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GGE Biplot Analysis of Multi-Environment Yield Trials in Soybean Promising Lines

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ABSTRACT

Soybean in Indonesia is grown in diverse agro-ecological environments. The performance of soybean yield often varies due to significant genotype × environment interaction (GEI), therefore the yield stability of performance is an important consideration in the breeding program. The aim of the research was to exploring the GEI pattern and yield stability of soybean promising lines in the tropics using GGE (Genotype and Genotype by Environment Interaction) biplot method. A total of 16 soybean promising lines were evaluated in ten environments during 2016 growing season. The experiment was arranged in a randomized completely block design with four replicates. The analysis of variance revealed that environments (E) explained the highest percentage of variation (51.45 %), meanwhile the genotypes (G) and genotype × environment interactions (GEI) contributed for 3.24 %, and 14.59 % of the total variation, respectively. Seed yield of 16 soybean promising lines ranged from 2.41 to 2.83 $t.ha^{-1}$ with an average of 2.74 $t.ha^{-1}$. Joint effects of genotype and interaction (G+GE) which was partitioned using GGE biplot analysis showed that the first two components were significant, explaining 60.88 % (37.89 % PC1 and 22.98 % PC2) of the GGE sum of squares. Indonesia can be divided into at least four putative mega environments for soybean production. The GGE biplot identified G10 as high yielding and stable promising line, thus recommended to be developed in multi-environment in tropical regions of Indonesia.

Keywords: GGE biplot, high yield, soybean, stable.

INTRODUCTION

Soybean, one of the major staple foods in Indonesia, is grown in diverse agro-ecological conditions. Soybean is planted in the wetland (paddy field/upland) after one or two planting seasons of rice, or in dry land (lowland) which planted in the beginning of the rainy season. However, the largest area of soybean cultivation is in the lowland during the second dry season (June/July–September/October). Thus, a large variation appears in soybean yield level could be due to the genotype by environment interaction (GEI).

GEI is a common phenomenon in a multi-environment yield trials (Hagos and Abbay, 2013), and can be defined as the failure of genotypes to achieve consistent performance (stability) across different environments (Baker, 1988). It has been reported that the GEI may reduces the correlation between phenotype and genotype as well as complicates in breeding program, such as during the testing and selection of superior genotypes (Rao *et al*., 2011; Atnaf *et al*., 2013; Hagos and Abbay, 2013; Kumar *et al*., 2014). The significant presence of GEI has been showed in previous studies in rice (Samonte *et al*., 2005), sorghum (Rakshit *et al*., 2010), maize (Tonk *et al*., 2011), potato (Gedif *et al*., 2014), and soybean (Kandil *et al*., 21012; Adie *et al*., 2013).

Multi-environment yield trials are widely used to identify high-yielding and stable genotypes across a wide range of environments (Fan *et al*., 2007). Seed yield, an economically most important trait in soybean, is a quantitative trait which controlled by many genes and a product of interaction between genotypes and environment (Liu & Herbert, 2002; Abady *et al*., 2012; Choi *et al*., 2016). Environmental factors, such as growing season, type of soil, planting pattern, and different elevations affect the adaptation of soybean varieties in Indonesia (Adie *et al*., 2015; Kuswantoro, 2016). Environmental changes may affect both crop growth and yield due to significant GEI (Luo *et al*., 2015).

Various statistical techniques have been developed to explore the patterns of GEI from multi-environmental yield data trial, such as joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968), Additive Main Effect and Multiplicative Interaction (AMMI) (Gauch, 1992), and Genotype plus Genotype × Environment interaction (GGE) (Yan *et al*., 2000). In this study, GGE biplot was used to display graphical examination the GEI pattern of multi-environmental yield data (Yan *et al*., 2000). According to Fan *et al*., (2007), GGE can be used to identify the least discriminating locations and representing test locations. Several studies also revealed that GGE provides mega-environment analysis through the 'Which-won-where' pattern' biplot, genotype evaluation (mean vs. stability), and test environment evaluation which provides the most desirable test location (discriminating power vs. representativeness) (Yan *et al*., 2007; Amira *et al*., 2013). Furthermore, GGE analysis was based on principal component analysis (PCA) which useful to fully explore multi-environment trials (Yan *et al*., 2001).

