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Genotypes x Environments Interaction of Soybean Lines in Various Shading Environments

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Authors' contributions

This work was carried out in collaboration among all authors. Authors YB and TS designed the study. Authors TS, GWAS, S and P performed the statistical analysis and wrote the protocol. Authors NN, YB and MJM wrote the first draft of the manuscript. Authors TS and MJM managed the analyses of the study. Authors GWAS and S managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Soybean (*Glycine max* (L) Merr.) planted in land space among stands of other crops especially forest trees experience shading stress due to less sunlight penetration. The objective of the study was to identify the performance and yield stability of soybean genotypes in various shading environments. Field research was conducted in 2018 on 15 soybean genotypes consisted of 12 promising soybean lines and three check varieties (Dena 1, Dena 2, and Grobogan) in 10 shading environments (cassava, maize, orange, teak, eucalyptus, oil palm, and no shading). Randomized block design and repeated four times was used in each location. Result of the study showed that the response of the genotypes to grain yield was significantly difference in each environment or location. Stability of genotypes were grouped into 3, namely 1 genotype classified as unstable and recommended for less optimal environments, 6 genotypes (5 promising lines and 1 check variety) which were classified as stable and adaptive in 10 test locations. Based on seed yield and yield components average, one line (Grob/Pander-395-2) had a high average seed yield (1.84 tha⁻)

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¹), high seeds weight per plant (14.8 g), high weight of 100 seeds (21.6 g), and stable in 10 location (indicated by non significant both regression coefficient and regression deviation). Therefore, Grob/Pander-395-2 could be recommended for being grown in shading environments across the country.

Keywords: Genotype; grain yield; shading; soybean; stability.

1. INTRODUCTION

Soybean (Glycine max (L) Merr.) is very important source of food and feed consumptions in Indonesia. Sovbean consumptions needs have increased from year to year and until now national soybean production has not been able to meet these needs. The inability of national soybean production in meeting national soybean needs was due to decreasing land area for monoculture soybean cultivation. Therefore, expansion of soybean planting was done by using land space available among stands of other trees, especially industrial forest trees, plantation crops, and horticulture trees, as well as food crops such as maize and cassava. In such conditions, soybean have the opportunity to experience shading stress due to less sunlight penetration. Shade stress causes reduced light received by soybean plants. Light plays role an important in the life of the plant, determine the rate of photo-morphogenesis and photosynthesis [1].

Light does not only play as a driving force of photosynthesis, but also affect the structure and function of photosynthetic organs. Therefore, light is important in determining photosynthesis and crop yields [2,3]. The rate of photosynthesis decreases with shade treatment. The reduced rate of photosynthetic potential among cultivars shows a difference [4]. Light directly affects the crop growth and yield potential. In a maizesoybean relay-strip intercropping system, growth period is essential for soybean growth because tall crops (maize) absorb major part of the light, whereas shorter crops (soybean) receive low amounts of light for photosynthesis and suffer shading from taller crops [5]. Shading affects plant growth, morphology, and anatomy of the soybean crop [6].

Soybean show different responses to various shading levels [7]. The response of crops to environmental stress was very important to understand in order to know the behavior of crops in the face of environmental changes [8,9]. Behavior of soybean often changes with changes

in the environment. These behavioral changes can be explained through the interaction of genotype x environmental [10,11,12,13].

To determine the superiority and stability appearance of a genotype, it was necessary to evaluate it in a number of locations, seasons or other environments [14]. The evaluation was intended to determine whether there was an influence or effect of interaction among genotype x environment. Information on the interaction of genotype x environment and stability was needed in determining the adaptation and recommendations of a certain genotype or line that will be released as a new variety [15] and makes it easier to select varieties in plant breeding programs [16].

The influence of genotype x environmental interactions can reduce genetic progress in plant breeding programs, therefore testing in a variety of environments is very important to identify superior genotypes in the final selection cycle Partitioning genotype x environment (G x E) interactions into adaptability and phenotypic stability will positively address the information gap on association of traits to yield [17].

During the breeding process, genetic material is tested in various shading environments for evaluation of posterior performance and evidence of genetic superiority. In this case, the occurrence of genotypic and environmental interactions (G x E) is common. Interactions will affect plant behavior in the face of environmental conditions. The objective of this field study was to identify the performance and seed yield stability of each soybean genotype in various shading environments.

2. MATERIALS AND METHODS

2.1 Research Site

Field research was conducted under the shading plantations in 10 locations of two Provinces of Indonesia (Table 1 and Fig. 1).

	Shading	plantation		Locations	
Code	Main plants or	Age of main	Regency	Distric	Village
	crops	plants (years)			-
L1	Oil palm trees	2.0	Langkat ^{a)}	Binjai	Tanjung Jati
L 2	Teak trees	2.0 – 2.5	Ngawi	Widodaren	Karangbanyu
L 3	Citrus trees	2.0 – 2.5	Banyuwangi	Cluring	Sembulung
L 4	Teak trees	3.0 – 3.5	Blitar	Panggung Rejo	Ngrampal Ombo
L 5	Eucalyptus trees	4.0	Lamongan	Mantub	Kedukbembem 1
L 6	Eucalyptus trees	4.0	Lamongan	Mantub	Kedukbembem 2
L 7	Cassava	The same time ^{b)}	Malang	Kepanjen	Jambegede
	(intercropped)				
L 8	Citrus trees	1.0 – 2.0	Banyuwangi	Purwoarjo	Kradenan
L 9	Maize	The same time ^{b)}	Malang	Pakisaji	Kendalpayak 1
	(intercropped)				
L10	Soybean	-	Malang	Pakisaji	Kendalpayak 2
	(monoculture)		-		-

Table 1.	. Shading	Plantations	of sov	vbean	adaptation	trials at	10	locations

^{a)} In North Sumatera province (9 other locations were in East Java province); ^{b)} Cassava and maize were planted at the same time with soybean



Fig. 1. Location of soybean adaptation trials in shading plantations

2.2 Plant Materials

A total of 15 soybean genotypes consisted of 12 promising lines (Grob/IT-7-1, Grob /IT-7-2, Grob/IT-7-3, Grob/IT-7-5, Grob/IT-7-7, Grob/IT-IBK/Argop-296-10, IBK/Argop-276-3, 17-1, Grob/Pander-395-2, Grob/Pander-397-6, Grob/Pander-428-1, and Grob/IAC-453-7) and three check popular varieties (Dena 1, and Dena 2, and Grobogan). Dena 1 and Dena 2 are shading tolerant varieties) and Grobogan is early maturing and large seed size variety. The 12 promising lines were derived from breeding program by making crosses of several elite varieties (Grobogan, Argopuro, and Panderman).

