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# Oil Content and Potential Region for Cultivation Black Soybean in Java as Biofuel Alternative

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#### Abstract

Oil content from black soybean (*Glycine max* (L.) Merr.) seed is potential as an alternative renewable energy source. The objectives of this study were to identify content of seven black soybean genotypes and to analysis stability of genotypes, widely adapted or specifically adapted. Oil content was determined using proximate analysis and observation procedure base on AOAC standard. Field experiments were conducted at ten locations across the island of Java, Indonesia i.e. Banyuwangi, Bogor, Cianjur, Cirebon, Jatinangor 1, Jatinangor 2, Madiun, Majalengka, Ngawi, and Yogyakarta. The experimental design was arranged in randomized complete block design with four replication at each environment was employed. The genotype main effect plus genotype-by-environment interaction biplots were applied to analyze and visualize pattern of the interaction component. The result elucidated that black soybean genotype that have high yield is KA 6 (2.21 t · ha<sup>-1</sup>), and potential to produce oil in amount of 445.65 L · ha<sup>-1</sup>. GGE biplot identified that KA 6 adaptive to be cultivated in the regions of Cirebon, Madiun and Banyuwangi, and environment similar to the three regions. The ideal environment in terms of being the most representative of the overall environments is Cianiur.

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\* Corresponding author. Tel.: +62 813 2104 1098. *E-mail address:* chindyuz@gmail.com Keywords: Black soybean; biofuel; GGE biplot; oil content.

#### Nomenclature

**GGE** Genotype plus Genotype-by-Environment interaction

**PC** Principal Component

AEC Average Environment Coordinate
GEI Genotype-by-Environment Interaction
AOAC Association of Official Analytical Chemists

t ton =  $10^3$  kg

#### 1. Introduction

Indonesia has potency to develop black soybean (*Glycine max* (L.) Merr.), due to its commodity has already known and cultivated in Indonesia. Soybean seed contains 38 % to 44 % protein and 18 % to 23 % oil on a dry basis [1]. Protein and oil content are two main traits of seed quality in soybean. In Indonesia, black soybean usually use for raw material of soy sauce. It can produce natural black colour instead of using yellow soybean.

Recently, beside used as a raw material of food, black soybean also can use as a biofuel alternative. Oil content of black soybean seed is source for biofuel. Despite the relatively low oil content of the seed (about 20% on moisture-free basis), black soybean is one of the largest source of edible oil and account for roughly 50% of the total oilseed production of the world [2]. Development of soybean as energy source in Indonesia is needed. Therefore, high oil content, high yield, stable and wide or specific adaptation are required to develop black soybean.

Yield performance of black soybean influenced by genotype, environment, and genotype-by-environment interaction. The GEI is a major problem to identify superior genotypes for quantitative traits, because it reduces the association between genotypic and phenotypic values [3]. Multilocation trials are conducted to evaluate genotypes which are stable or adapted to a wide or specific region. A genotype grown in different environments will frequently show significant fluctuations in yield performance [4,5].

Stability of a genotype across a range environment is important for variety recommendation. A stable genotype is capable of maintaining performances in all environment [6,7]. To development of black soybean in Indonesia need to know the potential of each region. Identification of stable and widely adapted and unstable but specifically adapted genotypes can give the information about potential region. The objectives of this study were to determine oil content of seven black soybean genotypes and to identify genotypes that are stable, widely adapted or specifically adapted.

#### 2. Material and method

## 2.1. Analysis of oil content

Oil content was determined using proximate analysis and observation procedure base on AOAC [8]. The analysis was conducted at Laboratory of Crop Physiology Indonesian Vegetable Research Institute, Lembang, Bandung.

## 2.2. Analysis of stability and adaptability

Field experiments were conducted at ten locations across the island of Java, Indonesia i.e. Banyuwangi, Bogor, Cianjur, Cirebon, Jatinangor 1, Jatinangor 2, Madiun, Majalengka, Ngawi, and Yogyakarta. Treatment consists of five Unpad lines, i.e. CK 12, CK 5, CK 6, KA 2, and KA 6, and two varieties comparators i.e. Detam 1 and Cikuray. The experimental design was a randomized complete block design with four replication. Combined analysis of variance was performed on grain yield data to examine the main effects of the environment and

genotypes and their interaction effect variances. Existences of significant genotype-by-environment interaction variance justify further partitioning of this variance component. Analysis of genotype-by-environment (GE) was computed using the genotype plus genotype-by-environment interaction (GGE) model [9]. The GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data [4]. The basic model for GGE biplot is:

$$Y_{ij} - \overline{Y_j} = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

$$\tag{1}$$

where:

 $Y_{ij}$  = genotype mean of the i<sup>th</sup> at the j<sup>th</sup> environment

 $\overline{Y_i}$  = mean yield over all genotypes at j<sup>th</sup> environment

 $\lambda_1$  and  $\lambda_2$  = singular values for the PC1 and PC2

 $\xi_{i1}$  and  $\xi_{i2}$  = PC1 and PC2 scores, respectively for genotype i

 $\eta_{i1}$  and  $\eta_{i2}$  = PC1 and PC2 scores, respectively for environment j

 $\varepsilon_{ij}$  = residual of the i<sup>th</sup> at the j<sup>th</sup> environment

To display PC1 and PC2 in a biplot, the equation is [9]:

$$Y_{ij} - \overline{Y_i} = \xi_{i1}^* + \xi_{i2}^* \eta_{i2}^* + \varepsilon_{ij}$$
 (2)

where:

$$\xi_{in}^* = \lambda_n^{1/2} \xi_{in} \text{ dan } \eta_{in}^* = \lambda_n^{1/2} \eta_{in}, \text{ where } n = 1, 2.$$

This scaling method has the advantage that PC1 and PC2 have the same unit (square root of the original unit, e.g.,  $t \cdot ha^{-1}$  in terms of yield).

# 3. Result and discussion

The result of proximate analysis showed that oil content of black soybean genotypes ranged between (164.80 to 185.20) g  $\cdot$  kg<sup>-1</sup> (Table 1). Grain yield ranged from (1.98 to 2.21) t  $\cdot$  ha<sup>-1</sup>. To obtain oil yield potential , then converted from oil content and seed yield per hectare. Oil yield varies from (369.57 to 445.65) L  $\cdot$  ha<sup>-1</sup>. Genotype that have high oil content and high yield is KA 6.

Genotypes	Oil content $(g \cdot kg^{-1})$	Grain yield (t · ha <sup>-1</sup> )	Oil yield (L · ha <sup>-1</sup> ) 380.43	
Cikuray	165.00	2.11		
CK 12	165.00	2.09	369.57	
CK 5	172.50	1.98	369.57	
CK 6	164.80	2.11	380.43	
Detam 1	165.00	2.40	434.78	
KA 2	172.40	2.06	380.43	
KA 6	185.20	2.21	445.65	
Means	169.99	2.14	394.41	

Table 1. Oil content, seed yield, and oil yield of seven black soybean genotypes

The result combined analysis of variance over environments presented in Table 2. Environment, genotype, and genotype-by-environment interaction variance were significant ( $P \le 0.05$ ). Environment accounted about 77.47 % of

the variation. Variation caused by genotype of 2.91 %. The genotype-by-environment interaction accounted about 9.77 % of the variation which is less than environment effect. The large environment effect suggest that the different performance of soybean genotypes due to environment effect. According to some report, that normal in multilocation data, environment accounts for about 80 % of the total variation [10]. In barley yield multilocation data reported as high as 81 % of variation being explained by environment [11]. However, another reported little lesser about 65 % contribution of location to the total variation in cassava multilocation data [12].

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Sources of variation	DF	SS	MS	F	ProbF	% SS
Environment (E)	9	75.75	8.42	103.77	0.00*	77.47
Replication (Env)	30	2.43	0.08			
Genotype (G)	6	2.85	0.47	2.68	0.02*	2.91
GE	54	9.55	0.18	4.42	0.00*	9.77
Error	180	7.20	0.04			
Total	279	97.79	0.35			

Table 2. Combined analysis of variance for grain yield (t · ha<sup>-1</sup>) of seven black soybean genotypes at 10 environments of Java

A significant GE interaction for a quantitative trait can limit progress in selection. Variance due to GE interaction is an important component of the variance of phenotypic means in selection experiments [13]. GE interactions complicate the identification of superior genotypes [7]. GGE biplot as one of the statistical modeling method can use to identify superior genotype.

## 3.1. GGE biplot analysis

GGE biplot provides the polygons to view or visualize the genotype-by-environment interaction pattern [14]. The polygon provides an effective and elegant tool for visualizing the "which-won-where" pattern. The polygon can be called a convex hull, and the cultivars at the corner of the polygon can be called the vertex cultivars [14]. Fig. 1 present a polygon view of seven black soybean genotypes tested at ten environments. Genotypes at the vertex of the polygon are either the best or poorest in one or more environments [15]. The genotype at the vertex of the polygon performs best in the environment falling within the sectors [16,17].