GGE has been recognized and applied as a popular method to analyse and visualize the pattern of GEI in multi-environment yield trials in various crops (Brar *et al*., 2010; Jandong *et al*., 2011; Ullah *et al*., 2012; Bhartiya *et al*., 2017). However, the use of GGE biplot in Indonesia have not very much implemented, particularly as a tool for determining the mega environments, the best genotype in each location, and stability of soybean genotypes. The research materials used in this study were promising lines derived from crossing and followed by preliminary and advanced yield trials to obtain genotypes with high and stable productivity (yield) which in accordance with farmer's preferences. During the advanced yield trials, the fourteen promising lines have relatively exhibited high yield performance (Adie *et al*., 2014). However, the multi-location trials are required for evaluating the yield stability of each promising line. Therefore, the aims of this study was to exploring the GEI pattern and yield stability of soybean promising lines in the tropics using GGE (Genotype Main Effect and Genotype by Environment Interaction) biplot method.

MATERIALS AND METHODS

Genetic Materials

The genetic materials consist of fourteen promising lines and two check varieties i.e., Anjasmoro and Argomulyo are having high yield and well known varieties, were used in this study (Table 1).

Field Trials

The field trials were conducted at several soybean production centers in Indonesia with different soil types, average annual rainfall, and altitude. The detail description of field trial locations is presented in Table 2. The study was conducted during the dry season from February to September 2016.

Table 1. Genotype and genotype code in soybean multi location trials at 10 locations

Code	Genotype	Pedigree
G1	G 511 H/Anjs/Anjs-2-13	G511H /Anjasmoro//Anjasmoro
G2	G 511 H/Anjs-1-1	G511H /Anjasmoro
G3	G 511 H/Arg//Arg///Arg-30-7	G511H /Argomulyo//Argomulyo////Argomulyo
G4	G 511 H/Kaba//Kaba///-4-4	G511H /Kaba//Kaba
G5	G 511 H/Kaba//Kaba///Kaba////Kaba 16-2	G511H /Kaba//Kaba///Kaba////Kaba
G6	G 511 H/Anjs/Anjs///Anjs-3-3	G511H /Anjasmoro//Anjasmoro///Anjasmoro
G7	G 511 H/Anjs/Anjs///Anjs-6-13	G511H /Anjasmoro//Anjasmoro///Anjasmoro
G8	G 511 H/Anjs//Anjs-1-2	G511H /Anjasmoro//Anjasmoro
G9	G 511 H/Anjs//Anjs-5-5	G511H /Anjasmoro//Anjasmoro
G10	G 511 H/Anjs/Anjs///Anjs-6-11	G511H /Anjasmoro//Anjasmoro///Anjasmoro
G11	G 511 H/Anjs/Anjs///Anjs-8-1	G511H /Anjasmoro//Anjasmoro///Anjasmoro
G12	G 511 H/Anjs//Anjs-1-3	G511H/Anjasmoro//Anjasmoro
G13	G 511 H/Anjs//Anjs///Anjs-6-12	G511H /Anjasmoro//Anjasmoro///Anjasmoro
G14	G 511 H/Anj//Anj///Anj////Anjs-6-8	G511H /Anjasmoro//Anjasmoro///Anjasmoro////Anjasmoro
G15	Anjasmoro	-
G16	Argomulyo	-

Table 2. Location, code and characteristics of the multi-environment trials, February to September 2016

No.	Location	Code	SoilType	Land Type	Climate^a	Altitude (masl)
1.	Bojong Pondok Terong, Cipayung, Depok, West Java	E1	Ultisol	Lowland	B	330
2	Banaran Wetan, Bagor, Nganjuk, East Java	E2	Regosol	Lowland	E	58
3	Kedunguneng, Bangsal, Mojokerto, East Java	E3	Gray Grumosol	Lowland	C3	72
4	Binangun, Binangun, Blitar, East Java	E4	Alluvial	Upland	C3	355
5	Sumber Banteng, Kejayan, Pasuruan	E5	Brown Mediteran	Upland	E	124
6	Tapan Rejo, Muncar, Banyuwangi	E6	Latosol	Lowland	D2	168
7	Gambiran, Genteng, Banyuwangi, East Java	E7	Latosol	Lowland	D2	168
8	Budeng, Jembrana, Jembaran, Bali	E8	Alluvial	Lowland	D2	74
9	Berabah, Kediri, Tabanan, Bali	E9	Latosol	Lowland	D3	20
10	Segara Anyar, Pajut, Central Nusa Tenggara	E10	Regosol	Lowland	C3	24

Remarks: ^{a}climate type based on Oldeman (1974) climate classification system: B = 7–9 wet months, 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; masl = meter above sea level.

