

Yield Stability of Soybean Genotypes in Tropical Environments based on Genotype and Genotype-by-Environment Biplot

Stabilitas Hasil Genotipe Kedelai pada Lingkungan Tropis Berdasarkan Biplot Genotipe dan Genotipe-Lingkungan

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ABSTRACT

Genotype \times environment interaction is universal phenomenon when different genotypes are tested in a number of environments. The objective of this experiment was to determine the seed yield stability of soybean genotypes. Seven soybean genotypes and two check cultivars were evaluated at eight soybean production centers during the dry season 2015. Stability analysis on seed yield was based on the GGE biplot method. The combined analysis showed that yield and yield components were significantly affected by genotype (G), environments (E), and genotype \times environment interaction (GEI), except for number of filled pods. The highest yield was G6 (3.07 ton ha⁻¹), followed by G7 (2.93 ton ha⁻¹). The “which-won-where” polygon mapping resulted two mega-environments. The best genotype for the first mega-environment was G1 (G511H/Anjasmoro//Anjasmoro-2-8) at E5 (Pasuruan2); and the second one was G6 (G511 H/Anj//Anj//Anj//Anj//Anjs-6-7) at E1 (Nganjuk), E2 (Mojokerto), E3 (Blitar), E4 (Pasuruan1), E6 (Jembrana), E7 (Tabanan), and E8 (Central Lombok). The G7 (G511 H/Anjasmoro-1-4-2) was closest to ideal genotype as indicated by relatively stable and produced high yield across environments. The analysis of multi-environment trials data using GGE is useful for determining mega-environment analysis and stability of genotype which focusing on overall performance to identify superior genotypes.

Keywords: GE interaction, GGE biplot, *Glycine max*, seed yield

ABSTRAK

Interaksi genotipe dengan lingkungan merupakan fenomena umum pada pengujian sejumlah genotipe pada berbagai lingkungan. Tujuan penelitian adalah menentukan stabilitas hasil dari beberapa galur harapan kedelai. Sebanyak 7 galur harapan disertai dua varietas pembandingan (Anjasmoro dan Grobogan) dievaluasi pada delapan sentra produksi kedelai selama musim kemarau tahun 2015. Analisis stabilitas hasil biji menggunakan metode GGE biplot. Sidik ragam tergabung menunjukkan bahwa hasil biji dan komponen hasil secara nyata dipengaruhi oleh genotipe (G), lingkungan (E) dan interaksi antara genotipe dan lingkungan (GEI), kecuali jumlah polong isi. Hasil tertinggi diperoleh oleh G6 (3.07 ton ha⁻¹) diikuti oleh G7 (2.93 ton ha⁻¹). Grafik poligon “which-won-where” mampu mengelompokkan lingkungan pengujian menjadi dua mega lingkungan. Galur terbaik pada mega lingkungan pertama (E1/Pasuruan2) adalah G1 (G511H/Anjasmoro//Anjasmoro-2-8), sedangkan galur terbaik pada mega lingkungan kedua (E1/Nganjuk, E2/Mojokerto), E3/Blitar, E4/Pasuruan1, E6/Jembrana, E7/Tabanan, dan E8/Lombok Tengah) adalah G6 (G511 H/Anj//Anj//Anj//Anj//Anjs-6-7). Genotipe terpilih yang terindikasi sebagai genotipe ideal adalah G7 (G511 H/Anjasmoro-1-4-2), yakni hasil relatif stabil dan berdaya hasil tinggi pada berbagai lingkungan. Analisis GGE pada penelitian secara lintas lingkungan berguna untuk menentukan mega lingkungan dan mengidentifikasi genotipe yang stabil dengan menekankan pada keragaan keseluruhan tanaman dalam identifikasi genotipe superior.