2.3 Field Methods

The randomized block design repeated four times was used at each location. The criteria of the treatment was the modification of the soybean technology described by Harnowo et al. [18]. In the all locations soybeans were planted at a spacing of 35 cm x 20 cm, 2 seeds hole⁻¹ and were fertilized 150 kg Phonska and 100 kg SP36 ha⁻¹ which were given at the age of 7-10 days after planting (DAP). In maize-soybean intercropping, maize were planted 3 weeks before soybeans, with a maize spacing of 210 cm x 35 cm x 20 cm and 1 seed hole⁻¹. While soybeans were planted 3 weeks after planting

maize at 210 cm of maize planting row. Maize were fertilized using 350 kg Urea + 300 kg Phonska ha⁻¹. Maize fertilization was carried out in 2 stages: at 7-10 DAP as much as 100 kg Urea + 300 kg Phonska ha⁻¹ and at 35-45 DAP as much as 250 kg Urea ha-1. In cassavasoybean intercropping, soybean were planted 2 weeks after planting (WAP) cassava. Cassava planting space was 2.1 m x 0.5 m x 0.75 m (which was 0.75 m within row), while soybeans were planted among 2.1 m of cassava planting row. Cassava were fertilized with 200 kg Urea + 100 kg SP36 + 100 kg KCl ha⁻¹, given in two plant stages, at 2 WAP with a dose of 100 kg Urea + 100 kg SP36 + 50 kg KCl ha⁻¹, and at 3 WAP with dose of 100 kg Urea + 50 kg KCl ha⁻¹.

2.4 Data Analysis

Observation of quantitative characters was carried out on seed weight area⁻¹ measured and weight of 100 seeds was observed based on population per plot. Observations of plant height, number of branches, number of fertile stem nodes, number of filled pods, and seed weight plant⁻¹ were carried out on 5 plant sample. Observations on supported data such as light intensity were carried out at 12.00 - 13.00 PM at a two-week interval, starting from planting to harvest. Fig. 1 shows the pattern of light and shading reception at each adaptation test location of shading adaptive soybean promising lines.

To find out the interaction of genotype x environment, a joint analysis was performed. If there was genotype x environment interaction, then it was continued with the stability analysis using the regression method according to Eberhart and Russell [19] based on the linear model:

Yij = Ui + bi Ij + dij. i = 1, 2. ... g. where:

Yi = average results of the i^{th} line at the j^{th} test environment

Ui = average ith line for all environments

bi = slope of response of yield of the ith line to the environment

Ij = environment index to j^{th} with the following magnitude:

ig Ι ΣΥ.j / g - ΣΣΥij / gl j i j

 S^2d = deviation from regression of ith line at the jth environment.

Stability tests were assessed based on Eberhart and Russell [19] model, with two parameters of stability: regression coefficient (bi) is considered as parameter of response and deviations from regressoin (Sij) as stability. Genotype is categorized as stable if the bi value is not different from 1 (bi = 1) and S^2 d not different from zero ($S^2d = 0$). The regression coefficient value will also be used as an appraisal of adaptability as follows: bi < 1.0 has above average stability, special adaptation in marginal environment; bi = 1.0: has average stability, well adapted to all environments; and bi> 1.0: has stability below average, is well adapted to especially in productive environments. Adaptation and yield stability of shade-adaptive soybean lines include early maturity, large seeds, and high yield potential among 10 locations.

3. RESULTS AND DISCUSSION

3.1 Performance of Soybean Lines

Analysis of the combined variance was carried out to determine the genotype response to the environments (locations). The mean square results of the combined variance analysis showed that genotypes, locations and interactions among genotypes and locations significantly affected plant height, number of branches, fertile stem nodes, filled pods, weight of 100 seeds, seed weight per plant, and seed yield per hectare (Table 2). This showed that the response of each genotype to the environment was different. In other words, each genotype gave different performance in each location. According to the research results by Jandong et al. [13] in testing a number of soybean lines in several locations, there was an effect of interaction among line x location, which showed that each line had a different adaptation boundary.

The highest soybean seed yield of 3.20 tha^{-1} was achieved in L8 (in a space among rows of citrus trees, Banyuwangi District 2, East Java) and the lowest seed yield of 0.9 tha⁻¹ was achieved in L9 (intercropping with maize, Malang District, East Java) (Table 3). The high yield average at L8 was due to the level of light reception in L8 higher than that in L9, especially in the critical period of soybeans against light deficiency, namely the generative phase, precisely in the filling phase of soybean pods. Light reception at L9 (intercropping of maize + soybeans) was reduced along with the growth

Plant characters		Coeff. of		
	Location (L)	Genotype (G)	LxG	Variation (%)
Plant height (cm)	2141.139**	1652.489**	101.451**	12.56
Number of branches/plant	18.389**	2.779**	0.905**	13.16
Number of nodes/plant	397.249**	96.918**	14.923**	9.21
Number of filled pods/plant	7514.050**	48.234**	104.337**	12.83
Days of flowering (day)	146.513**	56.881**	3.929**	2.35
Days of maturity (day)	392.208**	260.035**	14.155**	2.22
Weight of 100 seeds (g)	260.225**	211.059**	5.630**	5.83
Seed weight/plant (g)	2029.690**	35.276**	17.604**	13.65
Seed yield/ha (ton)	36.301**	0.236**	0.154**	12.45

 Table 2. Combining analysis of yield components characteristics and yield of 15 soybean genotypes in 10 locations

**significant at the 1% test level

and development of maize plants. The pattern of receiving light and the level of shading in each location were presented in Fig. 2. In maize-soybean intercropping systems, also cause changes in light intensity and light spectrum. These changes affect plant growth, morphology, and anatomy [6,7].

