The Yield Stability of Indonesian Soybean Promising Lines with High Isoflavone for Food Security

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Abstract. A soybean with both high yielding and high concentrations of desired seed quality components is an ideal cultivar. The objective of this study is is to examine the yield stability of soybean promising lines with high isoflavone contents across environments in Indonesia. In the present study, performance of 12 soybean genotypes over eight locations during the dry season 2012 was investigated using AMMI analysis. Environment (location) attributed higher proportion of the variation (36%), while the rest were genotype and GEI contributed 5.6% and 18.4% of total variation, respectively. Genotypes G1 (IAC100/K-60-1092-1141) and G9 (K/IAC100-997-1035) with both high yield and high isoflavone content were proposed to be released as new soybean cultivars for specific environment in Indonesia.

Keywords: soybean, yield stability, isoflavone

1. Introduction

High yielding cultivar is the main focus of the soybean development in Indonesia. But often most studies focus on high yields and overlook yield stability, which is also an important factor for food security [1]. The yield stability is influenced by several factors, i.e. environmental factors. The considerable variation in soil and climate has resulted in large variation in yield performance, thus genotype $\times$ environment interaction (GEI) is an important circumstance for plant breeders and agronomists.

Soybean is often described as the miracle golden bean, the pearl of the Orient, the Cinderella crop of the century, the meat that grows on vines, the protein hope of the future and the salvation crop among others. These attributions are mainly due to the relatively high protein content (about 40%) contained in soybean seeds [2]. Soybean-protein products also contain a high concentration of isoflavones, up to 1 g/kg [3]. Soybean isoflavones have shown to positively impact on the human health [4]. Indonesian as the largest soybean consumer and has long been consuming soybean in the form of processed products such as tofu, tempeh, salted soybean, and soy sauce. Strategic position of soybean as healthy food will increasingly important if there is availability of high yielding soybean cultivar with high isoflavone content.

The additive main effects and multiplicative interaction (AMMI) analysis model, combining the analysis of variance (ANOVA) and principal components analysis (PCA), has emerged as a powerful analytical tool to interpret the interaction and widely applied in breeding researches [5], [6]. The aim of this paper is to examine the yield stability of soybean promising lines with high isoflavone contents in several different agro ecological environments in Indonesia.

2. Materials and Methods

2.1. Field Evaluation

Research materials consists of ten soybean promising lines with high isoflavone content (IAC100/K-60-1092-1141; IAC100/K-67-1099-1147; B/IAC100-47-678-764; IAC100/SHR-W60-1-252-273; K/IAC100-

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71-1011-1041; IAC100/K-5-1037-1062; K/IAC100-64-1004-1037; IAC100/K-2-1034-1058; K/IAC100-997-1035; IAC100/SHR-W60-6-257-285) and two check varieties (Wilis and Anjasmoro). The experiments were done in eight locations (Depok, Sleman, Klaten, Mojokerto, Blitar, Pasuruan, Tabanan and West Lombok) during the dry season I (March – June 2012) and dry season II (June – September 2012). A randomized completely block design with four replicates was used in each location. Each line was planted on 2.4 m x 4.5 m plot size, 40 cm x 15 cm plant distance, two plants/hill. Fertilizer of 50 kg Urea, 100 kg SP36 and 75 kg KCl per ha were applied before sowing time. Weed, insect and disease were controlled intensively. Isoflavone extraction and HPLC analyses were done using a modified version of the protocol of [7].

2.2. AMMI Model Analysis

AMMI analysis combines ANOVA and principal component analysis (PCA) where the sources of variability in the genotype by environment interaction are partitioned by PCA. The AMMI model analysis of soybean seed yield was performed by a SAS program written by [8].

The ANOVA model is $Y_{ij.} = \mu + g_i + e_j + ge_{ij} + \varepsilon_{ij.}$, and the AMMI model is $Y_{ij.} = \mu + g_i + e_j + \sum_{k=1}^{x} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij.}$, where $Y_{ij.}$ is the mean of the ith cultivar in the jth environment, μ is the grand mean, g_i is the genotype effect, e_j is the site effect, λ_k is the singular value for principal components 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, and $\varepsilon_{ij.}$ is the error for genotype i and environment j. The results of the AMMI model analysis were interpreted by a biplot [9].

3. Results and Discussion

3.1. Genotype Performance

Average seed yield of 12 genotypes at eight locations was 2.62 t/ha. The seed yield of the check cultivars Wilis and Anjasmoro were 2.63 t/ha and 2.64 t/ha, respectively. Seed yields of 10 genotypes ranged from 2.49 t/ha to 2.82 t/ha. Five genotypes i.e G1 (2.82 t/ha), G2 (2.66 t/ha), G6 (2.69 t/ha), G7 (2.70 t/ha) and G9 (2.75 t/ha) had higher seed yield than the yield grand mean and the check cultivars.

Table I: Analysis of variance of AMMI model for seed yield (t/ha) of twelve soybean cultivars grown in 10 environments during dry season 2012.