Kata kunci: biplot GGE, *Glycine max*, hasil biji, interaksi GE

INTRODUCTION

Soybean (*Glycine max* L. Merrill) is a major legume crops in Indonesia, which is cultivated in various agro-

ecologies. Environmental conditions such as the growing season, cropping patterns, soil characteristics, temperature, photoperiod, and rainfall; determine the adaptability of each soybean variety. As a result, the performance of soybean cultivars is influenced by interaction with these environments [genotype \times environment interaction (GEI)].

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A multi-environment trial over several environments and years is a way to overcome the GEI problem, to recognize the selected genotype with high and stable performance over a wide range of environments (Gedif *et al.*, 2014; Rincent *et al.*, 2017; Tariku, 2017).

GEI is defined as the failure of genotypes to achieve a consistent phenotypic performance over diverse environments (Aswaf *et al.*, 2009), and it was resulted from the differential responses of genotypes across a range of environment. The presence of GEI was indicated by the differential ranking of genotypes over the various environments. Thus, this occurrence will reduce the correlation between phenotypic and genotypic values and complicates the selection process of the best genotypes (Rea *et al.*, 2016). GEI can be formed as qualitative (crossover) interaction or quantitative (non-crossover) interaction. Non-crossover type interaction, or the absence of GEI, is preferred when selecting genotypes for wide adaptation (Matus-Cadiz *et al.*, 2003), by selecting genotype that has good mean performance over a wide range of environments (Gurmu *et al.*, 2009). However, the presence of crossover type interaction is important, because it implies that the choice of the best genotype is determined by the environment (Malosetti *et al.*, 2012), hence, the breeding environments may be classified in to mega-environments and specifically adapted genotypes can be developed for each sub environment separately (Yan *et al.*, 2007). Mega environments is defined as a group of locations or environments that constantly share the same best genotypes (Yan *et al.*, 2000).

Numerous statistical methods have been proposed to analyze and determine the results of multi-location trials and GEI data (Ilker *et al.*, 2009; Tukamuhabwa *et al.*, 2012; Mitrovic *et al.*, 2012). There are two major groups of stability statistic, i.e. univariate and multivariate methods (Adugna 2008; Szarecki *et al.*, 2017). The newest popular multivariate method is GGE, which stands for the genotype main effect (G) and the genotype \times environment interaction (GE). GGE biplot is an effective method to quantify the GEI effects, which is based on principal component analysis (PCA). GGE analysis partitions G + GE into principal components through singular value decomposition of environmentally centered yield data (Yan, 2001). GGE-biplot graph shows which genotype won in which environments ('which-won-where'), and thus provides mega-environments identification (Yan *et al.*, 2000; Alwala *et al.*, 2010).

GGE biplot methodology has been recognize as useful method which provides comprehensive visualization of the GEI pattern of multi-environmental trials, and has been widely used in various crops, i.e., soybean (Amira *et al.*, 2013), maize (Sibiya *et al.*, 2013), mungbean (Ullah *et al.*, 2012), and sorghum (Rakshit *et al.*, 2012). This method is important for mega-environment analysis, genotype evaluation (mean vs. stability), and test environment evaluation which provides discriminating power vs. representativeness of the test environment (Yan *et al.*, 2007; Jalata, 2011; Atnaf *et al.*, 2013).

The objective of this study was to determine the seed yield stability of soybean promising lines by using GGE biplot method.

MATERIALS AND METHODS

The materials used nine soybean genotypes, consisting of seven lines and two check cultivars ('Anjasmoro' and 'Grobogan', Table 1). The field trials were conducted at eight soybean production centers (Nganjuk, Mojokerto, Blitar, Pasuruan1, Pasuruan2, Jembrana, Tabanan, and Central Nusa Tenggara) in 2015 (Table 2). The field experimental design for each location was randomized block design with four replicates. Each genotype was planted on 2.4 m x 4.5 m plot size, with 40 cm x 15 cm planting distance, and two seeds/hole. Fertilizer of 50 kg ha⁻¹ Urea, 100 kg ha⁻¹ SP36 and 75 kg ha⁻¹ KCl were applied at sowing. Pests, diseases, and weeds were controlled optimally, and drainage was applied to maintain optimum soil moisture. Pod was harvested when 95% of the leaf turned yellow in a population. Seed yield was recorded and analyzed by randomly taken from the seed yield per plot and converted to ton ha⁻¹. The following yield components were measured on all plots at each location: days to maturity, plant height, number of branches, number of nodes, number of filled pods, and 100 seed weight.