3.2 Stability of Soybean Lines

To determine the adaptation and stability of the genotype seeds yield tested in 10 locations, a varience of stability analyzes were carried out (Table 4). Based on Table 2, the interaction among genotypes and environment has a highly significant effect on the seed yield of 15 soybean genotypes tested. Suggested that the response of the 15 genotypes tested against the test locations showed a difference. Based on the regression coefficient (bi) and regression deviation (S²di), it was identified that the bi values of seed yield ranged from 0.80 to 1.21 and S²di ranged from -0.0062 to 0.0592.

Based on bi and S²di values according to Eberhart and Russell [19], the tested genotypes were grouped into: 1) genotypes with significant bi values less than 1 (bi <1) and S²di different from zero $(S^2 di \neq 0)$, recommended for environments with less optimal, namely Grob / IT-7-3 line; 2) genotypes with bi values not different from 1 (bi = 1) and S^2 di not different from zero (S^2 di = 0) were categorized as stable in 10 test locations, namely Grob/IT-7-2, Grob/IT-7-5, Grob/IT-7-7, Grob/Pander-395-2, Grob/Pander-397-6 and Grobogan lines; and 3) genotypes with bi values not different from 1 (bi = 1) and S^2 di at zero (S2 at \pm 0) were categorized as unstable in 10 test locations, namely Grob/IT-7-1, Grob/IT-17-1, IBK/Argop-296-10, IBK/Argop-276-3, Grob/Pander-428-1,

Grob/IAC-453-7, Dena 1, and Dena 2 lines (Table 5).

Based on the average yield of 10 locations, there was one line (namely IBK/Argop-276-3) had a higher average yield than the three check varieties (Dena 1, Dena 2, and Grobogan); there were five lines (Grob/IT-7-1, Grob/Pander-395-2, Grob/IAC-453-7, Grob/IT-7-5, and IBK/Argop-296-10) had higher yields than the twocheck varieties (Dena 1 and Dena 2); and six lines (Grob/IT-7-2, Grob/IT-7-3, Grob/IT-7-7, Grob/IT-17-1. Grob/Pander-397 -6. and Grob/Pander-428-1) had lower yields than the three check varieties (Dena 1, Dena 2, and Grobogan). Among the lines that had high vields. Grob/Pander-395-2 and Grob/IT-7-5 were classified as stable lines, while the other four lines (IBK/Argop-276-3, Grob/IT-7-1, Grob/IAC-453-7, and IBK/Argop-296-10) were classified as unstable lines (Table 5). This results showed that it is difficult to breed cultivars that simultaneously have high yields and high stability [20]. The mixture of lines is an efficient strategy to increase phenotypic stability in soybean [21].

3.3 Yield Components

The plant height of each genotype showed differences in 8 test locations, but not significantly different in the 2 test locations, namely at L1 (among the stands of oil palm trees, Langkat-North Sumatra) and L2 (among the stands of teak trees, Ngawi, East Java). The highest average of soybean plant height (61 cm) was reached in L9 namely intercropping with maize (Table 6). The shading level pattern in L9 was different from the other nine locations, namely at L9, the shading level continued to increase along with the increasing age of maize,

whereas in the other nine locations the shading level pattern was almost the same, which tends to be flat from the beginning to the end of the soybean growth period (Fig. 1). Plants growth under low light intensity experience an increase in plant height in an effort to compete for light [22].



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L9

Fig. 2. Pattern of light and shading reception at each adaptation test location of shading adaptive soybean promising lines

The number of filled pods showed differences among genotypes and locations (Table 7). The highest number of pods was reached in L8 (among the stands of citrus trees, Banyuwangi District 2, East Java), followed by L3 (among the stands of citrus trees, Banyuwangi District 1, East Java) with an average number of filled pods of 58 and 49 pods per plant. Soybean genotypes in L3 and L8 locations were tested among citrus trees in Banyuwangi 1 and 2. The large number of filled pods formed in L8 and L3 was also followed by high seed weight per plant achieved, namely 26.3 and 20.4 g plant⁻¹ (Table 8). Seed vield per unit area at L8 and L3 was also high, namely 3.2 and 2.7 t ha^{-1} (Table 3). According to Egli [23] the number of branches, bunches and number of pods were the most important components in determining seed yields, and have a high correlation with total yields.

The highest seed weight per plant (Table 8) and seed yield per hectare (Table 3) in each location were achieved by different genotypes. This showed the influence of interaction among genotypes and locations or the response of each genotype to the location was different. The differences in seed yields in each location was generally caused by differences in shading trees (palm, teak, citrus, eucalyptus, maize, and cassava). Differences in shading trees caused differences in light intensity and shading stress received by soybean plants in each location (Fig. 1). Sundari et al. [24] stated that the soybean yield in the shading environments partly was determined by the soybean variety, the type and age of the shading plants or trees.

Seed size (100 seed weight) was influenced by the interaction between the genotype and the location. The largest average seed size was achieved in L8 with a weight of 22.0 g 100⁻¹ seeds, while the lowest was 14.8 g 100⁻¹ seeds achieved in L7 (intercropping with cassava, Malang District, East Java) (Table 9). L8 was a location that was able to provide the highest average yield and largest seed size. This was due to the environment in L8 was the best environment among the 10 locations used for yield adaptability testing.

Table 10 shows the average of 10 locations of seed yield and yield components of 15 soybean genotypes. Based on seed yield and yield components average, one line (Grob/Pander-395-2) had a high average seed yield (1.84 tha⁻¹), high seeds weight per plant (14.8 g), high weight of 100 seeds (21.6 g), and stable in 10 location (indicated by non significant both regression coefficient and regression deviation). The Grob/Pander-395-2 also had number of filled pods/plant equal to the grand average (36.6). Grob/Pander-395-2 Therefore. could be recommended for being grown in shading environments across the country.

Soybean yield and yield components were significantly affected by interaction of genotype and environment. Shading increased soybean plant height, decreased stem diameter, decreased leaves per plant and decreased grain yield per unit area with increasing shading [25]. Adaptation test of certain genotype is necessary to determine the agronomic performance for breeder in identifying stable genotypes adapted to the specific conditions of cultivation. Some genotypes perform well in some environments but not so well in others. Plant breeders need to give attention to develop soybean genotypes with consistent high yield potential under varying environmental conditions [26, 27].

