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GENOTYPE BY ENVIRONMENT INTERACTION AND YIELD STABILITY OF SOYBEAN GENOTYPES

Interaksi Genotipe Kedelai dengan Lingkungan dan Stabilitas Hasilnya

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ABSTRACT

Soybean breeding program in Indonesia has been actively involved in improving the genetic yield potential to meet the needs of farmers in different parts of the country. The study aimed to determine the presence of soybean production mega-environments and to evaluate the yield performance and stability of 12 soybean genotypes. Soybean yield performances were evaluated in eight production centers in Indonesia during 2013 growing season. The experiment in each location was arranged in a randomized complete block design with four replications. Parameters observed included grain yield and yield components. The yield data were analyzed using GGE biplot and the yield components data were analyzed using analysis of variance. The results showed that the yield performances of soybean genotypes were highly influenced by genotype-environment interaction (GEI) effects. The yield components were significantly affected by GEI except per plant branch number. The partitioning of the G + GE sum of squares showed that PC1 and PC2 were significant components which accounted for 57.41% and 18.55% of G + GE sum of squares, respectively. Based on the GGE visual assessment, agro-ecology for soybean production in Indonesia was divided into at least three mega-environments. Genotypes 8 and 2 were the best yielding genotypes in the most discriminating environment, but adapted to specific environment, thus highly recommended for that specific location. Genotypes 9 and 10 were stable and had relatively high yield performances across environments. Those genotypes would be recommended to be proposed as new soybean varieties.

Keywords: environment, genotype, genotype-environment interaction, *Glycine max,* yields

ABSTRAK

Program pemuliaan kedelai di Indonesia difokuskan pada peningkatan potensi hasil genetik dalam rangka memenuhi kebutuhan petani di berbagai daerah. Tujuan penelitian adalah untuk mengidentifikasi keberadaan lingkungan mega-produksi dan mengevaluasi kinerja dan stabilitas hasil 12 genotipe kedelai. Penelitian dilakukan di delapan daerah penghasil kedelai utama di Indonesia pada musim tanam 2013. Penelitian di setiap lokasi menggunakan rancangan acak kelompok dengan empat ulangan. Parameter yang diamati meliputi hasil biji dan komponen hasil. Hasil biji dianalisis menggunakan GGE biplot, sementara data komponen hasil dianalisis menggunakan analisis varian. Hasil penelitian menunjukkan bahwa hasil biji kedelai dipengaruhi oleh efek interaksi antara genotipe dan lingkungan (GEI). Komponen hasil dipengaruhi oleh GEI, kecuali jumlah cabang per tanaman. Pemecahan nilai jumlah kuadrat G + GE menunjukkan bahwa PC1 dan PC2 menjadi faktor nyata yang dapat menjelaskan masing-masing 57,41% dan 18,55% dari total jumlah kuadrat G + GE. Berdasarkan visualisasi GGE biplot, agroekologi untuk produksi kedelai di Indonesia paling sedikit terbagi menjadi tiga mega-lingkungan. Genotipe 8 dan 2 berdaya hasil paling tinggi dan beradaptasi pada lingkungan spesifik sehingga direkomendasikan untuk lingkungan spesifik. Genotipe 9 dan 10 teridentifikasi stabil dan berdaya hasil tinggi pada lintas lingkungan. Kedua genotipe tersebut dapat direkomendasikan untuk dilepas sebagai varietas unggul baru.

Kata kunci: genotip, Glycine max, hasil, interaksi genotipe-lingkungan, lingkungan

INTRODUCTION

Soybean is one of the three most important food crops in Indonesia after rice and maize. Soybean production is dealing with two issues, which are the decrease in total acreage and the increase in soybean consumption. On the other hand, the number of people who consume processed soybean products also increased, even the processed soybean products have already spread beyond the island of Java. The combination of the level of consumption per year and the increasing population triggers the increased domestic soybean demand, and so far is unable to be fully met by domestic production. Hence, a key objective of soybean breeding in Indonesia is increasing yields per unit area.