Experimental Design and Plant Cultivation

The experiment was arranged in randomized complete block design with four replications in each location. Unit plot size and planting spacing for each line were 2.0 m × 4.5 m and 40 cm × 15 cm, respectively. Two seeds per hill were sown and plants were entirely fertilized with 250 kg.ha^{-1} Ponska, 100 kg.ha^{-1} SP36, and 1 t.ha^{-1} organic fertilizer after sowing the seeds. Weeds, pests, and diseases were intensively controlled by following common monitoring system. Irrigation was applied to maintain optimum condition for soil field capacity.

Observation and Data Analysis

Plant height, days to flowering, days to maturity, number of branch per plant, number of node per plant, number of the filled pod, 100 seed weight, and seed yield per plot were observed in this study. The plant height, number of branch per plant, number of node per plant, and number of the filled pod were randomly recorded from 10 sample plants. Seed yield per plot was converted to ton.ha^{-1}. Data were analyzed using analysis of variance (ANOVA) using SAS ver. 9.1.3 (SAS, 2007). The GGE analysis was used to determine the effects of GEI on yields. The results of the GGE analysis were visualized in biplot graphs (Yan *et al*., 2000; Rakshit *et al*., 2012).

RESULTS AND DISCUSSION

Analysis of Variance and GGE

The analysis of variance for seed yield and yield components of the sixteen genotypes tested in ten environments revealed that the mean squares of environments, genotypes, and genotype × environment interactions (GEI) were highly significant for all the evaluated traits (Table 3), and accounted for 51.45%, 3.24%, and 14.59% of treatment combination sum of squares, respectively. A highly significant GEI for yield trait indicating the necessity for the further analysis of stability.

The GGE analysis partitioned the sum of squares

Table 3. Analysis of variance for yield and yield components of 16 genotypes in 10 environments

Parameter	Mean Square				
	Replication|R	Environment (E)	Genotype (G)	G × E	CV (%)
Days to flowering (day)	38.3239**	315.3618**	219.1983**	4.7240**	3.35
Days to maturity (day)	15.1385ns	78.1243**	55.6666**	26.3613**	4.31
Plant height (cm)	143.2029ns	6097.5492**	1623.7875**	167.5997**	16.22
Number of branches/plant	1.1176 **	10.0441**	5.1976**	0.9250**	32.27
Number of node/plant	22.8506 **	646.3024**	88.9627**	14.5185**	22.83
Number of filled pod/plant	980.0025 **	7333.8095**	658.7600**	110.6048**	24.15
100 seed weight (g)	4.2251 **	171.9735**	8.9358**	3.2270**	8.59
Seed yield (ton/ha)	0.2154 **	11.6502**	0.4402**	0.2202**	12.88

Remarks: CV = coefficient of variation; ** = significant at 1 % probability level ($p < 0.01$), ns = not significant

Table 4. Analysis of variance for GGE

Principal Component	Degree of freedom	Eigen values	Total Eigen values (%)	Cumulative (%)
Genotipe (G)	15	6.6033**		
G × E	135	29.7347**		
PC1a	23	13.7704**	37.89	37.89
PC2b	21	8.3512**	22.92	60.87
Residual	91	14.2164	39.13	100
Total eigen valuesc	980.0025 **	36.3380a		

Remarks: CV = coefficient of variation; ** = significant at 1 % probability level (p < 0.01), ns = not significant

of GEI into nine interaction principal components (PCs), of which the first three PCs was significant. The partitioning of the G + GE sum of squares through GGE biplot showed that PC1 and PC2 were 37.89% and 22.98% of G + GE sum of squares, suggesting significant components (Table 4).