No.	Genotype	Seed yield (t/ha) at location ^{a)}										
		L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	Mean
1	Grob/IT-7-1	1.5	1.4	2.6	1.4	2.4	1.8	0.9	3.4	0.9	2.2	1.85
2	Grob /IT-7-2	1.1	1.6	2.5	1.2	1.9	1.5	1.0	3.1	0.9	2.3	1.70
3	Grob/IT-7-3	1.3	1.4	2.5	1.4	2.2	1.4	1.0	2.7	0.9	2.2	1.71
4	Grob/IT-7-5	1.3	1.6	2.7	1.2	1.9	1.8	0.9	3.5	0.8	2.6	1.82
5	Grob/IT-7-7	1.2	1.8	2.6	1.3	1.9	1.6	0.9	2.8	0.9	2.6	1.76
6	Grob/IT-17-1	1.6	1.7	2.4	1.0	1.8	1.3	0.7	2.8	0.8	2.2	1.63
7	IBK/Argop-296-10	1.4	1.7	2.9	1.4	1.8	1.5	0.7	3.6	0.8	2.4	1.82
8	IBK/Argop-276-3	1.4	1.5	3.5	1.2	2.3	1.7	0.7	3.4	0.8	2.4	1.90
9	Grob/Pander-395-2	1.5	2.0	2.7	1.2	2.2	1.5	0.8	3.2	0.9	2.6	1.84
10	Grob/Pander-397-6	1.5	1.5	2.4	1.3	1.6	1.5	0.9	3.1	0.9	2.2	1.69
11	Grob/Pander-428-1	1.4	1.7	2.2	1.5	1.9	1.5	1.0	3.0	1.0	2.6	1.77
12	Grob/IAC-453-7	1.1	1.5	3.2	1.2	1.9	2.2	0.8	3.2	0.9	2.4	1.84
13	Dena 1 (check 1)	1.2	1.7	2.7	1.2	2.4	1.5	0.9	3.5	0.8	2.3	1.81
14	Dena 2 (check 2)	1.5	1.4	2.5	1.1	1.7	2.0	0.9	3.6	0.9	2.4	1.80
15	Grobogan (check 3)	1.5	1.7	2.9	1.4	2.1	1.5	1.0	3.2	0.8	2.7	1.88
Average	e	1.4	1.6	2.7	1.3	2.0	1.6	0.9	3.2	0.9	2.4	1.79
Coeff. o	of Variation (%)	12.8	10.4	11.9	14.0	10.0	12.7	13.1	10.4	12.4	12.3	
LSD 5%	0	0.3	0.2	0.5	0.3	0.3	0.3	0.2	0.6	ns	ns	
			a)	The non	ne of locatio	n the same	as described	l at Tahla 1				

Table 3. Seed yield per ha of 15 soybean genotypes evaluated in 10 locations

Source of variation	DF ^{a)}	Sum of	Mean of	lean of F test ^{b)} F tab		
		square	square		5%	1%
Total	149	168				
Genotype (G)	14	82	5.83	192.003**	1.70	2.09
Location (L) + (G x L)	135	87				
Location linier	1	82	81.67	2687.840**		
G x L linier	14	1.2	0.085	2.805**	1.78	2.24
Combined deviation	120	3.6	0.0304			
Grob/IT-7-1	8	0.3	0.0400	3.2239**	1.94	2.51
Grob /IT-7-2	8	0.1	0.0074	0.5988 ns		
Grob/IT-7-3	8	0.2	0.0266	2.1492*		
Grob/IT-7-5	8	0.1	0.0122	0.9838 ns		
Grob/IT-7-7	8	0.2	0.0199	1.6072 ns		
Grob/IT-17-1	8	0.2	0.0261	2.1025*		
IBK/Argop-296-10	8	0.2	0.0246	1.9823*		
IBK/Argop-276-3	8	0.4	0.0538	4.3384**		
Grob/Pander-395-2	8	0.2	0.0230	1.8540 ns		
Grob/Pander-397-6	8	0.1	0.0183	1.4724 ns		
Grob/Pander -428-1	8	0.3	0.0383	3.0872**		
Grob/IAC-453-7	8	0.6	0.0728	5.8730**		
Dena 1	8	0.2	0.0253	2.0396*		
Dena 2	8	0.4	0.0516	4.1606**		
Grobogan	8	0.1	0.0160	1.2944 ns		
Combined error	420	52	0 0124			

Table 4. Analysis of the stability on seed yields per ha of 15 soybean genotypes evaluated in10 locations

^{a)} DF = degree of freedom; ^{b)} ns = not significant at the 5% test leve; * and ** = significant at the 5% and 1% test level, respectivelty

Table 5. Seed yield average of 10 location, regression coefficient (bi), and regression
deviation (S ² di) of 15 soybean genotypes

No.	Genotype	Seed yield average (t ha ⁻¹)	Regressi coefficie	ion nt (bi) ^{a)}	Regression (S ² di) ^{a)}	n deviation
1	Grob/IT-7-1	1.85	1.00	ns	0.0263	**
2	Grob /IT-7-2	1.70	0.92	ns	0.0062	ns
3	Grob/IT-7-3	1.71	0.80	*	0.0130	*
4	Grob/IT-7-5	1.82	1.10	ns	-0.0014	ns
5	Grob/IT-7-7	1.76	0.91	ns	0.0063	ns
6	Grob/IT-17-1	1.63	0.88	ns	0.0124	*
7	IBK/Argop-296-10	1.82	1.14	ns	0.0109	*
8	IBK/Argop-276-3	1.90	1.21	ns	0.0401	**
9	Grob/Pander-395-2	1.84	1.03	ns	0.0093	ns
10	Grob/Pander-397-6	1.69	0.89	ns	0.0046	ns
11	Grob/Pander -428-1	1.77	0.81	ns	0.0246	**
12	Grob/IAC-453-7	1.84	1.10	ns	0.0592	**
13	Dena 1	1.81	1.11	ns	0.0116	*
14	Dena 2	1.80	1.04	ns	0.0379	**
15	Grobogan	1.88	1.06	ns	0.0024	ns
Averac	ie	1.79				