In Indonesia, soybean is grown in diverse agro-ecological environments. The largest soybean area is in the lowland cultivated in the second dry season (June/July–September/October) following the cropping pattern of rice – rice – soybean. Fertile land, mainly the lowland such as paddy field, is the largest contributor of the national soybean production, i.e. 62% from the total 8.1 million hectares of lowland areas (Mulyani et al. 2016; Mulyani, et. al. 2009). This is due to (1) almost no important problems regarding with soil nutrients, (2) nearby accessable to the soybean industry for both food and feed raw materials, and (3) high productivity per unit area.

Soybean grain yield as a complex character is associated with some yield components and influenced by environmental fluctuations (Choi et al. 2016; El-Abady et al. 2012; Obalum et al. 2011). Soybean yield potential in various agro-ecological environments vary depending on the compatibility with the agro-ecosystem, biotic and abiotic stress magnitudes, and level of crop management (Penalba et al. 2007; Zanon et al. 2016). Environmental variables such as soil type, growing season, planting pattern and elevation often become a determinant of suitability adaptation of soybean varieties in Indonesia (Adie et al. 2013; Kuswantoro 2016). It also leads to the interaction between genotype and environment (GEI), which caused difficulties in selecting superior lines (Kumar et al. 2014). Optimization of such diverse environments can be achieved by the provision of high yielding and stable adaptating soybean varieties. So far, the Indonesian government has released 90 soybean improved varieties. Superior/improved variety is recognized as a cultivation technology component which is inexpensive, easy to adopt and compatible with other technological innovations as well as safe for the environment (Jain and Kharkwal 2003).

Multi-environment yield trials are widely used for selecting superior soybean advanced lines to be released as a new variety for target environments in Indonesian soybean breeding programs. Numerous methods for analyzing soybean multi-environment trial data have been developed to expose the patterns of GEI, for instance joint regression (Eberhart and Russell 1966; Finlay and Wilkinson 1963; Perkins and Jinks 1968), AMMI model analysis (Gauch 1992), and the newest and most popular method of GGE biplot (Yan et al. 2000) GGE (genotype main effect plus genotype by environment interaction) shows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions (Ding et al. 2007). The biplot tool is being increasingly used by plant breeders and agricultural researchers since its use in mega-environment investigation, genotype evaluation and test location evaluation (Yan et al. 2007). A mega-environment is defined as a group of locations that consistently share the same best cultivar(s) (Yan and Rajcan 2003).

The multi-environment analysis, especially GGE biplot, has been used in recent years for explaining GEI and quantifying the adaptability and stability of tested soybean genotypes (Asfaw et al. 2009; Atnaf 2013; Bhartiya et al. 2017). However, the use of GGE biplot in Indonesia has not been much documented, particularly as a tool for determining the mega-environments and the best performing soybean genotypes in each location. The aims of this study were to determine the presence of soybean production mega-environments and to evaluate the yield performances and the yield stability of soybean lines.

MATERIALS AND METHODS

The genetic materials used consisted of ten soybean promising lines which were developed in 2008 to obtain high yielding and early maturing varieties, i.e. Sin/Arg-8, Sin/Mal-16, Sin/Mal-19, Arg/Sin-34, Arg/Sin-47, Arg/Sin-52, Mal/Sin-66, Mal/Sin-68, L.Jateng/Sin-85, and Arg/Sin-98 (Table 1). Anjasmoro and Grobogan varieties as high yielding and popular varieties were used as check varieties.

The field trials were conducted at eight locations of soybean production centers in Indonesia. The detail

Table 1. Genetic materials used for soybean multi-location trials at eight locations during dry season, March–September 2013.

Code	Genotype	Pedigree	Source[a]	Remark
1	Sin/Arg-8	Sinabung × Argomulyo	ILETRI	Promising line
2	Sin/Mal-16	Sinabung × Malabar	ILETRI	Promising line
3	Sin/Mal-19	Sinabung × Malabar	ILETRI	Promising line
4	Arg/Sin-34	Argomulyo × Sinabung	ILETRI	Promising line
5	Arg/Sin-47	Argomulyo × Sinabung	ILETRI	Promising line
6	Arg/Sin-52	Argomulyo × Sinabung	ILETRI	Promising line
7	Mal/Sin-66	Malabar × Sinabung	ILETRI	Promising line
8	Mal/Sin-68	Malabar × Sinabung	ILETRI	Promising line
9	L.Jateng/Sin-85	L.Jateng × Sinabung	ILETRI	Promising line
10	Arg/Sin-98	Argomulyo × Sinabung	ILETRI	Promising line
11	Anjasmoro	-	ILETRI	Released variety
12	Grobogan	-	ILETRI	Released variety

[a]ILETRI = Indonesian Legume and Tuber Crops Research Institute.

