AMMI and GGE methods, and proposed to be released as a new high-yielding black soybean cultivar.**

***Keywords* – GEI, Black Soybean, Yield, AMMI, GGE Biplot.**

I. INTRODUCTION

Soybean has a high economic value in Indonesia because Indonesia is one of the largest soybean-consuming country in the world. Due to lower yield of national soybean production forced the government to import soybean, causes the value of soybean import continue to increase every year. Soybean also has undergone repositioning, initially only as food, this time also placed as the best source of functional food and industrial raw materials. Soybean with black seed coat (black soybean) not only prospective feedstock for the soy sauce but also contains high nutrients. Hence the provision and enhancement the national soybean production needs to be done.

In Indonesia, the main use of black soybean is for the soy sauce. In other countries such as China, Taiwan, Korea, and Japan; black soybean has been used in a wide range of processed foods, such as burgers and ice cream. The use of black soybean sauce for raw materials will improve the quality of soy sauce to brown black color and increase the nutritional value, especially protein.

The development of high-yielding black soybean cultivar with wider adaptability and stability is the ultimate aim of soybean breeders in Indonesia. However, attaining this goal is made more complicated by GEI, genotype × environment interactions [1]. The application of the different methods to describe GEI statistics and stability have been made [2]-[3]-[4]-[5]. Method that can be used to assess the adaptability and phenotypic stability are developed using data from repeated testing on a wide range of varying growing environments [6]. Analysis of variance is normally performed to measure whether GEI exist.

GEI is defined by [7] as a non-permanent differences between genotypes when planted in a single to another environment. GEI results from a change in the relative rank of genotype performance or a change in the magnitude of differences between genotype performances from one environment to another. This interaction is important to assess because affect selection of superior cultivars [8]-[9]-[10], and often difficult to obtain valid conclusions from varietal trials carried out over a wide range of environments [11]. Another undesirable effect of GEI includes low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance [12]-[13].

AMMI and GGE biplot model analysis combines the additive parameters of traditional ANOVA (analysis of variance) with multiplicative parameters of PCA (principal component analysis) into a single analysis model. The parameters used are the principal component [1]. The models are SVD-based, and the analysis provided by biplot increases tremendously the informativeness of the results. The difference between AMMI and GGE is that GGE biplot analysis is based on environment-centered PCA, whereas AMMI analysis refers to double-centered PCA. The AMMI model and GGE biplot has been used extensively with great success to analyze and understand various crop genotype × environment interaction in various crops [14]-[15]-[16].

The objective of this study was to evaluate the GEI using AMMI and GGE biplot analysis for black soybean yield in order to identify stable genotypes.

II. RESEARCH METHODS

The materials used were ten soybean genotypes, consisting of eight promising lines and two released varieties ('Detam 1' and 'Mallika') check cultivars. Genotypes and their code names are presented in Table 1.

The field experimental design for each location was completely randomized design with four replicates. The plot size was 2.8 m x 4.5 m with 40 cm x 15 cm plant distance, two plants/hill. Fertilizer of 50 kg Urea, 100 kg SP36 and 75 kg KCl per ha were applied before sowing time. Weed, insect and disease were controlled intensively.

To determine the effects of GEI on yields, the data were subjected to AMMI [17] and GGE Biplot [18] analysis using SAS software written by [19]. The results of AMMI and GGE analysis are presented by analysis of variance and biplot graph.

The AMMI model is

$$Y_{ijr} = \mu + g_i + e_j + \sum_{k=1}^{x} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ijr} ,$$

with Y_{ijr} = observation of the *r*th replicate of the *i*th genotype in the *j*th environment, μ = the overall mean, g_i = main effect of the *i*th genotype, e_j = main effect of the *j*th environment, x = matrix rank of $\{ge\}_{ij}$, λ_k = the singular value for principal component *k*, α_{ik} = the eigenvector score for genotype *i* and component *k*, γ_{jk} = the eigenvector score for environment *j* and component *k*, and ε_{ijr} = the error for genotype *i* and environment *j* and replicate *r*.