^{a)} ns = not significant at the 5% test level; * and ** = significant at the 5% and 1% test level, respectivelty

No.	Genotypes					Plant	height (cm) at locatio	n ^{a)}			
		L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	Mean
1	Grob/IT-7-1	54	43	60	50	51	36	39	39	64	43	47.7
2	Grob /IT-7-2	51	50	52	56	44	35	38	39	52	54	46.9
3	Grob/IT-7-3	59	52	50	57	47	37	44	43	55	50	49.4
4	Grob/IT-7-5	58	58	52	49	41	38	36	40	53	46	47.1
5	Grob/IT-7-7	48	47	51	60	49	36	44	41	67	47	48.9
6	Grob/IT-17-1	52	53	55	56	58	43	47	50	57	49	51.8
7	IBK/Argop-296-10	50	49	51	58	46	39	43	41	53	46	47.5
8	IBK/Argop-276-3	45	46	53	60	47	40	49	50	62	57	50.8
9	Grob/Pander-395-2	52	53	52	55	55	44	49	46	61	55	52.1
10	Grob/Pander-397-6	54	57	58	53	56	43	43	47	54	58	52.3
11	Grob/Pander -428-1	50	50	56	60	54	42	52	46	55	52	51.5
12	Grob/IAC-453-7	48	47	53	62	52	36	52	49	59	55	51.1
13	Dena 1	56	52	85	88	70	59	85	70	90	72	72.8
14	Dena 2	49	48	56	70	53	43	56	48	60	59	54.0
15	Grobogan	50	51	62	68	64	47	56	53	69	58	57.9
Averag	ge	52	50	56	60	52	41	49	47	61	53	52,1
Coeff.	of Variation (%)	14.3	11.7	14.1	12.8	10.9	11.0	12.6	12.5	12.8	10.3	
LSD 5	%	ns	ns	11.4	11.0	5.0	6.5	10.1	9.6	12.8	5.3	

Table 6. Plant height of 15 soybean genotypes evaluated in 10 locations

Sundari et al.; ARRB, 36(3): 77-92, 2021; Article no.ARRB.67282

No.	Genotype	Number of filled pods per plant at location ^{a)}										
		L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	Mean
1	Grob/IT-7-1	31	30	66	28	34	32	36	68	23	44	39
2	Grob /IT-7-2	30	29	41	28	28	27	34	45	25	41	33
3	Grob/IT-7-3	30	31	48	29	38	26	36	51	28	41	36
4	Grob/IT-7-5	34	24	43	25	27	32	35	47	25	46	34
5	Grob/IT-7-7	34	25	54	26	34	25	37	81	27	52	39
6	Grob/IT-17-1	35	29	49	26	30	27	33	61	29	50	37
7	IBK/Argop296-10	34	24	39	27	29	30	37	43	24	42	33
8	IBK/Argop-276-3	29	23	51	19	26	24	33	55	25	48	33
9	Grob/Pander-395-2	32	28	42	23	29	27	36	61	27	52	36
10	Grob/Pander-397-6	25	20	42	27	31	20	31	56	23	52	33
11	Grob/Pander-428-1	24	24	38	23	29	19	33	51	20	38	30
12	Grob/IAC-453-	38	26	48	26	34	31	37	50	33	45	37
13	Dena	33	32	41	41	31	30	41	80	35	57	45
14	Dena2	42	37	55	36	31	37	37	66	40	51	43
15	Grobogan	30	32	51	37	33	29	53	59	28	59	41
Avera	ge	32	28	49	28	31	28	37	58	27	48	36.6
Coeff.	of Variation (%)	13.3	6.1	11.9	13.2	14.2	11.2	9.6	14.6	11.7	11.9	
LSD 5	5%	5.0	2.4	8.3	5.3	6.3	4.4	5.8	14.1	5.3	9.4	
			a)	The name of	of location th	he same as	described a	at Table 1				

Table 7. Number of filled pods per plant of 15 soybean genotypes evaluated in 10 locations

No.	Genotype	Seed weight (g/plant) at location ^{a)}										
		L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	Mean
1	Grob/IT-7-1	10.6	12.3	26.4	10.0	11.4	11.1	11.3	28.5	8.6	17.9	14.8
2	Grob /IT-7-2	10.3	11.4	17.5	10.5	9.6	8.6	10.3	20.9	9.4	15.9	12.4
3	Grob/IT-7-3	10.3	11.8	21.7	11.3	12.9	8.4	10.0	23.4	10.0	15.6	13.5
4	Grob/IT-7-5	10.7	9.5	18.6	8.2	9.0	12.4	10.3	22.5	8.8	19.1	12.9
5	Grob/IT-7-7	12.2	10.0	22.7	9.1	11.8	8.4	10.0	36.0	8.8	18.2	14.7
6	Grob/IT-17-1	11.3	9.6	18.3	7.0	10.6	8.4	9.8	24.7	9.2	17.6	12.6
7	IBK/Argop-296-10	14.4	9.9	18.7	9.0	9.9	9.9	11.3	18.0	8.6	18.2	12.8
8	IBK/Argop-276-3	10.6	9.5	23.8	8.0	12.1	9.2	10.3	27.6	9.6	20.0	14.0
9	Grob/Pander-395-2	12.3	10.8	21.2	10.8	11.1	10.7	10.0	31.9	8.5	20.7	14,8
10	Grob/Pander-397-6	9.5	8.8	18.9	11.8	12.9	7.9	8.0	29.0	8.9	19.4	13.5
11	Grob/Pander -428-1	9.0	11.4	15.0	12.2	11.5	8.5	10.8	26.1	8.0	16.5	12.9
12	Grob/IAC-453-7	12.5	10.0	21.4	9.9	14.3	10.1	9.3	24.3	12.1	18.6	14.2
13	Dena 1	8.6	9.8	21.8	14.9	10.4	10.0	9.0	29.1	9.7	17.1	14.0
14	Dena 2	10.6	12.6	18.8	10.1	9.7	10.5	9.0	22.5	9.6	15.0	12.8
15	Grobogan	10.4	12.0	20.9	14.3	12.7	8.9	15.0	29.6	8.4	21.3	15.3
Averag	e	10.9	10.6	20.4	10.5	11.3	9.5	10.3	26.3	9.2	18.1	13.7
Coeff. o	of Variation (%)	14.1	14.7	11.7	11.4	8.2	12.9	12.2	14.2	9.8	11.7	
LSD 5%	6	2.2	2.2	3.4	1.7	1.3	1.8	2.1	6.1	1.5	3.5	
	a) The name of location the same as described at Table 1											