Table 2. Characteristics of the locations used for multi-environment trials of advanced soybean lines, March–September 2013.

Location	Code	Soil type	Land type	Climate[a]	Altitude (m asl[b])
Bojong Pondok Terong Village, Cipayung District, Depok Regency, West Java	S1	Ultisol	Lowland	B	330
Ngawen Village, Ngawen District, Klaten Regency, Central Java	S2	Entisol	Lowland	D3	62
Jati Kampir Village, Bagor District, Nganjuk Regency, East Java	S3	Regosol	Lowland	C3	58
Kedunguneng Village, Bangsal District, Mojokerto Regency, East Java	S4	Gray Grumosol	Lowland	C3	72
Kemiri Village, Kepanjen District, Malang Regency, East Java	S5	Association of Alfisol and Inceptisol	Lowland	C3	335
Binangun Village, Binangun District, Blitar Regency, East Java	S6	Alluvial	Upland	C3	355
Tapan Rejo Village, Muncar District, Banyuwangi Regency	S7	Latosol	Lowland	D2	168
North Ampenan Village, Ampenan District, Mataram Regency, West Nusa Tenggara	S8	Vertisol	Lowland	D3	62

[a]Climate 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, [b]m asl = meter above sea level.

description of each test location is presented in Table 2. The study was conducted for two growing seasons from March to September 2013. The study sites had different soil types, mean seasonal rainfalls and altitudes.

The experiment in each of the eight study sites was arranged in a randomized complete block design with four replications. Each line was planted using 2.4 m × 4.5 m plot size, 40 cm × 15 cm plant spacing, two grains per hill. Fertilizers used consisted of 50 kg ha^{-1} urea, 100 kg ha^{-1} SP36 and 75 kg ha^{-1} KCl that were applied after sowing the grains. Weeds, pests and diseases were intensively controlled. Irrigation was applied to maintain optimum soil moisture.

Parameters observed included plant height, per plant pod number, per plant branch number, per plant total node number, 100 grain weight, and per plot grain yield. Grain yield per plot was converted to t $ha^{-1.}$ Data were then analyzed using analysis of variance (ANOVA). GGE analysis was used to determine the effects of GEI on yields. The results were visualized in biplot graphs (Rakshit et al. 2012; Yan et al. 2000).

The GGE model was as the following:

$$\boldsymbol{Y}_{ijr} = \boldsymbol{\mu} + \boldsymbol{e}_j + \sum_{k=1}^{\chi} \boldsymbol{\lambda}_k \boldsymbol{\alpha}_{ik} \boldsymbol{\gamma}_{jk} + \boldsymbol{\varepsilon}_{ijr}$$

$\boldsymbol{Y}_{ijr}$ = observation of the r^{th} replicate of the i^{th} genotype in the j^{th} environment,
$\boldsymbol{\mu}$ = the overall means,
$\boldsymbol{e}_j$ = main effect of the j^{th} environment,
χ = matrix rank $\{gge\}_{ij}$ when $\{gge\}_{ij} = g_i + ge_{ij}$,
$\boldsymbol{\lambda}_k$ = the singular value for principal component *k*,
$\boldsymbol{\alpha}_{ik}$ = the eigenvector score for genotype *i* and component *k*,
$\boldsymbol{\gamma}_{jk}$ = the eigenvector score for environment *j* and component *k*, and
$\boldsymbol{\varepsilon}_{ijr}$ = the error for genotype *i* and environment *j* and replicate *r*.

RESULTS AND DISCUSSION

Analysis of Variance and GGE

The analysis of variance for grain yield and yield components of the 12 soybean genotypes tested in eight environments showed that the mean squares of environments, genotypes and genotype × environment interactions (GEI) were highly significant (Table 3) except for branch number per plant, The analysis of variance revealed that environments, genotypes and genotype × environment interactions accounted for 64.4%, 10.8% and 24.8% of sum of squares, respectively. A highly significant GEI indicates the necessity for further analysis for yield stability. The significance level of probability for grain yield indicates the extended genetic diversity of the parental materials used in this study.