Which-Won-Where Pattern and Mega Environment Classification

The GGE biplot was used to effectively identify the existing GEI pattern of the data (Fig.1). Polygon views of the GGE biplot showed the mega-environments and their respective highest yield cultivars (Fig. 1), and explicitly exhibited the "which-won-where pattern" as a concise summary of the GEI pattern derived from multi-environment yield trial data set.

In the present study, seven rays in Figure 1, the biplot was divided into seven sectors and the environments only into four of them. The rest three sectors in the polygon had no test environment. Four environments (E3, E7, E9, and E10), fell into the first sector or mega-environment. The first mega-environment and the vertex genotype were G10, suggesting this is the highest-yielding genotype for these four environments. The second mega-environment contained one environment (E8), and the vertex genotype was G7, suggesting this is the high-yielding genotype in E8. Other genotypes which located at this second mega-environment (G12 and G14) were also well adapted. Two environments (E1 and E6) fell into the third mega-environment. The vertex genotype for this mega-environment was G4, suggesting this genotype is the highest-yielding genotype for those environments. G11 and G13 which were also located at the similar sector, indicated those genotypes well performed at those environment. The fourth mega-environment contained three environments (E2, E4, and E5) with the two vertexes genotypes were G1 and G16. For this mega-environment, G1 had similar high yield with G16, and other genotypes (G5 and G8) also have good adaptation in those three environments. Vertex genotypes G6 and G3 were not winners at any test environment. Genotypes which fall in sectors where there

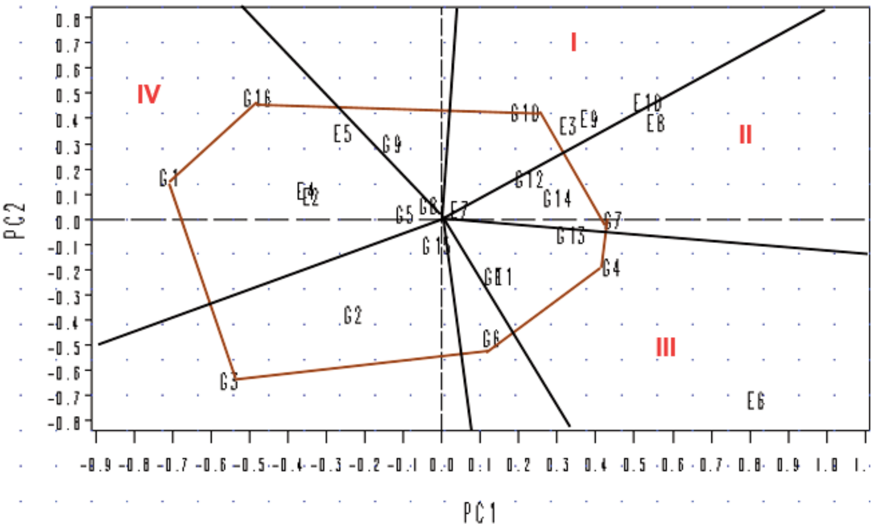

Figure 1. Polygon views of the GGE-biplot for the which-won-where pattern for genotypes and environments. Genotypes and environments code refer to Table 1 and Table 2, respectively. I = first mega-environment, II = second mega-environment, III = third mega-environment, IV = fourth mega-environment

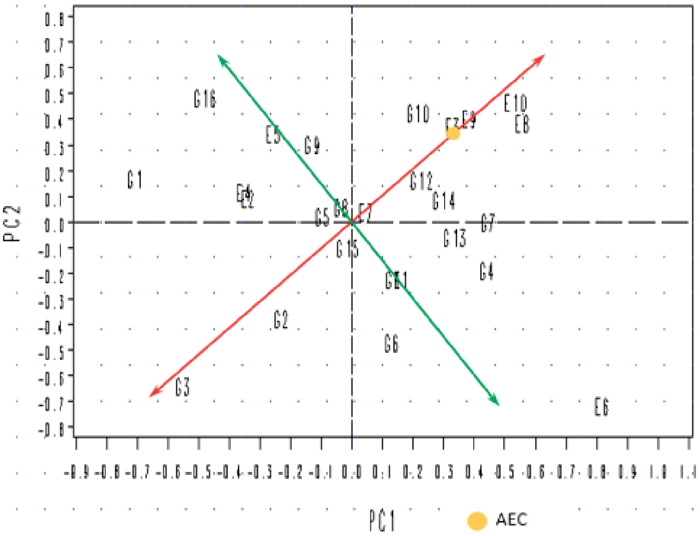

Figure 2. Polygon views of the GGE-biplot for the which-won-where pattern for genotypes and environments. Genotypes and environments code refer to Table 1 and Table 2, respectively. I = first mega-environment, II = second mega-environment, III = third mega-environment, IV = fourth mega-environment