Table 8. Seed weight per plant of 15 soybean genotypes evaluated in 10 locations

Genotype	Weight of 100 seeds (g) at location ^{a)}										
	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	Mean
Grob/IT-7-1	20.9	16.4	17.6	16.6	18.1	16.6	15.6	20.0	16.8	18.6	17.7
Grob /IT-7-2	19.7	16.9	20.9	15.7	16.9	17.7	16.1	20.7	17.2	18.3	18.0
Grob/IT-7-3	20.8	16.4	20.9	18.5	18.0	18.7	16.0	23.0	16.1	17.5	18.6
Grob/IT-7-5	19.1	16.0	20.4	16.0	17.6	16.5	15.0	22.9	15.6	17.9	17.7
Grob/IT-7-7	18.4	16.5	20.1	16.1	16.9	16.7	15.4	20.1	16.9	17.9	17.5
Grob/IT-17-1	20.4	16.8	20.7	17.6	19.1	19.2	13.9	21.5	16.6	18.4	18.4
IBK/Argop-296-10	21.0	17.5	20.3	16.3	16.6	15.7	15.0	22.3	16.6	19.4	18.0
IBK/Argop-276-3	20.5	17.4	19.8	16.6	20.4	18.7	13.7	21.1	17.8	19.2	18.5
Grob/Pander-395-2	24.2	20.0	25.2	19.4	22.5	23.3	14.7	25.8	19.8	21.6	21.6
Grob/Pander-397-6	23.4	21.7	24.0	21.7	24.3	24.4	16.3	26.2	20.5	20.6	22.3
Grob/Pander-428-10	24.1	21.5	25.0	21.7	21.0	23.4	17.7	26.6	20.1	20.8	22.2
Grob/IAC-453-7	18.6	15.9	22.5	17.2	18.4	15.8	14.0	21.4	19.5	21.3	18.5
Dena 1	18.9	13.7	17.2	15.7	17.0	17.0	12.7	19.4	14.6	16.1	16.2
Dena 2	14.6	14.3	15.1	12.7	13.1	13.3	11.4	14.8	11.6	12.4	13.3
Grobogan	21.1	17.2	20.4	20.6	21.4	20.7	14.1	24.4	17.3	18.5	19.6
	20.4	17.2	20.7	17.5	18.7	18.5	14.8	22.0	17.1	18.6	18.5
/ariation (%)	4.4	4.5	3,9	4.4	3.9	4.9	4.5	8.9	4.2	9.1	
	1.3	1.1	1.2	1.1	1.0	1.3	1.1	3.2	1.2	2.8	
,	Genotype Grob/IT-7-1 Grob/IT-7-2 Grob/IT-7-3 Grob/IT-7-5 Grob/IT-7-7 Grob/IT-17-1 IBK/Argop-296-10 IBK/Argop-276-3 Grob/Pander-395-2 Grob/Pander-397-6 Grob/Pander-428-10 Grob/IAC-453-7 Dena 1 Dena 2 Grobogan /ariation (%)	Genotype L1 Grob/IT-7-1 20.9 Grob /IT-7-2 19.7 Grob/IT-7-3 20.8 Grob/IT-7-3 19.7 Grob/IT-7-7 18.4 Grob/IT-7-7 18.4 Grob/IT-7-7 18.4 Grob/IT-7-7 20.5 Grob/IT-7-7 20.5 Grob/Pander-395-2 24.2 Grob/Pander-397-6 23.4 Grob/Pander-428-10 24.1 Grob/IAC-453-7 18.6 Dena 1 18.9 Dena 2 14.6 Grobogan 21.1 20.4 20.4	Genotype L1 L2 Grob/IT-7-1 20.9 16.4 Grob /IT-7-2 19.7 16.9 Grob/IT-7-3 20.8 16.4 Grob/IT-7-3 19.7 16.9 Grob/IT-7-3 19.1 16.0 Grob/IT-7-7 18.4 16.5 Grob/IT-17-1 20.4 16.8 IBK/Argop-296-10 21.0 17.5 IBK/Argop-276-3 20.5 17.4 Grob/Pander-395-2 24.2 20.0 Grob/Pander-397-6 23.4 21.7 Grob/Pander-428-10 24.1 21.5 Grob/IAC-453-7 18.6 15.9 Dena 1 18.9 13.7 Dena 2 14.6 14.3 Grobogan 21.1 17.2 /ariation (%) 4.4 4.5 1.3 1.1 1.3	Genotype L1 L2 L3 Grob/IT-7-1 20.9 16.4 17.6 Grob /IT-7-2 19.7 16.9 20.9 Grob/IT-7-3 20.8 16.4 20.9 Grob/IT-7-3 20.8 16.4 20.9 Grob/IT-7-3 20.8 16.4 20.9 Grob/IT-7-3 19.1 16.0 20.4 Grob/IT-7-7 18.4 16.5 20.1 Grob/IT-17-1 20.4 16.8 20.7 IBK/Argop-296-10 21.0 17.5 20.3 IBK/Argop-276-3 20.5 17.4 19.8 Grob/Pander-395-2 24.2 20.0 25.2 Grob/Pander-397-6 23.4 21.7 24.0 Grob/Pander-428-10 24.1 21.5 25.0 Grob/IAC-453-7 18.6 15.9 22.5 Dena 1 18.9 13.7 17.2 Dena 2 14.6 14.3 15.1 Grobogan 21.1 17.2 2	Genotype L1 L2 L3 L4 Grob/IT-7-1 20.9 16.4 17.6 16.6 Grob/IT-7-2 19.7 16.9 20.9 15.7 Grob/IT-7-3 20.8 16.4 20.9 18.5 Grob/IT-7-3 19.1 16.0 20.4 16.0 Grob/IT-7-5 19.1 16.0 20.4 16.0 Grob/IT-7-7 18.4 16.5 20.1 16.1 Grob/IT-17-1 20.4 16.8 20.7 17.6 IBK/Argop-296-10 21.0 17.5 20.3 16.3 IBK/Argop-276-3 20.5 17.4 19.8 16.6 Grob/Pander-395-2 24.2 20.0 25.2 19.4 Grob/Pander-397-6 23.4 21.7 24.0 21.7 Grob/Pander-428-10 24.1 21.5 25.0 21.7 Grob/Pander-428-10 24.1 21.5 25.0 21.7 Dena 1 18.9 13.7 17.2 15.7	Weight ofL1L2L3L4L5Grob/IT-7-120.916.417.616.618.1Grob /IT-7-219.716.920.915.716.9Grob/IT-7-320.816.420.918.518.0Grob/IT-7-519.116.020.416.017.6Grob/IT-7-718.416.520.116.116.9Grob/IT-17-120.416.820.717.619.1IBK/Argop-296-1021.017.520.316.316.6IBK/Argop-276-320.517.419.816.620.4Grob/Pander-395-224.220.025.219.422.5Grob/Pander-397-623.421.724.021.724.3Grob/Pander-428-1024.121.525.021.721.0Grob/Pander-428-1024.121.525.021.721.0Grob/IAC-453-718.615.922.517.218.4Dena 118.913.717.215.717.0Dena 214.614.315.112.713.1Grobogan21.117.220.420.621.420.417.220.717.518.7/ariation (%)4.44.53.94.43.91.11.21.11.010	Weight of 100 seedsL1L2L3L4L5L6Grob/IT-7-120.916.417.616.618.116.6Grob /IT-7-219.716.920.915.716.917.7Grob/IT-7-320.816.420.918.518.018.7Grob/IT-7-519.116.020.416.017.616.5Grob/IT-7-718.416.520.116.116.916.7Grob/IT-7-718.416.520.116.316.615.7IBK/Argop-296-1021.017.520.316.316.615.7IBK/Argop-276-320.517.419.816.620.418.7Grob/Pander-395-224.220.025.219.422.523.3Grob/Pander-397-623.421.724.021.724.324.4Grob/Pander-428-1024.121.525.021.721.023.4Grob/IAC-453-718.615.922.517.218.415.8Dena 118.913.717.215.717.017.0Dena 214.614.315.112.713.113.3Grobogan21.117.220.420.621.420.720.417.220.717.518.718.5/ariation (%)4.44.53.94.43.94.91.31.11.21.11.01.3	Weight of 100 seeds (g) at locatL1L2L3L4L5L6L7Grob/IT-7-120.916.417.616.618.116.615.6Grob /IT-7-219.716.920.915.716.917.716.1Grob/IT-7-320.816.420.918.518.018.716.0Grob/IT-7-519.116.020.416.017.616.515.0Grob/IT-7-718.416.520.116.116.916.715.4Grob/IT-17-120.416.820.717.619.119.213.9IBK/Argop-296-1021.017.520.316.316.615.715.0IBK/Argop-276-320.517.419.816.620.418.713.7Grob/Pander-395-224.220.025.219.422.523.314.7Grob/Pander-397-623.421.724.021.724.324.416.3Grob/Pander-428-1024.121.525.021.721.023.417.7Grob/Pander-428-1024.121.525.021.721.023.417.7Dena 118.913.717.215.717.017.012.7Dena 214.614.315.112.713.113.311.4Grobogan21.117.220.717.518.718.514.8'ariation (%)4.44.53.9 <td< td=""><td>Weight of 100 seeds (g) at location "L1L2L3L4L5L6L7L8Grob/IT-7-120.916.417.616.618.116.615.620.0Grob/IT-7-219.716.920.915.716.917.716.120.7Grob/IT-7-320.816.420.918.518.018.716.023.0Grob/IT-7-519.116.020.416.017.616.515.022.9Grob/IT-7-718.416.520.116.116.916.715.420.1Grob/IT-17-120.416.820.717.619.119.213.921.5IBK/Argop-296-1021.017.520.316.316.615.715.022.3IBK/Argop-276-320.517.419.816.620.418.713.721.1Grob/Pander-395-224.220.025.219.422.523.314.725.8Grob/Pander-397-623.421.724.021.724.324.416.326.2Grob/Pander-428-1024.121.525.021.721.023.417.726.6Grob/Pander-428-1024.121.525.021.721.023.417.726.6Grob/Pander-428-1024.121.525.717.017.012.719.4Dena 118.913.717.215.717.017.012.7</td><td>Weight of 100 seeds (g) at location "L1L2L3L4L5L6L7L8L9Grob/IT-7-120.916.417.616.618.116.615.620.016.8Grob/IT-7-219.716.920.915.716.917.716.120.717.2Grob/IT-7-320.816.420.918.518.018.716.023.016.1Grob/IT-7-519.116.020.416.017.616.515.022.915.6Grob/IT-7-718.416.520.116.116.916.715.420.116.9Grob/IT-7718.416.520.316.316.615.715.022.316.6IBK/Argop-296-1021.017.520.316.316.615.715.022.316.6IBK/Argop-276-320.517.419.816.620.418.713.721.117.8Grob/Pander-397-623.421.724.021.724.324.416.326.220.5Grob/Pander-397-623.421.724.021.721.023.417.726.620.1Grob/Ac-453-718.615.922.517.218.415.814.021.419.5Dena 118.913.717.215.717.017.012.719.414.6Grob/Pander-428-1024.121.525.021.721.1<!--</td--><td>Genotype Weight of 100 seeds (g) at location " L1 L2 L3 L4 L5 L6 L7 L8 L9 L10 Grob/IT-7-1 20.9 16.4 17.6 16.6 18.1 16.6 15.6 20.0 16.8 18.6 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-5 19.1 16.0 20.4 16.0 17.6 16.7 15.4 20.1 16.9 17.9 Grob/IT-7-1 20.4 16.8 20.7 17.6 19.1 19.2 13.9 21.5 16.6 18.4 IBK/Argop-296-10 21.0 17.5 20.3 16.3 16.6 15.7 15.0 22.3 16.6 19.4 IBK/Argop-276-3 20.5 17.4 19.8</td></td></td<>	Weight of 100 seeds (g) at location "L1L2L3L4L5L6L7L8Grob/IT-7-120.916.417.616.618.116.615.620.0Grob/IT-7-219.716.920.915.716.917.716.120.7Grob/IT-7-320.816.420.918.518.018.716.023.0Grob/IT-7-519.116.020.416.017.616.515.022.9Grob/IT-7-718.416.520.116.116.916.715.420.1Grob/IT-17-120.416.820.717.619.119.213.921.5IBK/Argop-296-1021.017.520.316.316.615.715.022.3IBK/Argop-276-320.517.419.816.620.418.713.721.1Grob/Pander-395-224.220.025.219.422.523.314.725.8Grob/Pander-397-623.421.724.021.724.324.416.326.2Grob/Pander-428-1024.121.525.021.721.023.417.726.6Grob/Pander-428-1024.121.525.021.721.023.417.726.6Grob/Pander-428-1024.121.525.717.017.012.719.4Dena 118.913.717.215.717.017.012.7	Weight of 100 seeds (g) at location "L1L2L3L4L5L6L7L8L9Grob/IT-7-120.916.417.616.618.116.615.620.016.8Grob/IT-7-219.716.920.915.716.917.716.120.717.2Grob/IT-7-320.816.420.918.518.018.716.023.016.1Grob/IT-7-519.116.020.416.017.616.515.022.915.6Grob/IT-7-718.416.520.116.116.916.715.420.116.9Grob/IT-7718.416.520.316.316.615.715.022.316.6IBK/Argop-296-1021.017.520.316.316.615.715.022.316.6IBK/Argop-276-320.517.419.816.620.418.713.721.117.8Grob/Pander-397-623.421.724.021.724.324.416.326.220.5Grob/Pander-397-623.421.724.021.721.023.417.726.620.1Grob/Ac-453-718.615.922.517.218.415.814.021.419.5Dena 118.913.717.215.717.017.012.719.414.6Grob/Pander-428-1024.121.525.021.721.1 </td <td>Genotype Weight of 100 seeds (g) at location " L1 L2 L3 L4 L5 L6 L7 L8 L9 L10 Grob/IT-7-1 20.9 16.4 17.6 16.6 18.1 16.6 15.6 20.0 16.8 18.6 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-5 19.1 16.0 20.4 16.0 17.6 16.7 15.4 20.1 16.9 17.9 Grob/IT-7-1 20.4 16.8 20.7 17.6 19.1 19.2 13.9 21.5 16.6 18.4 IBK/Argop-296-10 21.0 17.5 20.3 16.3 16.6 15.7 15.0 22.3 16.6 19.4 IBK/Argop-276-3 20.5 17.4 19.8</td>	Genotype Weight of 100 seeds (g) at location " L1 L2 L3 L4 L5 L6 L7 L8 L9 L10 Grob/IT-7-1 20.9 16.4 17.6 16.6 18.1 16.6 15.6 20.0 16.8 18.6 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-3 20.8 16.4 20.9 18.5 18.0 18.7 16.0 23.0 16.1 17.5 Grob/IT-7-5 19.1 16.0 20.4 16.0 17.6 16.7 15.4 20.1 16.9 17.9 Grob/IT-7-1 20.4 16.8 20.7 17.6 19.1 19.2 13.9 21.5 16.6 18.4 IBK/Argop-296-10 21.0 17.5 20.3 16.3 16.6 15.7 15.0 22.3 16.6 19.4 IBK/Argop-276-3 20.5 17.4 19.8