Combined analysis of variance for yield and yield components was used to determine the effects of genotype (G), environment (E) and genotype \times environment interaction. Stability analysis on seed yield was based on singular value decomposition that is represented by GGE (Genotype and Genotype \times Environment) Biplot.

The GGE model is
$$Y_{ijr} = \mu + e_j + \sum_{k=1} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ijr}$$
,

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

The results of GGE analysis were presented by analysis of variance and biplot graph. A biplot was an enhanced scatter plot that summarizing two factors in such

Table 1. Genotype and genotype code in soybean multi-environment trials at 8 locations

No.	Genotype	Genotype Code
1	G511H/Anjasmoro//Anjasmoro-2-8	G1
2	G511H/Arg//Arg///Arg///Arg-12-15	G2
3	G511H/Anj//Anj///Anj-6-3	G3
4	G511H/Arg//Arg///Arg///Arg-19-7	G4
5	G511H/Anjasmoro-1-7	G5
6	G511 H/Anj//Anj///Anj///Anjs-6-7	G6
7	G511 H/Anjasmoro-1-4-2	G7
8	'Anjasmoro'	G8
9	'Grobogan'	G9

Table 2. Location, code and characteristic of the multi-environment trials

No.	Location	Code	Soil Type	Land Type	Previous crop	Planting date / Environment	Climate ^a	Altitude (masl) ^b
1	Jati Kampir Village, Bagor District, Nganjuk Regency	E1	Regosol	Lowland	paddy	24 February 2015 (dry season I)	C3	58
2	Kedunguneng Village, Bangsal District, Mojokerto Regency	E2	Vertisol	Lowland	paddy	20 March 2015 (dry season I)	C3	72
3	Binangun Village, Kesamben District, Blitar Regency	E3	Entisol	Upland	maize	22 February 2015 (dry season I)	C3	355
4	Sumber Banteng Village, Kejayan District, Pasuruan Regency	E4	Alfisol	Upland	maize	10 January 2015 (dry season I)	E	124
5	Sumber Banteng Village, Kejayan District, Pasuruan Regency	E5	Alfisol	Lowland	soybean	26 June 2015 (dry season II)	E	124
6	Budeng Village, Jembrana District, Jembrana Regency	E6	Entisol	Lowland	paddy	10 April 2015 (dry season I)	D2	168
7	Beraban Village, Kediri District, Tabanan Regency	E7	Inceptisol	Lowland	paddy	6 March 2015 (dry season I)	D2	174
8	Segala Anyar Village, Pajut District, Central Nusa Tenggara Regency	E8	Inceptisol	Lowland	paddy	10 March 2015 (dry season I)	D3	20

Note: ^aclimate type based on Oldeman classification system: C3 = 5-6 wet months and 4-6 dry months, D2 = 3-4 wet months and 2-3 dry months, D3 = 3-4 wet months and 4-6 dry months, E = < 3 wet months and < 2 dry months; ^bmasl = meter above sea level

a way that relationships among the factors and underlying interactions between them can be visualized. The GGE biplot showed the first two principal components (PC1 and PC2, also referred as primary and secondary effects, respectively) derived from subjecting environment centered yield data (the yield variation due to GGE) to singular value decomposition. The first interaction principal component axes (IPCA1) represented genotype productivity, and the second interaction principal component axes (IPCA2) described the genotype stability (Yan *et al.*, 2000; Rakshit *et al.*, 2012).

