Research Article

Stability analysis on yield of several winged bean lines (*Psophocarpus tetragonolobus* L.) in three environments

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ABSTRACT

Winged bean is a plant with a high seed protein content equivalent to soybeans. Indonesia is one of the central origins in southern Asia. However, there are still only a few superior varieties that can be widely cultivated. One effort to increase productivity is by growing improved varieties. This study aimed to identify promising winged bean lines with high and stable yield potential. The experiment was conducted in three environments, i.e., two planting seasons in Bogor and one in Palembang from January 2019 to June 2020. A total of 11 winged bean genotypes were tested and observed for grain yield characters. Parametric analysis methods were used to obtain information on the stability of 11 winged bean genotypes across the three environments. Grain yield was significantly affected by G x E interaction and, therefore, was subjected to stability analyses. Genotypes H1(P), L2, and H4(P) were classified as stable. This genotype had similar characteristics with stable grain yield in three test environments.

Keywords: G x E interaction; seed yield; parametric stability, underutilized legume

INTRODUCTION

The winged bean (*Psophocarpus tetragonolobus* (L.) DC) belongs to the Fabaceae family, which is an underutilized legume plant [\(Akinyosoye et al., 2023;](#page-6-0) [Ng, Samsuri,](#page-7-0) et al., [2020\)](#page-7-0). It grows well on various types of soil, including marginal land. The underuse of this plant is primarily due to insufficient awareness of its potential. In line with the food diversification initiative, winged beans should be recognized as a viable alternative source of nutrition (Kuswanto [et al., 2024\)](#page-7-1). Winged bean plants have good prospects as a significant multipurpose food crop in tropical areas, including Asia, Africa, and Latin America, providing human nutrition, animal feed, and environmental protection [\(Alalade](#page-6-1) [et al.,](#page-6-1) 2016). Even though dozens of species are consumed globally, only 20 crops comprising cereals, legumes, roots, and other food crops provide most of the world's calories [\(Mohanty et al., 2020\)](#page-7-2). Every component of the winged bean plant, such as flowers, leaves, young pods, seeds, and tubers, can be consumed [\(Mohanty et al., 2015;](#page-7-3) [Eagleton, 2020\)](#page-7-4).

Several winged bean accessions have produced edible tubers with high protein content and significant fiber, energy, and minerals [\(Sriwichai et al., 2021\)](#page-8-0). Winged bean seeds contain 33% protein, 39% carbohydrates, 19% fat, and various vitamins and minerals recommended for humans [\(Adegboyega et al., 2019;](#page-6-2) [Lepcha et al., 2017;](#page-7-5) [Ishthifaiyyah et al., 2023\)](#page-7-6). Winged beans are known for their potent antioxidant content,

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antihypertensive, and antifungal, in addition to their excellent nutritional value [\(Singh et](#page-8-1) [al., 2019;](#page-8-1) [Koley et al., 2019;](#page-7-7) [Chay et al., 2018;](#page-6-3) [Zakuan et al., 2018\)](#page-8-2). Winged beans have also been utilized as a component in several earlier trials to treat conditions like diabetes, cancer, infections, migraines, eye disorders, muscle weakness, and asthma [\(Singh et al.,](#page-8-1) [2019;](#page-8-1) [Ng, Yong, et al., 2020\)](#page-7-8). With this potential, winged beans can be one way to increase vegetable protein consumption in developing countries.

Indonesia is one of the centres of winged bean plant diversity worldwide. However, the lack of superior genotypes is a significant obstacle in the widespread use of winged beans [\(Popoola et al., 2019\)](#page-8-3). The yield and productivity of winged beans could be increased by breeding and introducing superior cultivars. Data on production shows that winged bean produces 2000 kg ha -1 of dry seeds and up to 10,000 kg ha -1 of young green pods [\(Tanzi et al., 2019\)](#page-8-4). A thorough survey was carried out at several cultivation centers across several provinces. This investigation identified 69 different local lines that exhibit a high degree of variation in seed color [\(Kuswanto, et al., 2024\)](#page-7-1). Local crop accessions have been successfully collected, and genetic diversity has been enhanced through crossbreeding. To obtain genotypes with high and stable yields, genotype studies must be conducted through environmental interactions $(G \times E)$. Interactions $(G \times E)$ are important for the development of enhanced genotypes in various contexts. When $G \times E$ interaction effects are non-significant, the means of assessed varieties across environments serve as sufficient indications of genotypic performance across those environments [\(Mafouasson](#page-7-9) [et al., 2018\)](#page-7-9).