Table 9. Weight of 100 seeds of soybean genotype evaluated in 10 locations

No.	Genotype	Seed yield average (t ha ⁻¹)	Seed weight (g/plant)	100 seeds weight	Number of filled pods/	bi ^{a)}	S ² di ^{D)}
				(g)	plant		
1	Grob/IT-7-1	1.85	14.8	17.7	39	ns	**
2	Grob /IT-7-2	1.70	12.4	18.0	33	ns	ns
3	Grob/IT-7-3	1.71	13.5	18.6	36	*	*
4	Grob/IT-7-5	1.82	12.9	17.7	34	ns	ns
5	Grob/IT-7-7	1.76	14.7	17.5	39	ns	ns
6	Grob/IT-17-1	1.63	12.6	18.4	37	ns	*
7	IBK/Argop-296-10	1.82	12.8	18.0	33	ns	*
8	IBK/Argop-276-3	1.90	14.0	18.5	33	ns	**
9	Grob/Pander-395-2	1.84	14,8	21.6	36	ns	ns
10	Grob/Pander-397-6	1.69	13.5	22.3	33	ns	ns
11	Grob/Pander -428-1	1.77	12.9	22.2	30	ns	**
12	Grob/IAC-453-7	1.84	14.2	18.5	37	ns	**
13	Dena 1	1.81	14.0	16.2	45	ns	*
14	Dena 2	1.80	12.8	13.3	43	ns	**
15	Grobogan	1.88	15.3	19.6	41	ns	ns
Aver	age	1.79	13.7	18.5	36.6		

Table 10. Seed yield and yield components average of 10 locations of 15 soybean genotypes

^{a)} bi = Regression coefficient; ^{b)} S²di = Regression deviation

4. CONCLUSIONS

The response of soybean genotypes tested 3. against the shading environments showed significant differences. Stability of genotypes were grouped into three, namely 1 genotype classified as unstable and recommended for less optimal environments, 6 genotypes (5 promising lines and 1 check variety Grobogan) were classified as stable and adaptive in 10 test locations, and eight genotypes (6 promising lines and 2 check varieties) classified as unstable in 10 test locations. Based on seed yield and yield components average, line Grob/Pander-395-2 had a high average seed yield, high seeds weight per plant, high weight of 100 seeds, and stable in 10 location. Therefore, Grob/Pander-395-2 line could be recommended for being grown in shading environments across the country.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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