In this present study, the GEI was small in genotypic variation, whereas genotype (G) and environment (E) explained most of the variations. This indicated that genotypes and environments are both important in governing the expression of this trait (Gedif et al.

Table 3. Analysis of variance for yield and yield components of 12 soybean genotypes tested in eight environments.

Parameter	Mean squares			CV (%)
	Environment (E)	Genotype (G)	G × E	
Days to maturity (days after planting)	46.24**	213.94**	3.38**	0.78
Plant height (cm)	1,310.44**	1,349.03**	76.34**	7.23
Branch number per plant	30.81**	4.43**	0.56^{ns}	25.42
Node number per plant	630.28**	164.86**	16.85**	18.49
Filled pod number per plant	5,311.03**	964.23**	146.18*	22.65
100 grain weight (g)	54.90**	147.56**	6.12**	8.50
Grain yield (t/ha)	46.3**	9.05**	20.64**	15.72

*, ** = significantly different at 5% and 1% level, respectively; ns = not significant; CV = coefficient of variation.

2014). Another report demonstrated that GEI effects were higher than those shown by the genotypic and the environmental effects (Bhartiya et al. 2017), and environmental effect was three times higher than the G and GE effects (Cravero et al. 2010; Suwarto 2010).

The GGE analysis partitioned the sum of squares of GEI into seven interaction principal components (PCs), of which the first two PC were significant (Table 4). The partitioning of the G + GE sum of squares through GGE biplot showed that PC1 and PC2 were significant components that explained 57.41% and 18.55% of G + GE sum of squares, respectively. This result revealed that there were differential yield performances among soybean genotypes across testing environments due to the presence of GEI. According to Gauch (1992), the presence of GEI could complicate the selection process of superior genotypes and might reduce the selection efficiency in a breeding program.

Table 4. Analysis of variance for GGE.

Principal component	Degree of freedom	Sum of Squares	P > F
Genotype (G)	11	9.05**	<0.0001
G × E	77	20.64**	0.0013
PC1	17	17.05**	0.0000
PC2	15	5.51**	0.0042
Residual	45	7.01	
Total eigen values*		29.69*	

PC = Principal component; * = total of eigen values are equal with total of G + GE sum of squares; ** = significantly different at 1% level.

Which-Won-Where Pattern and Mega-Environment Classification

The GGE biplot was used to effectively identify the existing GEI pattern of the grain yield data (Figure1). GGE biplot is an essential tool for addressing the mega-environment issues, by showing which cultivar won in which environments, and thus it is an effective visual tool in mega-environment identification (Yan et al. 2000). The term of mega-environment analysis 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). Polygon views the GGE biplot showing the mega-environments and their respective highest yielding cultivars (Figure 1), and explicitly displays the "which-won-where pattern" as a concise summary of the GEI pattern derived from multi-environment yield trial data set. The "which-won-where pattern" is one of the most attractive GGE biplot features which is able to graphically address essential concepts, such as mega-environment differentiation and specific adaptation of a genotype (Rakshit et al. 2012).

The polygon of the GGE biplot for the which-won-where pattern is formed by connecting the markers of the genotypes that are further away from the biplot origin in a way that all other genotypes are contained in the polygon (Cravero et al. 2010). In the present study, five lines in Figure 1 divided the biplot into five sectors or five mega-environments (I to V) and the environments fall only into three of them (I, III and IV). The vertex genotypes in this study were genotypes 11, 8, 2, 3 and 12. According to Yan and Tinker (2006), the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction. Three environments (S3, S4 and S5) fell into the first mega-environment. The vertex genotype for this mega-environment was genotype 11. Another genotype (genotype 8) also performed well in those three environments. Four environments (S2, S6, S7 and S8) fell into the second mega-environment and the vertex genotype for this mega-environment was genotype 2, suggesting that this is the most responsive genotype for these four environments. Genotype 1 which also located in this mega-environment, performed well in S2, S6, S7 and S8. A single environment, S1 fell into the third mega-environment. The vertex genotype for this mega-environment was genotype 3 suggesting that this genotype is classified as a winning genotype for this