Source of variation	Degree of freedom	Sum of Squares	Mean Square	P value	Percentage of GEI SS	Cumulative percentage of GEI SS
Environment	7	28.928	4.132	<.0001		
Rep (Env)	24	5.786	0.241	<.0001		
Genotype	11	4.472	0.406	<.0001		
GEI	77	14.791	0.192	<.0001		
PC1	17	6.053	0.356	0.00000	40.92	40.92
PC2	15	3.094	0.206	0.00003	20.92	61.84
PC3	13	2.768	0.212	0.00412	18.71	80.55
Residual	32	2.876	0.304		19.45	100
Error	264	26.430	0.100			

3.2. AMMI Analysis

The analysis of variance results are presented in Table I. The ANOVA showed that seed yield were significantly affected by E and G. The highest percentage of variaton was explained by E main effect (36%), while G and GE effects explained the rest of variation (5.6% and 18.4%, respectively). A similar pattern was obtained from previous studies [10], [11].

A large yield variation explained by environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in seed yield. Environment seed yields (averaged across cultivars) ranged from 2.11 t/ha (E8) to 3.02 t/ha (E6). Cultivar seed yields (averaged across environment) ranged from 2.47 t/ha (G10) to 2.87 t/ha (G1). The GEI was a crossover type with different yield ranking of genotypes across environments.

The AMMI analysis partitioned the sum of squares of GEI into ten interaction principal components axes (IPCA), of which the first three IPCA were significant. Result from AMMI model showed that the first principal axes (PCA) captured 40.92% of the $SS_{G \times E}$, the second 20.92%, and the third 18.71%. The criterion of postdictive success of the AMMI model identified the first three IPCA axes in the model and the three principal component axes of the interaction were significant fo the AMMI model. Hence, this is led to the selection of the AMMI3 model. However, two interaction principal component axes for AMMI model was sufficient for predictive model. Other interaction principal component axes captured mostly non-predictive random variation (noise) and did not fit to predict validation observations [12]-[14]. Therefore, the interaction of the 12 genotypes with 8 environments was best predicted by the first two interaction principal components of genotypes and environments.

AMMI biplots are given in Figure 1 (AMMI1) and Figure 2 (AMMI2). Figure 1 plots PCA axes 1 versus mean yield of both genotypes and environments, showed the main and IPCA effects of both G and E on seed yield. According to [15], cultivars that had IPCA1 scores > 0 responded positively (adapted) to the environments that had IPCA1 scores > 0 but responded negatively to environments that had IPCA1 scores < 0, and the reverse applies for cultivars that had IPCA1 scores < 0. On this basis, genotypes G3, G5, G9, and G10 were adapted to E2, E3, E7, and E8. In contrast, genotypes G1, G2, G6, G7, G8, and G11were adapted to E1, E4, E5, and E6.
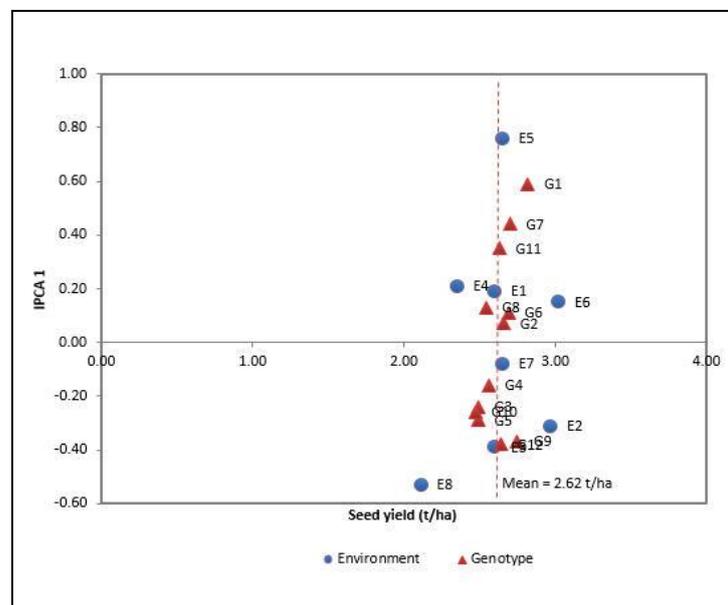

Fig. 1: Biplot of Principal Component Analysis (PCA) Axis 1 versus Mean Yield (t/ha) for 12 soybean genotypes grown in eight environments during dry season 2012.

The differences among cultivars in terms of direction and magnitude along the x axis (yield) and y axis (IPCA1 scores) were also important. The cultivar with a lower absolute IPCA score would produce a lower absolute GEI effect than the cultivar with a higher absolute IPCA score and have a less variable (more stable) yield across environments [15], [16]. The cultivar stability ranking based on lower absolute IPCA scores was genotypes G2, G6, G8, G4, G3, G10, G5, G11, G9, G12, G7, and G1. Genotype G2 prove to be stable genotypes but low on seed yield. Genotype G6 was also stable but had average yield. Genotypes G1 and G9 had the highest yield but relatively low on stability, thus both genotypes may perform well under specific environmental conditions.