The best genotype in each environment and mega-environment differentiation was identified by a polygon that exposed the pattern of “which-won-where” (Gedif *et al.*, 2014). “Which-won-where” graph was created by joining the most distance genotypes to form a polygon. Furthermore, perpendicular lines were drawn, starting from the origin of the biplot to each side of the polygon and dividing the biplot into several sectors with one genotype at the vertex of the polygon. Within a sector, genotype located at the vertex polygon is the best genotypes in all environments in the sector, and genotypes are well adapted in environments that are in the same sector (Yan, 2001). Performance of yield and stability of a genotype were evaluated by the method of average environment coordinate or AEC (Yan, 2001; Yan and Hunt, 2002; Yan, 2002).

RESULTS AND DISCUSSION

Analysis of variance showed that for seed yield the interaction between genotype × environment (GEI) was significant ($p < 0.001$), with GEI significantly explained 36.15% of the total variation. However, the occurrence of GEI in multi-environment trials is inevitable, due to the presence of either genetic diversity or the diverse in agro ecology. The magnitude of the GEI effect was larger than that for genotypes, indicating that there were considerable differences in genotypic response across environments. This result is in agreement with those of Rasyad and Idwar (2010) and Purbokurniawan *et al.* (2014). Another research found the E effect was about three times higher than G and GE effects (Cravero *et al.*, 2010). Suwanto (2010) also reported that E attributed to 74.43% of the total variation, while G and GE each explained for about 5.60% and 19.67% of variation, respectively.

The average seed yield of nine soybean genotypes was 2.65 ton ha⁻¹ (Table 3). The highest yield was G6 (3.07 ton ha⁻¹), followed by G7 (2.93 ton ha⁻¹), and the lowest yield was G3 (2.41 ton ha⁻¹). The yield of check cultivars G8 and G9 (Anjasmoro and Grobogan) were 2.47 and 2.44 ton ha⁻¹, respectively. A total six lines produced higher yield than the check cultivars, but only four lines (G2, G4, G6, and G7) showed higher than the average yield.

GEI refers to inconsistent phenotypic performance of genotypes across environments, which can be formed as quantitative interactions (non-crossover type) in which case there is no change in ranking of genotypes; or qualitative interactions (crossover type) when there is changes in the relative ranking of the genotypes (Ayalew *et al.*, 2014). In this study, the GEI was a crossover type, as revealed by differential yield ranking of genotypes across environments trial (Table 3). Genotype G6 was the top ranking at four environments while G1, G2, G4, and G7, each was top ranking at one environment. G7 recorded the top yield 3.72 ton ha⁻¹ at the highest yielding environment (E1) whereas G2 was the highest yielder (2.60 ton ha⁻¹) at the lowest yielding environment (E5).

Analysis of variance for GGE is presented in Table 4. The partitioning of the G + GE sum of squares through GGE biplot showed that PC1 and PC2 were significant components that explained 61.49% and 18.84% of G + GE sum of squares, respectively. The presence of GEI was clearly demonstrated by the GGE model, when the interaction was partitioned among the first two interaction principal component axes, as they were significant ($P < 0.001$). Due to the presence of GEI, yield become unpredictable and cannot be interpreted only based on genotype and environmental means (Hongyu *et al.*, 2014; Rea *et al.*, 2016). Furthermore, these imply that the interaction of nine soybean genotypes

with eight environments was predicted by the first two principal components of genotypes and environments.

The pattern of “which-won-where” polygon showed the biplot was divided into five sectors (S1 to S5) with different winning genotypes, and the environments fall into two of them (Figure 1). Seven environments (E1, E2, E3, E4, E6, E7, and E8) fell into sector 1 (S1) and the vertex genotype for this sector was genotype 6 (G6). A single environment, E5 fell into sector 5 (S5). The vertex genotype for this sector was genotype 1 (G1). These sectors (S1 and S5) were identified as two mega-environments. The polygon also explores associations between genotypes and environments. In this case, G1 was the winning genotype in E5, whilst G6 as the winning genotype in the rest of the E areas. Within S1, genotype G1, G4, and G7 performed well in all E areas except E5. Furthermore, within S5, genotype G1 and G2 were shows better performance in E5 than within other test environments. G3, G5, G8, and G9 had poor yield performance over tested environments.