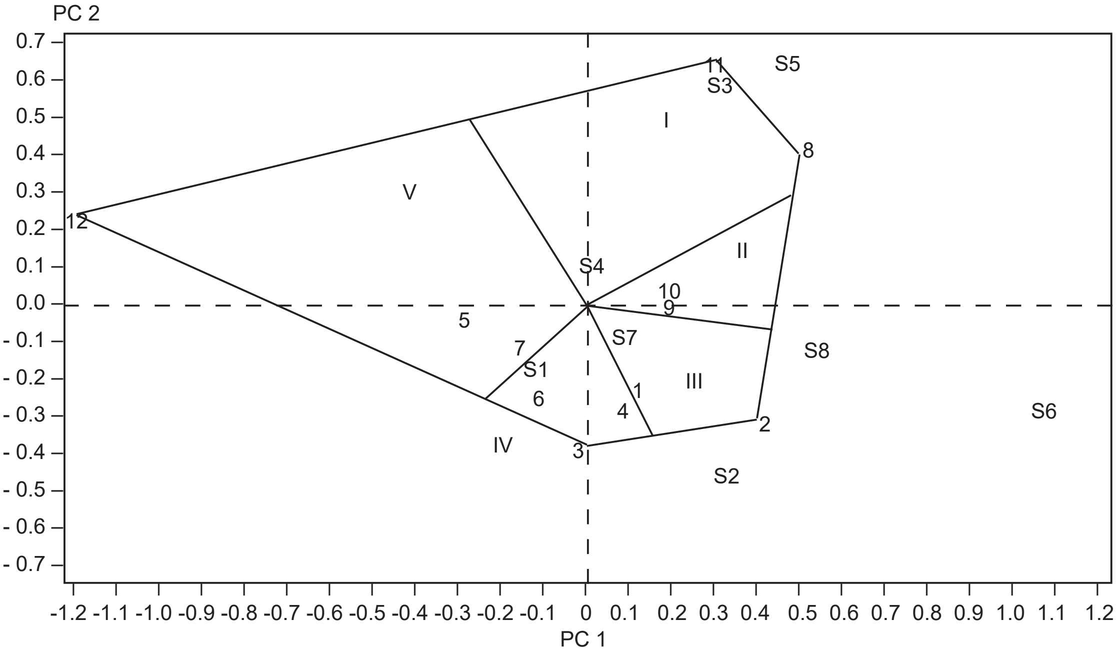

Fig. 1. Polygon views of the GGE-biplot of grain yield for the which-won-where pattern for genotypes and environments. PC1 = first principal component, PC2 = second principal component, S1 = Depok, S2 = Klaten, S3 = Nganjuk, S4 = Mojokerto, S5 = Malang, S6 = Blitar, S7 = Banyuwangi, S8 = Mataram.

single environment. Genotypes 4 and 6 also located at the similar sector, indicated that those genotypes performed well at those environments. Other genotypes (genotypes 5, 7 and 12) fell in sectors where there were no locations at all, showing that those genotypes were poorly adapted in all of the eight tested environments.

Yield and Yield Component Performances and Yield Stability

Yield performance and yield stability of the tested soybean genotypes were graphically visualized through GGE biplot (Figure 2). This can be evaluated by the average environmental coordinate (AEC) method (Yan 2002, 2001). In this method, a straight line passing through AEC with the biplot origin is as AEC abscissa, and a straight line through the origin and perpendicular biplot is as AEC ordinate. Directions to the AEC ordinate that move away from the origin biplot showed increased stability. AEC ordinate splitted the genotypes under and above the general yield average.

Referring to Figure 2, seven high yielding soybean genotypes (genotypes 1, 2, 4, 8, 9, 10 and 11) performed over the general yield average. Genotype 8 demonstrated the highest yield, but adapted to a specific environment. This genotype adapted to lowland with C3 climate, and could be cultivated in the area up to 400 m asl with the soil type of Regosol or association of Alfisol and Inceptisol, such as in Bagor District (Nganjuk) or Kepanjen District (Malang). Another high yielding genotypes which also adapted to specific environments were genotypes 2 and 11. These results showed a number of similarities with the previous reports showing that three top high yielding genotypes out of twenty soybean genotypes tested were unstable their performances when evaluated across different locations, and hence such genotypes were recommended for a specific environment (Gurmu et al. 2009).