Table 5. Seed yield of 16 soybean genotypes planted in ten environments

Code[a]	Seed yield (t ha^{-1})										Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	
G1	2.19	3.18	2.88	3.32	2.69	2.02	2.45	2.79	3.04	2.83	2.74
G2	2.14	3.00	2.84	3.06	2.18	2.77	2.15	2.81	2.78	3.05	2.68
G3	1.97	2.82	2.58	2.90	1.74	2.39	1.77	2.74	2.87	2.33	2.41
G4	2.44	2.64	3.28	2.75	1.90	3.00	2.27	3.25	3.32	3.25	2.81
G5	2.01	2.62	2.85	2.72	2.30	2.39	2.06	3.03	3.15	3.23	2.64
G6	2.49	2.94	2.80	3.03	2.14	3.16	2.06	2.89	2.94	3.37	2.78
G7	2.12	2.58	3.05	2.67	2.06	2.88	2.12	3.50	3.26	3.45	2.77
G8	2.32	2.90	3.04	3.03	2.53	2.66	2.38	3.07	3.32	3.12	2.83
G9	1.84	2.81	3.19	2.88	2.39	2.28	2.02	3.07	3.19	3.34	2.70
G10	2.14	2.79	3.29	2.87	2.38	2.46	2.03	3.49	3.35	3.52	2.83
G11	2.25	2.73	3.09	2.84	2.30	2.96	2.41	3.07	3.11	3.11	2.79
G12	1.81	2.91	2.97	3.01	1.82	2.65	2.27	3.50	3.52	3.32	2.78
G13	2.24	2.82	3.17	2.90	1.86	2.87	2.45	3.41	3.44	3.13	2.83
G14	2.22	2.75	3.29	2.85	2.22	2.82	1.75	3.26	3.52	3.27	2.80
G15	2.13	2.69	3.23	2.79	2.46	2.71	2.50	3.16	2.92	2.92	2.75
G16	2.08	3.16	3.13	3.28	2.19	1.77	2.10	3.11	3.19	3.21	2.72
Mean	2.15	2.83	3.04	2.93	2.20	2.61	2.17	3.13	3.18	3.15	2.74

Remarks: [a]Genotypes and environments code refer to Table 1 and Table 2, respectively.

were no locations at all, showed that those genotypes were poorly adapted in all tested environments.

The Performance of Yield and Yield Components and Stability of Genotypes

Yield performance and stability of soybean genotypes were graphically visualized through GGE biplot (Fig. 2). This can be evaluated by average environment coordination (AEC) method (Yan, 2001; Yan, 2002). In this biplot graph, the AEC was indicated by a yellow circle, which is defined by the average of PC1 and PC2 scores of all environments. A straight (red) line passing through AEC with the biplot origin is AEC abscissa, and point towards higher mean values (Farshadfar *et al.*, 2012). A straight (green) line through the origin and perpendicular biplot is AEC ordinate. Directions to the AEC ordinate that move away from the origin biplot showed a lower stability or greater GEI effect. AEC ordinate

Table 6. Overall yield and agronomic means of 16 soybean genotypes planted in ten environments.