Developing varieties that can adapt to various environments (broad adaptation) is the ultimate goal of plant breeders in crop improvement programs [\(Khalili & Pour-](#page-7-10)[Aboughadareh, 2016\)](#page-7-10). Therefore, genotype evaluation in a multi-environment is crucial for accurate candidate genotype ranking and discrimination and for identifying stable and high-yielding genotypes. The interaction between genotype and environment provides an effective assessment of genotypes regarding stability, and a stable genotype may be utilized for broader cultivation [\(Tiwari et al., 2022\)](#page-8-5). Stability has been widely studied by biometrics and genetics. Genetic \times environment interactions (G \times E) are crucial to developing better genotypes in various contexts. The means of examined variety across environments are sufficient markers of genotypic performance across environments when the effects of the $G \times E$ interaction are not considerable [\(Mafouasson et al., 2018;](#page-7-9) [Mebratu et al., 2019\)](#page-7-11). Finding significant crossover rank changes of the genotypes in various settings is critical when $G \times E$ exists such that distinct winners are selected in various contexts. The most common method is the parametric method. This method relies on a series of assumptions, including the hypothesis of a normal distribution with a zero mean and homogeneous variance.

The stability of the results of new candidate varieties can be analyzed using several methods, namely the parametric method based on [Wricke](#page-8-6) (1962), Shukla [\(1972\),](#page-8-7) and [Francis and Kannenberg \(1978\).](#page-7-12) This study aimed to identify promising winged bean lines with high and stable yield potential that can adapt widely to diverse environments.

MATERIALS AND METHODS

The research was conducted in three environments, Bogor1, Bogor2, and Palembang, from January 2019 to June 2020. The description of the three environments is presented in [Table 1.](#page-2-0) The genetic material used was 9 selected progeny of the 7th generation (F_7) from pedigree selection and 2 parent genotypes i[n Table 2.](#page-2-1)

Location	Geographic location			Mean annual	Temperature $(^{\circ}C)$	
	Longitude	Latitude	Altitude	rainfall (mm)	Min	Max
Bogor 1	$106^{\circ}43E$	$6^{\circ}33S$	201 m	285	26	35
Bogor 2	$106^{\circ}43E$	$6^{\circ}33S$	201 m	351	28	36
Palembang	$104^{\circ}48E$	$2^{\circ}57S$	8 m	187	28	37

Table 1. Description of the three research environments.

N ₀	Genotype code	Origin	Grain color
1	L1	Selected F ₇ progeny	Dark purple
2	L ₂	Selected F ₇ progeny	Dark purple
3	L ₃	Selected F ₇ progeny	Dark purple
4	L4	Selected F ₇ progeny	Dark purple
5	H1(P)	Selected F ₇ progeny	Brown
6	H1(U)	Selected F ₇ progeny	Dark purple
	H ₂	Selected F ₇ progeny	Brown
8	H3(U)	Selected F ₇ progeny	Dark purple
9	H4(P)	Selected F ₇ progeny	Brown
10	P ₂	Male parent (local green-winged	Brown
		bean from Cilacap, Indonesia	
11	P1	Female parent (purple winged	Dark purple
		bean, introduced from Thailand)	

Table 2. The list of winged bean genotypes evaluated.

The combined variance analysis of each environment refers to the fixed model [\(Table](#page-2-2) [3\)](#page-2-2). Analysis of yield stability was carried out using parametric methods: Wricke [\(1962\),](#page-8-6) Shukla [\(1972\),](#page-8-7) an[d Francis and Kannenberg \(1978\).](#page-7-12)

Wricke (1962)

Wricke's method uses ecovalence (Wi 2) as a stability parameter. Ecovalence is a measurement of the contribution of each genotype to the total square of interaction with the environment. The calculation used is :

$$
W_i^2 = \sum_{j=1}^q (\bar{X}_{ij} - \bar{X}_{i.} - \bar{X}_{.j} - \bar{X}_{..})
$$

Shukla (1972)

[\(Shukla, 1972\)](#page-8-7) method uses stability variance (σ^2) as the stability parameter. The stability variance is the difference between two sums of squares so that the value can be negative. The calculation used is :

$$
\sigma_i^2 = \frac{p}{(p-2) - (q-1)} \sum_{j=1}^q (\bar{X}_{ij} - \bar{X}_{i.} - \bar{X}_{.j} - \bar{X}_{..}) + \frac{SS(GE)}{(p-1)(p-2)(q-1)}
$$

Francis and Kannenberg (1978)