Table 1: Genotype and genotype code in soybean multi location trials at 16 locations. 2011.

Genotype	Genotype Code
Cikuray × W9837-171	G1
Cikuray × W9837-105	G2
W9837 × Cikuray-66	G3
W9837 × 100H-236	G4
MLG 3102 × Cikuray-435	G5
Cikuray × W9837-181	G6
Cikuray × W9837-184	G7
W9837 × Cikuray-26	G8
'Detam 1'	G9
'Mallika'	G10

Table 2: Description of the multi-location trials. 2011.

Code	Location (District)	Soil type	Land type	Climate	Elevation (masl)	Season
E1	Pasir Jaya, Bogor Barat, Bogor	Ultisol	Lowland	B	330	DS1
E2	Pasir Jaya, Bogor Barat, Bogor	Ultisol	Lowland	B	330	DS2
E3	Karang, Delanggu, Klaten	Entisol	Lowland	D3	62	DS1
E4	Karang, Delanggu, Klaten	Vertisol	Lowland	D3	62	DS2
E5	Bendungan, Prambanan, Sleman	Gray Regosol	Lowland	C3	86	DS1
E6	Madurejo, Prambanan, Sleman	Gray Regosol	Lowland	C3	86	DS2
E7	Kedung Uneng, Bangsal, Mojokerto	Gray Grumosol	Lowland	C3	72	DS1
E8	Peterongan, Bangsal, Mojokerto	Gray Grumosol	Lowland	C3	72	DS2
E9	Kademungan, Wonorejo, Pasuruan	Brown Mediteran	Lowland	E	124	DS1
E10	Sumberbanteng, Kejayan, Pasuruan	Brown Mediteran	Lowland	E	124	DS2
E11	Muneng, Sumberasih, Probolinggo	Brown Regosol	Lowland	E	10	DS1
E12	Muneng, Sumberasih, Probolinggo	Brown Regosol	Lowland	E	10	DS2
E13	Genteng, Genteng, Banyuwangi	Asosiasi Latosol	Lowland	D2	168	DS1
E14	Genteng, Genteng, Banyuwangi	Asosiasi Latosol	Lowland	D2	168	DS2
E15	Sesele, Gunung Sari, Lombok Barat	Gray Regosol	Lowland	C3	24	DS1
E16	Sesele, Gunung Sari, Lombok Barat	Gray Regosol	Lowland	C3	24	DS2

Note: masl = meter above sea level; DS1 = dry season 1 (February – May 2011); DS2 = dry season 2 (June – September 2011); climate type based on Oldeman classification system.

The GGE model is

$$Y_{ijr} = \mu + e_j + \sum_{k=1}^{x} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ijr} ,$$

with Y_{ijr} = observation of the *r*th replicate of the *i*th genotype in the *j*th environment, μ = the overall mean, e_j = main effect of the *j*th environment, x = matrix rank $\{gge\}_{ij}$ when $gge_{ij} = g_i + ge_{ij}$, λ_k = the singular value for principal component *k*, α_{ik} = the eigenvector score for genotype *i* and component *k*, γ_{jk} = the eigenvector score for environment *j* and component *k*, and ε_{ijr} = the error for genotype *i* and environment *j* and replicate *r*.

III. RESULT AND DISCUSSION

The average yield of ten black soybean genotypes was 2.59 t/ha. The yield of promising lines ranged from 2.51 to 2.88 t/ha. Check cultivar 'Detam 1' (2.66 t/ha) have higher yield than 'Mallika' (2.46 t/ha). Genotype G3 (2.88 t/ha) has the highest yield compared with seven other promising lines, even higher than the check cultivars 'Detam 1' and 'Mallika'.

The combined analysis of variance showed that seed yield were significantly affected by environment (E), genotype (G) and genotype × environment interaction (GEI) (Table 3).

Table 3: Analysis of variance from 10 genotypes in 16 environments.