In this study, genotypes 9 and 10 showed the highest yield stability and relatively high yield. The poorest yield performance and also the unstable genotype was genotype 12. Numerous studies have been conducted to investigate soybean yield stability. Atnaf (2013) found three ideal soybean genotypes as it exhibits both high mean yield and high stability performances across the test environments. Another study reported that soybean genotype C1 (PS1539) was considered as an ideal genotype with high yield and high stability as demonstrated by low GEI (Bhartiya et al. 2017). Asfaw et al. (2009) reported that GEI was an important source of soybean yield variation. The use of biplots was effective to graphically visualize the GEI pattern of genotypes and environments, and to determine the stability and adaptability of the genotypes.

Table 5 presents the grain yield of each soybean genotype in each location. Average of 12 genotypes, the

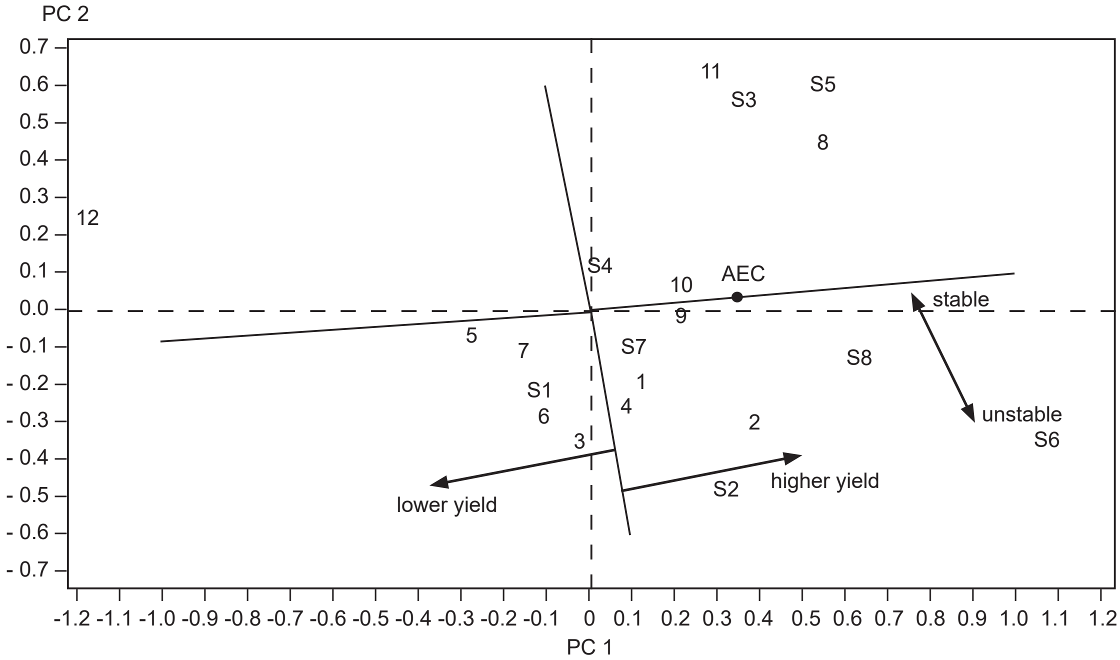

Fig. 2. Average environment coordinate (AEC) of the GGE biplot based on symmetrical scaling. The genotypes and environmental codes used in this figure can be referred to Table 1 and Table 2, respectively.

Table 5. Mean grain yield of 12 soybean genotypes tested in eight environments.