[Francis and Kannenberg \(1978\)](#page-7-12) stated that the stability of a genotype is determined by the value of environmental variation and the coefficient of variation (CV_i) . The value of the coefficient of variation (CVi) is determined from the value of the average standard deviation of the results of a genotype based on the general average.

$$
CVi = \left(\frac{\sqrt{s_i^2}}{\bar{Y}_{i.}}\right) x \quad 100\% = \left(\frac{\sqrt{\frac{\sum_i (\bar{Y}_{ij} - \bar{Y}_{.j})^2}{q - 1}}}{\bar{Y}_{i.}}\right) x \quad 100\%
$$

Where CVi is the coefficient of diversity, S_i^2 is the environmental variance, Y_i . is the mean of the ith genotype across all jth locations, \bar{Y}_{ij} is the mean of the ith genotype and the jth environment, \bar{Y}_i is the mean of the jth environment for all genotypes, q is the number of the ith environment. The outline of the mixed model analysis of variance is shown i[n Table](#page-2-1) [2.](#page-2-1) Analysis of variance and stability analyses used PBSTAT-GE on www.pbstat.com.

Source		Mean square	F-value
Environments (E)	(l-1)	M5	M5/M4
Replications/E	$l(r-1)$	M4	$\overline{}$
Genotype (G)	$(g-1)$	M ₃	M3/M1
$G \times E$	$(g-1)(l-1)$	M ₂	M2/M1
Error	$l(g-1)(r-1)$	M1	$\overline{}$

Table 3. Model of combined analysis of variance across environments.

Note: l, r, and g are the numbers of location, replication, and genotype, respectively; Genotype and environment were regarded as fixed effects, while replication within the environment was regarded as a random effect.

RESULTS AND DISCUSSION

Analysis of variance [\(Table 4\)](#page-3-0) showed that environmental factors and their interactions (G x E) significantly affected grain yield in the genotypes tested. Analysis of variance also indicated that the sum of the squares of the environment contributed 43.76% to the character of grain yield variance. The interaction of genotype x environment contributed 33.65% to grain yield variance, while the genotype contributed 22.59% to grain yield variance. The large and significant sum of the mean squares of the environment indicates that environmental conditions cause diversity in response between environments [\(Chimonyo et al., 2019\)](#page-7-13).

Table 4. Combined analysis of variance for grain yield.

Source	df	SS	MS	F-value	Contribution $(\%)$
Environment (E)		35.03	17.52	18.25**	43.76
Replication/E	6	5.75	0.96	$3.03*$	
Genotype (G)	10	18.09	1.81	$5.71**$	22.59
$G \times E$	20	26.94	1.35	$4.25**$	33.65
Error	59	18.70	0.32		
Total	97	104.513			

Note: $*$ = significant at α = 0.05; $**$ = significant effect at α = 0.01; ns = not significant.

The interaction between genotype and environment causes differences in response in each genotype. The effects of both factors, both genotype and environment, determine the phenotype of an individual, but they are not always additive because of the interaction between the two. The analysis of highly significant genotype and environment interactions indicates that character performance and environmental changes fluctuate [\(Lodhi et al., 2015\)](#page-7-14).

[Figure 1](#page-4-0) shows the grain yield of 11 genotypes tested in three environments and the interaction between genotype x environment. This interaction was caused by changes in the response of each genotype tested in different locations and seasons. This showed that the genotypes tested provided different productivity responses to the three growing environments. The values of young pod productivity and grain yield that differed between genotypes in three environments and had a significant G x E interaction met the requirements for stability analysis. This was done to explain the effect of interaction.

Figure 1. Genotype x environment interaction on grain yield.

The number of seeds per pod of winged bean [\(Table 5\)](#page-4-1) tested in three environments ranged from 10.46 to 17.37. The purple elder genotype P1 showed the highest average number of seeds per pod, with 18.86 seeds, which was significantly different from all genotypes. The environment showed no significant difference in the number of seeds per pod. The average seed weight per plant tested in the three environments ranged from 1.39 to 79.55 g. Genotype H3(U) had the highest average seed weight per plant with 58.23 g and was not significantly different from genotypes L4, L1, L2, H4(P), and P1 (purple parents). The test environment showed a significant difference, whereas the Palembang environment had the heaviest seed weight per plant, with 60.59 g.