SV	df	SS	MS	P > F
Env (E)	15	12.664	0.8443**	<0.0001
Genotype (G)	9	7.538	0.8376**	<0.0001
G × E	135	23.378	0.1732**	<0.0001
Error	432	44.070	0.1020	

Note: SV= source of variation, df = degree of freedom, SS = Sum of Squares, MS = Mean of Squares, Env = environment, ** = significant at 1% probability level (p<0.01), coefficient of variation = 12.31%.

A significant environment indicates that there are differences in their productivity. The significant GEI indicated that there was differences on genotype performance over locations.

A. AMMI analysis

The AMMI analysis partitioned the sum of squares of GEI into nine interaction principal components (PC), of which the first three PC were significant. Result from AMMI model showed that the PC1 of the interaction captured 37.66% of the interaction sum of squares. The PC2 and PC3 explained 18.19% and 17.63% of the GEI sum of squares, respectively (Table 4). According to [20]-[21], two interaction principal component for AMMI model was sufficient for predictive model. Other interaction principal component captured mostly non-predictive random variation (noise) and did not fit to predict validation observations.

Table 4: Analysis of variance for AMMI.

Source of Variation	df	SS	MS	P > F
G × E	135	23.3783	0.8443**	<0.0001
PC1	23	8.8042	0.3828**	0.00000
PC2	21	4.2533	0.2025**	0.00616
PC3	19	4.1205	0.2168**	0.00396
Residual	62	6.2001	0.4306	

Note: df = degree of freedom, SS = Sum of Squares, MS = Mean of Squares, ** = significant at 1% probability level (p<0.01), PC = Principal Component.

In AMMI1 biplot, the IPCA 1 scores of genotypes and environments are plotted against their respective means and in AMMI2 biplot, the IPCA1 and IPCA2 scores of genotype and environments are plotted against each other. AMMI1 biplot for soybean seed yield of the 10 genotypes at 16 environments is presented in Fig.1.

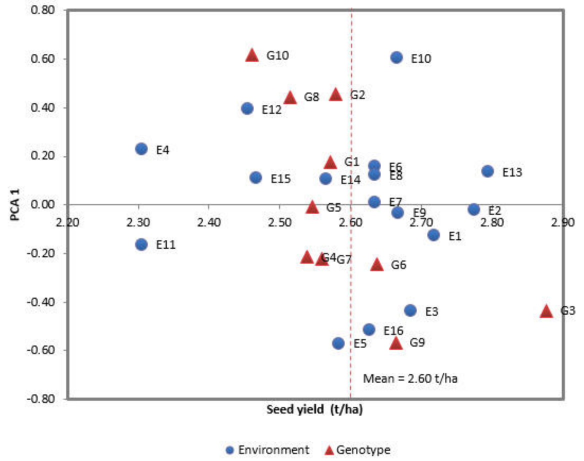

Fig.1. AMMI1 biplot from average seed yield and PC1 of genotype and environment.

The x-axis represents the mean seed yield, the y-axis (PCA1) represents the differences in the effect of the interaction (stability). Genotype/environment that has a lower of absolute PC1 value had the lower GEI effect than the genotype/environment that have a higher absolute PC1 value. Genotype and environment codes refers to Table 1 and Table 2, respectively.

AMMI1 biplot shows the genotype and environment means (additive mean effects) in the abscissa, and scores of the IPCA1 (multiplicative interaction) in the ordinate. A same sign on the IPCA of a genotype and environment, shows their positive interaction; if different, their interaction is negative [22]. Genotypes G1, G2, G8 and G10 are well adapted to E4, E10, E12, E14, E15, E6, E8, E7, and E13 environments; but not suitable for environments E11, E5, E16, E9, E3, E1, and E2. On the contrary, genotypes G4, G5, G6, G7, G9, and G3 are adapted to E11, E5, E16, E9, E3, E1, and E2.

Assessment of individual genotype performances can be based on their positions relative to the X and Y axis. Based on Fig.1, the yield of genotypes G3, G9, and G6 above the mean yield, but genotype G3 showed the lowest stability. Genotypes G3 and G6 have yield above the check cultivar (G9 and G10). Of the three high yielding genotypes (G3, G9, and G6), G9 showed the lowest stability, whereas G6 proved to be the most stable.