Code	Genotypes	Grain yield (t ha^{-1})								Mean
		S1	S2	S3	S4	S5	S6	S7	S8	
1	Sin/Arg-8	2.12	2.42	3.09	2.39	2.32	3.07	2.36	2.83	2.58 ab
2	Sin/Mal-16	2.15	2.42	2.60	2.35	2.72	3.11	2.29	3.63	2.66 ab
3	Sin/Mal-19	2.31	2.37	2.57	2.19	2.47	2.99	2.17	2.84	2.49 b
4	Arg/Sin-34	2.21	2.54	2.91	2.08	2.41	2.72	2.26	3.40	2.57 ab
5	Arg/Sin-47	2.12	2.15	3.00	2.12	2.21	2.28	2.23	3.19	2.41 bc
6	Arg/Sin-52	2.18	2.23	2.74	2.35	2.31	2.63	2.17	3.26	2.48 b
7	Mal/Sin-66	2.37	2.33	3.11	2.16	2.27	2.52	2.09	3.07	2.49 b
8	Mal/Sin-68	2.21	2.23	3.23	2.60	3.28	3.05	2.27	3.49	2.79 a
9	L.Jateng/Sin-85	2.32	2.21	3.15	2.46	2.58	2.98	2.37	3.32	2.67 ab
10	Arg/Sin-98	2.14	2.21	3.04	1.94	2.76	2.98	2.16	3.21	2.56 ab
11	Anjasmoro	1.92	2.00	3.58	2.19	3.03	2.84	2.13	3.10	2.60 ab
12	Grobogan	2.35	1.69	2.54	2.43	2.30	1.34	2.07	2.45	2.15 c
	Mean	2.20	2.23	2.96	2.27	2.56	2.71	2.21	3.15	2.54

Notes : all S symbols refer to table 2.

Mean values with the same letter within a column are not significantly different at 5% probability level.

grain yields across eight environments ranged from 2.20 t ha^{-1} in environment 1 (S1) to 3.15 t ha^{-1} in environment 8 (S8), suggesting that there was almost 1 t ha^{-1} difference between these two environments.

Table 6 presents the grain yield and yield components of the 12 soybean genotypes tested in eight environments. Genotype 8, as the unstable genotype but showed the highest yield was early maturing comparable to Grobogan, but nine days earlier than that of Anjasmoro. Genotype 8 also had medium grain size compared to Anjasmoro and Grobogan. Furthermore, the stable genotypes (9 and 10) with high per se performances (over the general mean) demonstrated medium maturity and medium grain size.

Table 6. Grain yield and agronomic performance means of 12 soybean genotypes tested in eight environments.

Code	Genotypes	Days to maturity (DAP)$^{a)}$	Plant height (cm)	Branch number per plant	Node number per plant	Filled pod number per plant	100 grain weight (g)	Grain yield (t ha^{-1})
1	Sin/Arg-8	77.22	73.68	2.84	15.44	42.09	12.47	2.58
2	Sin/Mal-16	77.66	66.51	3.09	18.06	49.28	11.49	2.66
3	Sin/Mal-19	77.78	75.20	3.69	20.55	52.44	11.51	2.49
4	Arg/Sin-34	78.09	71.80	3.30	20.87	50.07	12.36	2.57
5	Arg/Sin-47	77.34	73.91	3.04	16.50	39.98	12.85	2.41
6	Arg/Sin-52	77.19	72.22	3.14	17.58	42.44	11.96	2.48
7	Mal/Sin-66	80.72	69.48	3.70	20.84	42.66	13.86	2.49
8	Mal/Sin-68	74.88	73.22	2.57	15.22	38.67	11.80	2.79
9	L.Jateng/Sin-85	80.25	72.74	3.43	19.54	50.45	12.26	2.67
10	Arg/Sin-98	80.78	76.01	3.13	17.87	43.06	12.98	2.56
11	Anjasmoro	83.50	76.71	3.10	18.73	52.68	13.58	2.60
12	Grobogan	74.44	52.55	2.53	14.22	37.64	19.43	2.15
	Mean	78.32	71.17	3.13	17.95	45.12	13.05	2.54
	LSD $^{b)}$	0.669	3.884	0.537	2.414	7.220	0.896	0.275

$^{a)}$ DAP = days after planting.

$^{b)}$ LSD = Least significant difference at 5% probability level.

CONCLUSION

Yield performances of soybean genotypes were highly influenced by GEI effects. Indonesia can be divided into at least three mega-environments for soybean production. Among 12 tested soybean genotypes, genotypes 9 and 10 demonstrated the highest yield stability and relatively high yield. Genotype 12 showed the poorest and unstable yield performance, while genotypes 8 and 2 were highly recommended for specific locations. Genotypes 9 and 10 demonstrated stable performance with relatively high yield and were recommended to be released as new soybean varieties.

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