The length of an environmental vector is related to the discriminating power of the environment, and it is proportional to the standard deviation of genotypes in that particular environment. This is also served as an estimation of discriminating power of the environment, but if the experimental errors of the test environments are comparable (Yan *et al.*, 2007). In this study, E3 as well as E8 as the

Table 3. Mean seed yield (ton ha⁻¹) of the 9 soybean genotypes (G1 to G9) in 8 environments (E1 to E8)

Code	Environments ^a								Mean ^b
	E1	E2	E3	E4	E5	E6	E7	E8	
G1	2.71	<u>2.67</u>	3.16	2.46	2.24	2.68	2.46	2.33	2.59cde
G2	2.95	2.24	2.87	2.69	<u>2.60</u>	2.82	2.51	2.60	2.66cd
G3	2.52	2.30	2.16	2.26	2.32	2.43	2.76	2.56	2.41e
G4	2.99	2.43	2.49	<u>2.93</u>	2.06	3.08	2.95	3.05	2.75bc
G5	3.03	2.44	2.07	1.98	2.05	2.52	2.76	3.10	2.49de
G6	3.71	2.61	<u>3.49</u>	2.42	2.03	<u>3.40</u>	<u>3.51</u>	<u>3.42</u>	3.07a
G7	<u>3.72</u>	2.25	2.96	2.72	2.44	3.17	3.20	3.03	2.94ab
G8	2.75	2.07	2.53	1.91	2.20	2.98	2.63	2.68	2.47de
G9	2.65	2.33	2.49	2.26	2.52	2.43	2.43	2.47	2.45e
Mean	3.00	2.37	2.69	2.40	2.27	2.83	2.80	2.80	2.65

Note: ^aUnderlined values are highest yields at each test environments. ^bValue within the same column followed by the same letter are not significantly different at the 0.05 level according to LSD test

Table 4. Analysis of variance for GGE

Principal component	Degree of freedom	Eigen values	Total Eigen values (%)	Cumulative (%)
PC1	14	19.4299**	61.500	61.50
PC2	12	5.9528**	18.842	80.34
Residual	30	6.213	19.658	100.00
Total Eigen values*		31.5959*		

Note: * = total of Eigen values are equal with total of G + GE sum of squares; ** = significant at α 1% ($p < 0.01$)

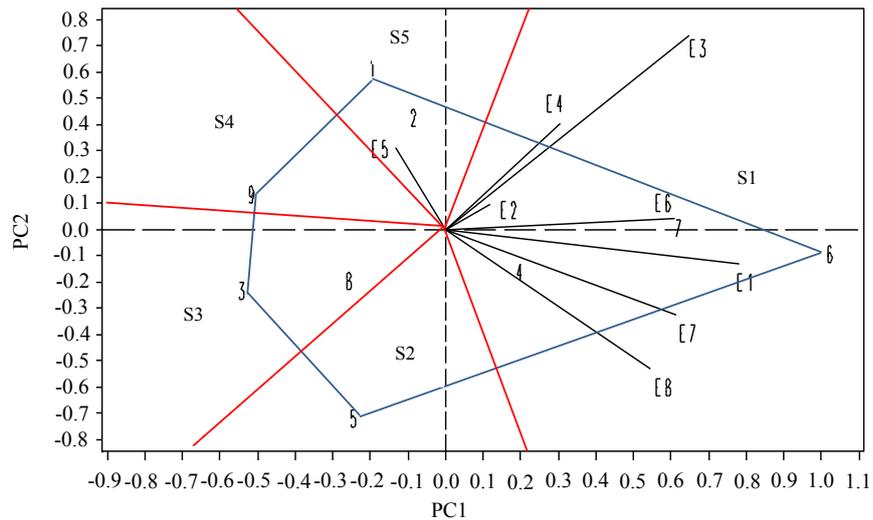


Figure 1. Polygon views of the GGE-biplot based on symmetrical scaling for the “which-won where pattern”. S = sector (S1- S5), E = environment (E1-E8), number 1-9 represent genotype 1-9