Fig. 2 gives the AMMI2 biplot for yield. A genotype or an environment with an IPCA score close to zero showed the small interaction effect and considered as stable [23].

Distribution of genotype points in the AMMI2 biplot revealed that the genotypes G3 and G4 scattered close to the origin, indicating minimal interaction of these genotypes with environments. The remaining eight genotypes scattered away from the origin indicating that the genotypes were more sensitive to environmental interactive forces. Genotype G4 showed the most stable one, but have lower yield than G3. Based on AMMI biplot, genotype G3 was identified as the best genotype because has highest yield and stable performance.

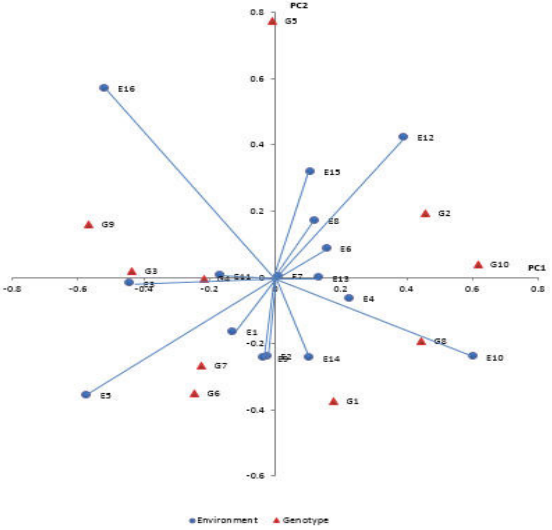

Fig.2. AMMI2 biplot from PC1 and PC2 of genotype and environment. The x-axis represents the PC1 value, the y-axis represents PC2 value. The more the PC scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled. Genotype and environment codes refers to Table 1 and Table 2, respectively.

Evaluation of seed yield from 27 soybean lines at three locations (Anhembi, Areão and Esalq) in Brazil using AMMI was done by [24]. First interaction principal component axis (IPCA1) was significant. USP 93-5082 and USP 93-5243 genotypes had high adaptability and stability. Another research [25], AMMI model 2 was the best fit for the data set, and soybean genotype DKC 80-10 showed the best adaptation to all environments.

B. GGE analysis

The partitioning of the G + GE sum of squares through GGE biplot showed that PC1, PC2, PC3, and PC4 are significant components that explain 45.19%, 13.94%, 13.50%, and 12.78% of G + GE sum of squares, respectively (Table 5).

Table 5: Analysis of variance for GGE.

Principal Component	df	Sum of Squares	P > F
Genotipe (G)	9	7.5387**	<0.0001
G × E	135	23.3783**	<0.0001
PC1	23	13.9019**	0.00000
PC2	21	4.2905**	0.00560
PC3	19	4.1536**	0.00362
PC4	17	3.9322**	0.00283
Residual	55	0.3552	
Total			
Eigen values*		30.91707*	

Note: PC = Principal Component; df = degree of freedom; * = total of Eigen values are equal with total of G + GE sum of squares; ** = significant at 1% probability level (p<0.01).

A polygon that shows the pattern of "which-won-where" in Fig. 3 graphically addresses crossover GE, mega-environment differentiation, specific adaptation, and identify the best genotype in each environment [26]-[18]-[27]-[28]-[29].