The rays in Fig. 1 are lines that are perpendicular to the sides of the polygon or their extensions. Four rays divide the biplot into four sectors, and the environment fall into four of them. Genotypes KA 6, CK 5, Cikuray, and Detam 1 were vertexes of polygon. Genotype KA 6 performed best in Cirebon, Madiun, and Banyuwangi. Detam 1 performed best in Majalengka, Cianjur, Yogyakarta, and Bogor. Cikuray performed best in Ngawi, while CK 5 being the best in Jatinangor 1 and Jatinangor 2.

Yield performance and stability of genotypes was done using AEC [9]. The average environment is defined by the average values of PC1 and PC2 of all environments, represented by a small circle (Fig. 2). A line pass through average environment and the biplot origin, this line is called the average environment axis and serves as the abscissa of the AEC. The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa. This line separates genotypes that have grain yield above-average means (right of the line) with genotypes that have grain yield below-average means (left of the line). Genotypes that have grain yield above-average means are KA 6, KA 2, and Detam 1 (Fig. 2). Genotypes that have grain yield below-average means are CK 5, CK 12, CK 6, and Cikuray. Stability of the genotypes depends on their distance from the AEC line. Genotype KA 2 is more stable as well as high yielding. Conversely, CK 12 and CK 6 were stable but low yielding.

# Scatter plot (Total - 85.15%)

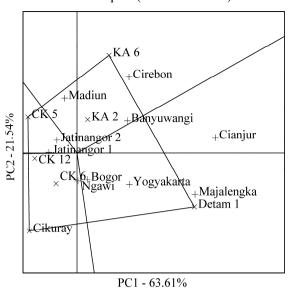


Figure 1. Polygon view of GGE biplot and their winning genotypes.

# Ranking biplot (Total - 85.15%)

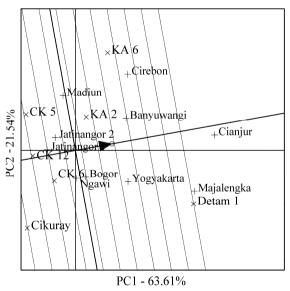
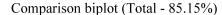


Figure 2. AEC views of the GGE-biplot based on genotype-focused scaling for the means performance and stability of genotypes.

Ideal genotype was determined by genotype that has highest mean performance and stable. Such an ideal genotype is equal to the longest vector of all genotypes and with zero GEI, as represented by an arrow pointing to it (Fig. 3). The closest genotype to the ideal genotype is Detam 1, in terms of higher yielding ability and stability. In addition KA 6 located on the next concentric circle, may be regarded as desirable genotypes.



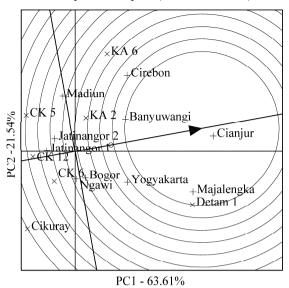


Figure 3. GGE biplot showing ideal genotype based on genotype-focused scaling.

Besides ideal genotype, ideal environment also needed as a reference for genotype selection in the multienvironment trial. The ideal test environment should have small (absolute) PC2 scores (more representative of the overall environment) and large PC1 score (more power to discriminate genotype in terms of the genotypic main effect) [4]. Such an ideal environment is represented by an arrow pointing to it (Fig. 4). Cianjur which fell into the center of concentric circles, it was closest to the ideal environment, in terms of being the most representative of the overall environments. Other environments which can be favorable environments were Cirebon and Banyuwangi.

# Comparison biplot (Total - 85.15%)

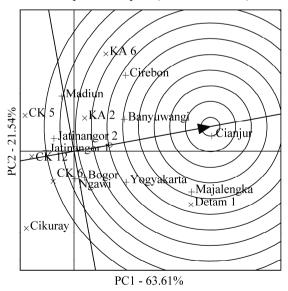


Figure 4. GGE biplot showing ideal environment based on environment-focused scaling.

#### 4. Conclusion

Black soybean genotype that have high yield is KA 6 (2.21 t  $\cdot$  ha<sup>-1</sup>), and potential to produce oil in amount of 445.65 L  $\cdot$  ha<sup>-1</sup>. According to GGE biplot analysis, KA 6 was adaptive to cultivate in the regions of Cirebon, Madiun and Banyuwangi, and environment similar to the three regions. The most stable genotype as well as high yielding is KA 2. An ideal genotype is Detam 1. The ideal environment in terms of being the most representative of the overall environments is Cianjur.

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