environments with longer vectors were more discriminating of the genotypes for seed yield. If an environment is close to the biplot origin, as E2 and E5 (Figure 1), meaning that those genotypes performed similarly and therefore resulted in insufficient information about the differences of genotypes' yield. Furthermore, a high discriminating environment maximizes the observed genotypic variation among genotypes for a given trait. The efficiency and accuracy within selection of genotype for a particular trait is greatly enhanced in high discriminating environments compared with non-discriminating ones (Cravero *et al.*, 2010).

Evaluation of performance for yield and stability of a genotype was illustrated by an average environment coordinate (AEC) as defined by the mean PC1 and PC2

scores of environments, and was illustrated by a small circle on the GGE biplot graph (Figure 2). AEC abscissa is the single line (blue line) that passes through the biplot origin, whereas the AEC ordinate is the single line (green line) that passes through the biplot origin and is perpendicular to the AEC abscissa (Figure 2). AEC ordinate separates genotypes which had seed yield higher than the general average with genotypes which had seed yield lower than the general average. Genotypes with seed yield higher than the general average were G1, G2, G4, G6, and G7, whereas G3, G5, G8, and G9 produce yield lower than the general average. The highest yielding genotype was G6 followed by G7. AEC ordinate, either direction away from the biplot origin indicates a greater GEI effect and reduced stability (Yan,

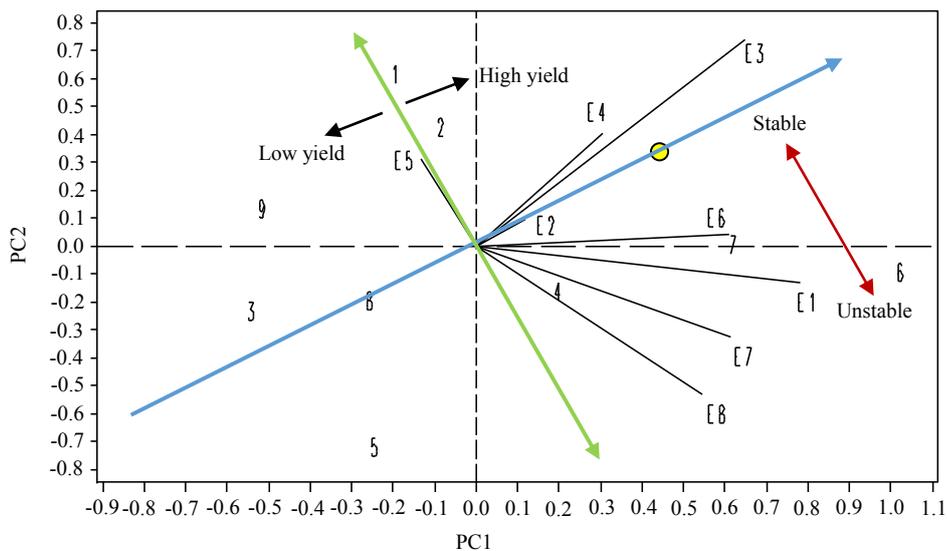


Figure 2. Average environment coordinate (AEC) of the GGE Biplot based on symmetrical scaling. Straight line (square dot) passing through AEC (black dot) with the biplot origin as AEC abscissa, a straight line (long dash) through the origin and perpendicular biplot as AEC ordinate. Directions to the AEC ordinate that move away from the biplot origin showed increased stability. AEC ordinate split genotypes under general average (low yield) and above the general average (high yield). E = environment (E1-E8), number 1-9 represent genotype 1-9

2002; Yan and Hunt, 2002). Thus, the most stable genotype was G8, followed by G3, G4, and G7.