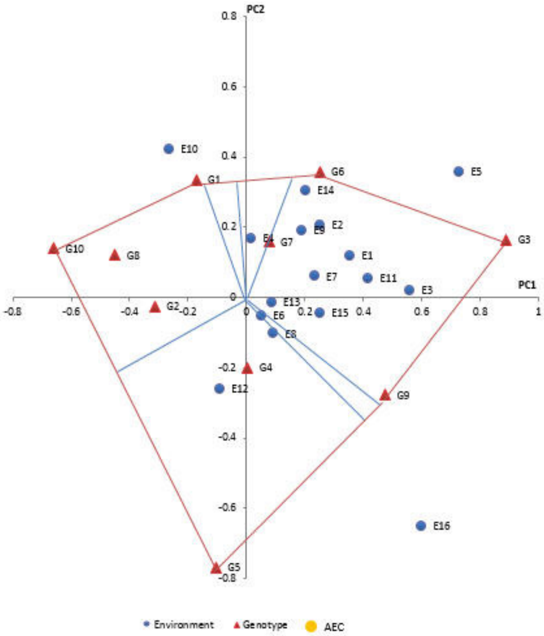

Fig.3. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won where pattern. A quadrant/sector is formed of a straight line that starts from the origin biplot which cut perpendicular to the connection line on each side, and divide into six sectors. Within a sector, genotype located at the peak polygon is the best genotypes in all environments in the sector, and genotypes are well adapted in environments that are in the same sector. Genotype and environment codes refers to Table 1 and Table 2, respectively.

In Fig. 3, the 16 environments are grouped into three sectors. Genotypes G1, G2, G8, and G10 were most suited for environment E10, with G1 as the highest yielding genotype. Genotypes G3, G6, G7, and G9 were most suited for environments E1, E2, E3, E5, E7, E9, E11, E13, E14, and E15; with G3 as the highest yielding genotype. Genotypes G4 and G5 were most suited for environments E8, E12, and E16; with G5 as the highest yielding genotype. According to [30], selection of superior genotypes for each environment ensures the effective exploitation of both G and GE interaction.

Performance of yield and stability of a genotype can be evaluated by the method of average environment coordinate or AEC [31]. Referring to Fig. 4, there were four high yielding genotypes (G3, G7, G8, and G9) above the general average yield, with G3 produced the highest yield. Genotypes with high stability were G2 and G3. The most stable genotype (G2) has lower yield than the high yielding genotype G3.

Since farmers are more interested in the varieties that produce consistent yields across environments [32], an ideal genotype should have the highest mean performance with high stability across environments (i.e. perform the best in all environments) [33].

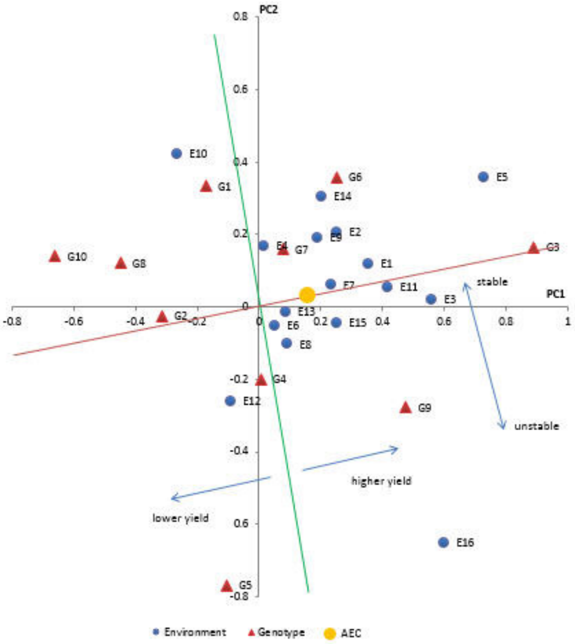

Fig.4. Average environment coordinate of the GGE biplot based on symmetrical scaling. Straight line passing through AEC with the biplot origin as AEC abscissa, a straight line through the origin and perpendicular biplot as AEC ordinate. Directions to the AEC ordinate that move away from the origin biplot showed increased stability. AEC ordinate split genotypes under and above the general average yield. Genotype and environment codes refers to Table 1 and Table 2, respectively.

Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation, because a genotype which is located closer to the ideal genotype is most desirable one [34]. Hence, the selected genotype based on this method (GGE biplot) is genotype G3 which has high yield performance among all genotypes and relatively stable.

In this research, AMMI and GGE biplot method provide similar analytical results in determining the best genotype. Both methods conclude genotype G3 as the best genotype. The similar result was previously obtained by [15]-[35].