Code[h]	Seed yield (t ha^{-1})						
	DTM[a]	PH[b]	NOB[c]	NON[d]	NOP[e]	SW[f]	Yield[g]
G1	80	66.68	2.54	15.21	39.56	17.55	2.74
G2	82	60.40	2.46	13.51	44.07	16.34	2.68
G3	79	64.79	2.66	13.59	36.54	15.85	2.41
G4	79	61.70	2.92	17.10	38.78	16.56	2.81
G5	80	76.43	2.04	16.68	44.98	16.64	2.64
G6	80	50.23	2.43	13.69	37.99	16.40	2.78
G7	81	68.91	2.63	14.36	43.73	15.84	2.77
G8	81	70.61	3.13	16.93	49.49	16.08	2.84
G9	80	64.17	1.85	13.71	37.20	16.46	2.70
G10	79	58.83	2.77	13.84	38.90	16.99	2.83
G11	82	63.99	2.03	12.97	44.69	16.09	2.79
G12	80	55.17	2.18	12.70	43.27	15.86	2.78
G13	80	66.33	2.96	14.81	45.69	16.05	2.83
G14	81	66.71	2.30	13.04	39.09	16.12	2.79
G15	80	69.89	2.69	15.69	48.10	15.76	2.75
G16	78	59.66	2.49	12.84	38.56	16.17	2.72
Mean	80	64.03	2.50	14.41	41.91	16.30	2.74

split genotypes with below the general average yield from those of above the general average yield.

Accordingly, the high yielding genotypes towards the upper right of AEC abscissae, such as G10, G12, G13, and G14. On the contrary, genotypes towards the lower left of AEC abscissa showed the low average yield. In this study, G8 showed the highest stability, followed by G12, G15, G5, and G10. Among the stable genotypes, G10 and G8 were the best performing genotypes in terms of seed yield, followed by G13 and G14.

The soybean seed yields of 16 genotypes planted in ten environments were presented in Table 5. The average seed yield in ten environments was ranged from 2.41 to 2.83 ton.ha^{-1} with an average of 2.74 ton.ha^{-1}. The high yielding genotypes were G8, G10, and G13. When we summarized both the yield performance and the yield stability genotypes, G8 and G10 were stable genotypes with high average yield. Nevertheless, G10 produced the highest yield in four environments, whereas G8 never won at all environments (Table 5). Furthermore, G8 was stable andconsistently had lower yield across environments than G10, thus, it could be discarded. Two genotypes, i.e., G13 and G14, were also discarded due to unstable even though it had high average yield. The other stable genotypes (G12, G15, and G5) produced a relatively low yield.

Table 6 presented the overall means of yield and yield components of 16 soybean genotypes in ten environments. The days to maturity of all tested genotypes consisted of early maturity (< 80 days) and medium maturity (80–90 days). The seed size of all tested genotypes was categorized as large seeded size (> 14 g/100 seed). Genotype 10, the stable and highest yielding genotype, had characteristics of early days to maturity (79 days) and large seed size (16.99 g/100 seed).

Discussion

Soybeans are planted in various agro-ecologies. Therefore, yield stability of a cultivar across a wide range of production environments is one of the farmer's preferences in Indonesia. In this study, the significance level of probability for seed yield from the analysis of variance showed the extended of genetic diversity in the material selection or wide diversity between the parental materials used in this study. A highly significant of the GEI for yield suggests that some genotypes were more stable than others across environments (Alghamdi, 2009).

The genotype (G) effect was small in genotypic variation, whereas environment (E) and GEI explains most of the variation. The E showed 51.45% of the variation which is more than three times of the GEI effects of the total variation, whereas the GEI accounted about 14.59% of the variation which is more than four times of the G effects. According to Kaya *et al.*, (2006), a large sum of squares for environments indicates the presence of variation in the test environments. The results of this study imply that environment and GEI are important in controling the expression of yield trait (Gedif *et al*., 2014). Similar findings in the same crop were also obtained in various studies (Asfaw *et al*., 2009; Gurmu *et al*., 2009; Bueno *et al*., 2013; Atnaf *et al*., 2013; Jandong *et al*., 2011; Bhartiya *et al*., 2017).

The large GEI effect found in this study proposes the differential yield performance among soybean genotypes across testing environments or the possible existence of different mega-environments with different winning genotypes (Yan and Kang, 2003). In this study, the seven environments out of ten had different winner genotypes. Yan and Kang (2003) reported that seed yield across environments could serve as sufficient measurement of genotypic performance when the genotype by environment interaction was absent, but in the presence of the GEI effect could complicate the selection process of superior genotypes and also may reduce the selection efficiency in breeding programs (Gauch, 2006; Rao *et al*., 2011; Kumar *et al*., 2014).