The yield of G8 and G3 as stable genotypes, as it located near the AEC abscissa, produce yield below average. G4 which also categorized as stable, showed average performance. G7 had similar yield stability with G4, occupy the second highest yield. On the other hand, the highest yielding genotype (G6) was located far away from the AEC abscissa, indicates more responsive to the environment change (unstable). But since an ideal cultivar, as proposed by Yan *et al.*, (2007), should have both high mean performance and high stability within a mega-environment, hence, G7 was considered as the closest genotype to the ideal cultivar, followed by G4. The closest ideal genotype, G7, performed best at E1, while near average yielded at E2 and E5. According to Rakshit *et al.* (2012), it would be difficult to conceive from mean table alone (Table 3), since the presence of high crossover GEI, i.e. the rank of genotypes' performance varied depend on the testing environment. However, varieties that are adapted to wider environments become the breeders' main goal, since it is easier and cost effective both in terms of variety evaluation and seed multiplication (Matus-Cadiz *et al.*, 2003; James

and Lawn, 2011).

According to the GGE biplot analysis, there are two ideal test environments, i.e. environments with large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments) (Yan *et al.*, 2000; Yan and Rajcan, 2002). The first environment is useful for clearly sorting the differences between genotypes. This environment is useful for testing the segregated population. The second environment is useful for selecting the best genotype for a trait, without having to test at multiple locations. The selection results at this location reflect the test results at other locations (Suwanto, 2010). Thus, the ideal test environment for discriminating genotypes was E1, and E6 as the representative environment for soybean yield testing.

The analysis of variance on agronomic characters of yield components (Table 5) showed significant GEI for all parameters studied, except for number of filled pod. The mean performance of yield components of nine genotypes in pooled environments was presented in Table 6, whereas the mean performance of yield components of eight environments in pooled genotypes was presented in Table 7.

Table 5. Analysis of variance for yield components of 9 genotypes in 8 environments

Parameter	Mean Square			σ^2_e	σ^2_g	σ^2_{ge}	CV (%)
	Environment (E)	Genotype (G)	G × E				
Days to maturity (day)	58.88**	133.61**	3.33**	1.24	4.07	0.52	1.42
Plant height (cm)	3,195.99**	1,596.23**	111.04**	48.67	46.41	15.59	11.64
Number of branches/plant	7.36**	6.00**	0.97*	0.64	0.15	0.08	38.08
Number of node/plant	65.53**	23.78*	8.82**	9.58	0.46	0.00	23.54
Number of filled pod/plant	1,292.55**	331.47**	112.38ns	90.02	6.84	5.58	21.05
100 seed weight (g)	51.95**	89.67**	5.01**	1.61	2.64	2.64	7.48

Note: ** = significant at α 1% ($p < 0.01$), * = significant at α 5% ($p < 0.05$), CV = coefficient of variation

Table 6. Yield components of 9 genotypes in pooled environments

Code	Yield components					
	DTM	PH	NOB	NON	NOP	SW
G1	74-79	39.75-59.34	1.75-3.42	11.50-15.59	34.09-53.75	15.31-20.97
G2	74-78	50.50-72.34	1.45-3.42	9.75-14.67	35.95-46.25	14.44-18.94
G3	77-83	43.50-82.59	0.25-2.25	10.38-16.42	33.35-58.75	14.12-18.03
G4	75-81	48.75-73.42	1.63-3.50	11.25-15.92	30.50-55.34	14.43-18.69
G5	77-82	49.10-89.42	0.13-3.25	9.38-16.75	28.30-56.88	14.59-19.69
G6	77-82	58.75-95.25	1.75-3.67	11.50-17.75	35.27-64.50	14.26-18.13
G7	77-81	56.00-92.08	1.80-3.00	11.50-17.17	35.81-59.50	14.49-16.06
G8	81-84	56.75-91.92	1.75-2.50	11.25-17.75	36.10-59.00	15.44-17.19
G9	74-78	43.50-64.33	1.30-2.67	9.75-14.25	32.45-47.00	16.66-25.37
Mean	77	56.43	2.76	15.13	43.17	16.27