IV. CONCLUSION

The results indicate a significant effect of genotype, environment, and GEI with respect to yield. According to AMMI and GGE biplot methods, genotype G3 (W9837 × Cikuray-66) was identified as the best genotype. This genotype produced highest yield and stable performance, therefore suggested to be released as a new improved black soybean cultivars.

REFERENCES

[1] H. G., Gauch and R.W. Zobel. AMMI analysis of yield trials. In Kang MS and Gauch HG. (Eds.). *Genotype-by-Environment Interaction*. CRC Press, Boca Raton. New York, United States of America, 1996.

[2] J.M. Cotes, J. Crossa, A. Sanches,and P.L. Cornelius. A Bayesian approach for assessing the stability of genotypes. *Crop Sci*. 2006, 46, pp. 2654-2665.

[3] S. Alwala, T. Kwolek, M. McPherson, J. Pellow, and D. Meyer. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. *Field Crops Research*, 2010, 119, pp. 225–230.

[4] L. Gulluoglu, H. Arioglu, and C. Kurt. Adaptability and stability of new soybean cultivars under double cropped conditions of Turkey. *Afric. J. of Agric. Res.* 2011, 6(14), pp. 3320-3325.

[5] A.A. Kandil, A.E. Sharief, A.R. Morsy, and A.I.M. El-Sayed. Performance of some promising genotypes of soybean under different planting dates using biplots analysis. *J of Basic and App. Sci*. 2012, 8, pp. 379-385.

[6] R.K. Singh and B.D. Chaudhary. 1979. *Biometrical Method in Quantitative Genetic Analysis.* Kalyani Publisher. New Delhi. 267p.

[7] R.C. Yang and R.J. Baker. Genotype × Environment interactions in two wheat crosses. *Crop.Sci.* 1991, 31, pp. 63-87.

[8] S.A. Eberhart and W.A. Russell. Stability parameters for comparing varieties. *Crop Sci*. 1966, 6, pp. 36-40.

[9] R. Magari and M.S. Kang. Genotype selection via yield-stability statistic in maize yield trials. *Euphytica*, 1993, 70, pp. 105-111.

[10] J.S. Ebdon and H.G. Gauch. Additive Main Effect and Multiplicative Interaction Analysis of national Turfgrass performance trials. II cultivar recommendations. Crop Sci. 2002, 42, pp. 497–506.

[11] Nasrullah. A Modified procedure for indentifying varietal stability. *Agric. Sci*. 1981, 3 (4), pp. 153- 159.

[12] R.E. Comstock and R.H. Moll. Genotype × Environment Interactions. *Symposium on Statistical Genetics and Plant Breeding*. National Academy Science National Research Council, Washington, D.C., 1963, pp. 164-196.

[13] S.S. Alghamdi. Yield stability of some soybean genotypes across diverse environments. *Pakistan J. of Biological Sci*. 2004, 7, pp. 2109-2114.

[14] R.C. Misra, S. Das, and M.C. Patnaik. AMMI Model analysis of stability and adaptability of late duration finger millet (*Eleusine coracana*) genotypes, *World Applied Sciences Journal*, 2009, 6(12), pp. 1650-1654.

[15] E. Ilker, F.A. Tonk., O. Caylank, M. Tosun, and I. Ozmen. Assessment of genotype × environment interactions for grain yield in maize hybrids using AMMI and GGE biplot analyses. *Turkish J. of Field Crops*, 2009, 14(2), pp. 123 – 135.

[16] M.R.N. Rad, M. A. Kadir, M.Y. Rafii, H.Z.E. Jaafar, M. R. Naghavi and F. Ahmadi. Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. AJCS, 2013, 7(7), pp. 956-961.

[17] H.G. Gauch. *Statistical analysis of regional yield trials: AMMI analysis of factorial designs*. Elsevier Science Pub. Amsterdam, Netherland, 1992.

[18] W. Yan, L.A. Hunt, Q. Sheng, and Z. Szlavnies. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop. Sci.* 2000, 40, pp. 597-605.