The GGE refers to the genotype main effect (G) and the genotype × environment (GE) interaction. The G and GEI are the most important sources of variation for cultivar evaluation in a multi-environment trials (Yan *et al*., 2007; Fan *et al*., 2007). In the GGE biplot, the complex GEI is simplified in different Principal Components (PCs) and the data are graphically visualized against various PCs. PC1 approximates the genotype main effects (mean performance), whereas the PC2 approximates the GEI effect (a measure of instability) for each genotype (Yan and Tinker, 2006). The soybean genotypes mean performance and stability were graphically visualized through GGE biplot (Fig 1, Fig 2). However, the GGE biplots are essential tools for addressing the mega-environment issue, by showing which cultivar won in which environments, and thus an effective visual tool in mega-environment identification (Yan *et al*., 2000).

The visualization of which-won-where patterns of multi-environment yield trials identifies the existence of different mega-environments in soybean growing regions (Fig. 1). The "which-won-where pattern" is one of most attractive GGE biplot feature which able to graphically address essential concepts, such as mega-environment differentiation and specific adaptation of a genotype (Rakshit *et al*., 2014). Figure 1 presents a polygon view of "which-won-where pattern" of sixteen soybean genotypes tested at ten environments. The polygon of the GGE-biplot for the which-won-where pattern is formed by connecting the vertex of the farthest genotypes from the biplot origin in a way that all other genotypes fall inside the polygon (Cravero *et al*., 2010). The vertex genotype(s) for each sector has (have) higher (sometimes the highest) yield than the others in all environments that fall in the sector (Yan, 2002).

The polygon view of this biplot (Fig.1) showed that the test environments and genotypes fell into four and seven sectors, respectively. Three of the sectors in the polygon had no test environment, hence there were four constructed mega-environments with different "winning" genotypes. The term mega-environment defines the partition of a crop growing region into different target zones. It consists of an irregular polygon and lines drawn from the biplot origin (Gauch and Zobel, 1996). According to Yang and Tinker (2006), the most responsive genotypes were located at the vertexes of the polygon, since they have the longest distance from the origin in their direction. Thus, the G10 was the most responsive genotype in the E3, E7, E9, and E10. Furthermore, the G7 was the most responsive genotype in E8, whereas the G4 was the most responsive genotype in E1 and E6. In addition, G1 and G6 were two of the most responsive genotypes in E2, E4, and E5.

The evaluation of genotypes for the yield potential and stability was examined by an average environment coordination method (Yan, 2002). In this study, G10 was showed the highest yield and stable among all genotypes. Thus, G10 was the most desirable genotype and categorized as "ideal" genotype. An ideal genotype is defined as the genotype that produced the highest yielding across test environments, which should have the highest mean performance and be absolutely stable (Yan and Kang. 2003). So far, the soybean breeding program in Indonesia has been focused on developing a high yielding and stable genotype, in accordance with the farmer's preferences. A number of soybean superior varieties with targeted characters have been released (ILETRI, 2015). Superior variety is recognized as an important component of technology which easily adopted, compatible with other technological innovations, environmentally friendly, and sustainable (Jain and Kharkwal, 2012; Chikoye *et al*., 2017).

In this study, based on the yield components, G10 showed early days to maturity and also has large seed size. The user's preferences are high yielding variety, and also with characteristics of large seed size and early days to maturity (Adie *et al*., 2015). The soybean farmers prefer an earliest maturing variety due to avoid the drought stress and pest infestation through drought escape mechanism (Adie and Krisnawati, 2017; Purwantoro *et al*., 2017) especially during the dry season. Early maturing variety also useful to increase the cropping index especially in regions with limited water availability (ILETRI, 2011). Beside early days to maturity, soybean with large seed size is also desirable for tempeh production (Antarlina *et al*., 2002; Krisnawati and Adie, 2015). Based on these facts, therefore G10 was potentially developed and introduced as a new cultivar, particularly for tropical regions.

CONCLUSIONS

The yield performance of soybean was highly influenced by GEI effects. The GGE analysis revealed that Indonesia can be divided into at least four putative mega-environments for soybean production. G10 was suitable with farmers' preference, stable and has higher yield compared with other genotypes, therefore it could be recommended for developing and releasing as new stable and high yielding variety for tropical regions.

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