Note: DTM = Days to maturity (days), PH = Plant height (cm), NOB = Number of branches per plant, NON = Number of node per plant, NOP = Number of filled pod per plant, SW = 100 seed weight (g)

Most of genotypes have early days to maturity (< 80 days), except G8 which had medium maturity. All genotypes have large seed size (> 14g/100 seed).

The farmers' preference of soybean improved variety were not only had high yield and performance over of a wide range of environments, but also must have the early days to maturity and large seed size (Krisdiana 2014). In this study, the stable genotypes were G8, G3, G7, and

G4. However, based on their yields, only G7 with highest yield performance among them (Table 3). This genotype (G7) have early days to maturity, large seed size, and also produced the highest number of filled pods (Table 6). These agronomic characters are preferred by farmers, thus this genotype could be categorized as ideal genotype and could be recommended to be released as new improved soybean variety.

Table 7. Yield components of 8 environments in pooled genotypes

Code	Yield components					
	DTM	PH	NOB	NON	NOP	SW
E1	76-82	50.08-77.17	0.84-3.33	12.67-17.33	30.50-59.50	14.84-22.79
E2	74-82	48.25-66.75	1.75-3.25	10.25-14.75	40.50-56.88	14.49-17.76
E3	75-82	59.34-94.25	0.75-3.67	12.50-17.75	39.08-64.50	16.06-25.37
E4	76-82	44.00-71.40	0.25-2.20	10.20-14.85	28.30-40.95	15.44-16.66
E5	74-81	46.50-68.88	0.13-2.25	9.38-15.00	33.79-38.38	15.67-19.73
E6	77-82	43.50-58.75	1.75-2.75	11.75-16.75	45.50-58.50	14.12-21.50
E7	76-83	47.75-68.50	0.83-2.67	9.75-12.42	36.92-50.42	15.25-21.59
E8	78-84	39.75-69.75	1.25-2.50	10.75-14.50	37.50-59.00	15.68-23.57
Mean	78	59.9	2.11	13.15	45.06	16.97

Note: DTM = Days to maturity (days), PH = Plant height (cm), NOB = Number of branches per plant, NON = Number of node per plant, NOP = Number of filled pod per plant, SW = 100 seed weight (g)

CONCLUSION

The combined analysis showed that yield and yield components were significantly affected by GEI, except for number of filled pods. The significant GEI in soybean yield revealed differential response of the genotypes across testing environments. The "which-won-where" polygon graph of GGE results two mega-environments. The best genotype for the first mega-environment was G1 (G511H/Anjasmoro//Anjasmoro-2-8) at E5 (Pasuruan2); and the second one was G6 (G511 H/Anj//Anj//Anj//Anj//Anjs-6-7) at E1 (Nganjuk), E2 (Mojokerto), E3 (Blitar), E4 (Pasuruan1), E6 (Jembrana), E7 (Tabanan), and E8 (Central Nusa Tenggara). According to GGE stability analysis, genotypes G8 (Anjasmoro), G3 (G511H/Anj// Anj//Anj-6-3), G7 (G511 H/Anjasmoro-1-4-2), and G4 (G511H/Arg//Arg//Arg//Arg-19-7) were found to be stable. However, only G7 produced the highest yield performance across environments among the stable genotypes, and thus, it is recommended to be proposed as new soybean variety with stable yield performance. The GGE biplot method was found useful for visualize the interaction between genotypes and environments, identifying environments/locations that optimize genotypes performance, and the performance of yield and stability.

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