[19] M.V. Hernandez and J. Crossa J. 2000. *The AMMI analysis and graphing the biplot*. CIMMYT. INT. Mexico.

[20] S. Admassu, M. Nigussie, and H. Zelleke. Genotype × environment interaction and stability analysis for grain yield (*Zea mays* L.) in Ethiopia. Asian J. *Plant Sci.* 2008, 7 (2), pp.163-169.

[21] R.W. Zobel, M.J. Wright, and H.G. Gauch. Statistical analysis of a yield trial. *Agron. J.* 1988, 80, pp. 388–393.

[22] B. Mitrović, D. Stanisavljevi, S. Treski, M. Stojaković, M. Ivanović, G. Bekavac, and M. Rajković. Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analyses. *Turkish Journal of Field Crops*, 2012, 17(1), pp. 35-40.

[23] J. Crossa. Statistical analyses of multilocation trials. *Adv.Agron*. 1990, 44, pp. 55-85.

[24] M. Rocha, N.A. Vello, A.C. Lopes, M.C.C. Maia. Yield stability of soybean lines using additive main effects and multiplicative interaction analysis - AMMI. Crop Breeding and Applied Biotechnology. Brazilian Society of Plant Breeding. 2004. Available at http://www.cababstractsplus. org/abstracts/ Abstract.aspx?AcNo=200531 (9 June 2009).

[25] M.J.A. Alberts. A comparison of statistical methods to describe genotype × environment interaction and yield stability in multi-location maize trials. *Thesis*. Faculty of Agriculture, Dept. of Plant Breeding. Univ. of the Free State, Bloemfontein, South Africa.

[26] H.G. Gauch and R.W. Zobel. Identifying mega-environments and targeting genotypes. *Crop. Sci.* 1997, 37, pp. 311 – 326.

[27] P.S. Rao, P.S. Reddy, A. Ratore, B.V.S. Reddy, and S. Panwar. Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype 9 environment interaction and seasonal adaptation. *Indian J. Agric. Sci.* 2011, 81, pp. 438–444.

[28] Rakshit, S., K. N. Ganapathy, S. S. Gomashe, A. Rathore, R. B. Ghorade, M. V. N. Kumar, K. Ganesmurthy, S. K. Jain, M. Y. Kamtar, J. S. Sachan, S. S. Ambekar, B. R. Ranwa, D. G. Kanawade, M. Balusamy, D. Kadam, A. Sarkar, V. A. Tonapi, and J. V. Patil. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica*, 2012, 185, pp. 465–479.

[29] P. Tukamuhabwa, H. Oloka, T. Sengooba, and P. Kabayi. Yield stability of rust-resistant soybean lines at four mid-altitude tropical locations. *Euphytica*, 2012, 183 (1), pp. 1-10.

[30] E.A. Jandong, M.I. Uguru, and B.C. Oyiga. Determination of yield stability of seven soybean genotypes across diverse soil pH levels using GGE biplot analysis. *J. Appl. Biosci.* 2011, 43, pp. 2924-2941.

[31] W. Yan. Singular value partitioning in biplot analysis of multienvironment trial data. *Agron. J.* 2002, 94, pp. 990 – 996.

[32] P. Tarakanovas and V. Ruzgas. Additive main effect and multiplicative interaction analysis of grain yield of wheat varieties in Lithuania. *Agron. Res*., 2006, 4(1), pp. 91-98.

[33] W. Yan and N.A. Tinker. Biplot analysis of multi-environment trial data: principles and applications. *Can J Plant Sci*. 2006, 86, pp. 623–645.

[34] Y. Kaya, C. Palta, and S. Taner. Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. *Turk J. Agric. For.* 2002, 26, pp. 275-279.

[35] A. Krisnawati. Analysis of multi-environment trial from soybean lines using regression and singular value decomposition. Thesis. Faculty of Agriculture, Gadjah Mada University, Yogyakarta, 2013, 88p.

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Adie, M.M. and A. Krisnawati. Soybean opportunity as source of new energy in Indonesia. International J. of Renewable Energy Development. 2014, 3 (1), pp. 37-43

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