The second biplot (Figure 2) is of PCA axis 1 versus PCA axis 2 for both genotypes and environments. Distribution of genotype points in the AMMI2 biplot revealed that the genotypes 6 and 8 scattered close to the origin, indicating minimal interaction of these genotypes with environments. The remaining 10 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. For example, the genotypes G4 had moderate positive interaction and genotypes G6 had negative interaction in the location E2.
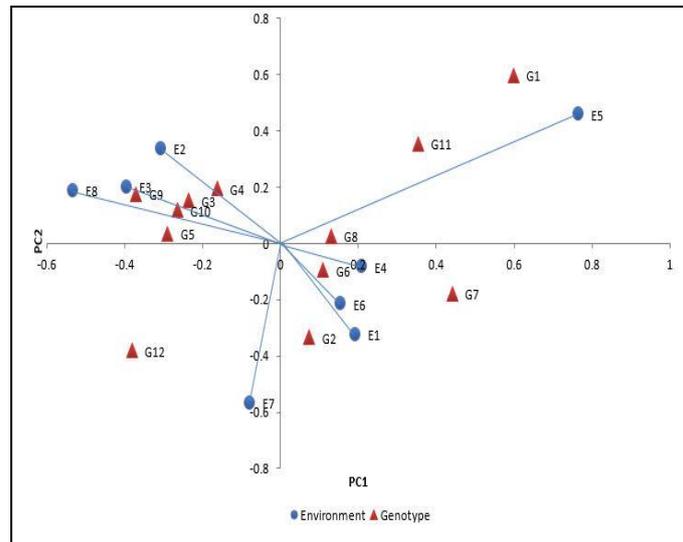
Fig. 2: Biplot of Principal Component Analysis (PCA) Axis 1 versus PCA Axis 2 for 12 soybean genotypes grown in eight environments during dry season 2012.
Abbreviations: G1=IAC100/K-60-1092-1141; G2=IAC100/K-67-1099-1147; G3=B/IAC100-47-678-764; G4=IAC100/SHR-W60-1-252-273; G5=K/IAC100-71-1011-1041; G6=IAC100/K-5-1037-1062; G7=K/IAC100-64-1004-1037; G8=IAC100/K-2-1034-1058; G9=K/IAC 100-997-1035; G10=IAC100/SHR-W60-6-257-285; G11=Wilis; G12=Anjasmoro; E1=Depok, E2=Klaten, E3=Sleman, E4=Mojokerto, E5=Blitar, E6=Pasuruan, E7=Tabanan, E8=West Lombok.

3.3. Soybean Isoflavone

The total isoflavone content of soybean genotypes is listed in Table II. Measurement of isoflavone of 12 genotypes derived from seed yield obtained from location of Probolinggo and Blitar. The high yielding genotypes G1 and G9 also had high of isoflavone content (394.77 ppm and 396.69 ppm, respectively). The five soybean varieties that have the highest total isoflavone content were genotypes G7, G1, G9, G6, and Wilis. The overall range in average total isoflavone content was 149.71 to 398.50 ppm.

Table II: The total isoflavone content of twelve soybean promising lines. 2012.

No.	Genotipe	Total isoflavone (ppm)			Seed yield (t/ha)
		Probolinggo	Blitar	Average	
1	IAC 100/K-60-1092-1141	449.00	340.53	394.77	2.82
2	IAC 100/K-67-1099-1147	240.88	257.46	249.17	2.66
3	B/IAC 100-47-678-764	133.89	203.02	168.46	2.49
4	IAC 100/SHR-W60-1-252-273	316.57	217.61	267.09	2.56
5	K/IAC 100-71-1011-1041	149.11	187.46	168.29	2.49
6	IAC 100/K-5-1037-1062	280.03	369.24	324.64	2.69
7	K/IAC 100-64-1004-1037	347.58	449.42	398.50	2.70
8	IAC 100/K-2-1034-1058	271.34	157.89	214.62	2.54
9	K/IAC 100-997-1035	364.42	428.96	396.69	2.75
10	IAC 100/SHR-W60-6-257-285	123.45	175.96	149.71	2.47
11	Wilis	267.05	418.93	342.99	2.63
12	Anjasmoro	188.44	166.21	177.33	2.64
	Average	260.98	281.06	271.02	2.62

Ideal soybean production systems achieve both high seed yield and high concentrations of desired seed quality components. The positive relationship between total isoflavone concentration and seed yield have been reported by [17], as it suggests that high soybean yield could be compatible with high quality from an isoflavone-based functional food perspective. Tthe availability of soybean cultivar with high isoflavone content play important role for the provision an inexpensive and healthy functional food in Indonesia.

4. Conclusion

There were five genotypes (G1, G2, G6, G7, and G9) had higher seed yield than the yield grand mean and the check cultivars. Genotypes G1 (IAC100/K-60-1092-1141) and G9 (K/IAC100-997-1035) had both high yield and high isoflavone content were recommended to be developed in specific environment.

5. Acknowledgements

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