Lines	Number of seeds per pod	Weight of seeds per plant (g)	100 seed weight (g)	Weight of young pod(g)
L1	10.60c	47.94ab	34.05e	10.60e
L ₂	11.38 _{bc}	48.59ab	36.99cd	10.40e
L ₃	11.44 _{bc}	35.54c	36.61cd	10.94de
L ₄	11.08c	53.73ab	35.25de	10.81de
H1(P)	11.62 _{bc}	42.31 _b	38.35 _{bc}	10.81de
H1(U)	11.72bc	42.46b	40.41a	11.10de
H ₂	11.62 _{bc}	36.45c	35.67de	11.65cd
H3(U)	14.62b	58.23a	39.83ab	12.40 _{bc}
H4(P)	12.11bc	47.36ab	35.18de	11.62cd
P ₁	18.86a	53.65ab	40.14a	12.69b
P ₂	11.47bc	22.77d	34.08e	13.96a

Table 5. Yield component of winged bean grain yields.

Note: Numbers in the same column followed by the same letter are not significantly different based on the DMRT test at α = 0.05.

The weight of 100 seeds tested in three environments ranged from 32.80 to 46.43 g. According to [Eagleton](#page-7-15) (2019), the average weight of 100 seeds of local accessions of winged beans was 48.30 g. In comparison, soybeans' weight of 100 seeds ranged from 15.29 to 16.69 g. Genotype H1(U) had an average weight of 100 in the three test environments and was not significantly different from genotype P1 (purple parents) and genotype H3U. The environment with a real effect was due to high temperature and rainfall in the Bogor 2 environment, resulting in flowering age in the Bogor 2 environment appearing later than the other two environments.

Wricke (1962)

Ecovalence was a stability parameter employed by [Wricke \(1962\).](#page-8-6) The contribution of each genotype to the overall interaction of all genotypes with the environment is measured by ecovalence. It is, therefore, a technique for analyzing dynamic stability. According to [\(Mulusew et al., 2014\)](#page-7-16), genotypes with low ecovalence scores exhibit less variability in yield across all settings, hence being categorized as stable genotypes. Wricke stability analysis is presented in [Table 5.](#page-4-1) The most stable genotypes were H1(P), L2, and H4(P), in that order. Conversely, the least stable genotypes were L1, L4, and L3.

Shukla (1972)

Shukla['s \(1972\)](#page-8-7) method uses stability variance (σ^2) as a parameter, where genotypes with small variance values indicate stable genotypes. Based on [Table 5,](#page-4-1) genotypes H1(P), L2, and H4(P) were classified as stable genotypes, while genotype P2 was unstable. The same results were obtained using the Wricke method analysis. This is in line with the statement of [\(Goksoy et al., 2019\)](#page-7-17), which states that the Shukla method is a dynamic stability concept whose results resemble the Wricke method.

Table 6. Average grain yield, Wricke ecovalence, Shukla stability variance, and Francis and Kannenberg coefficient of variation.

Genotype	Y (tons ha-1)	W^2	σ^2	CV _i
L1	2.64	1.64	0.95	8.75
L ₂	2.55	0.06	-0.02	29.33
L ₃	1.81	1.36	0.78	57.36
L4	2.74	1.54	0.89	15.12
H1(U)	2.46	0.38	0.18	34.69
H1(P)	2.29	0.04	-0.03	49.77
H ₂	2.09	0.94	0.52	65.91
H3(U)	2.22	0.16	0.05	38.31
H4(P)	2.71	0.15	0.04	18.10
(P1)	2.44	0.29	0.13	19.21
(P2)	1.23	2.49	1.47	150.06
Mean	2.29			

Note: Y= average grain yield; W²i = Wricke's ecovalence; σ^2 _i = stability variance; CV_i = coefficient of variability.

Francis and Kannenberg (1978)

This method uses the coefficient of diversity (CV_i) value. The coefficient of diversity (CVi) value is determined from the standard deviation value of the average yield of a genotype based on the general average. The smaller the coefficient of diversity value, the higher the level of stability of a genotype.

The relationship between the coefficient of diversity (CV_i) and the average productivity of each genotype is presented in [Figure 2.](#page-6-4) The average production results against the coefficient of diversity (CV) are divided into four groups. Group I is genotypes that have high production with low diversity. Group II is genotypes that have high yields with high diversity. Meanwhile, groups III and IV are genotypes that have low production with low and high diversity, respectively.

Figure 2. Relationship between the coefficient of variance (CVi) and mean of grain yield.

Genotypes in group I are genotypes with high and stable production. According to the Francis and Kanennberg method, only group I is considered stable. So, although group III is classified as stable, it shows low results in other environments. [Figure 2](#page-6-4) shows that genotypes L1, L2, L4, H1(P), H4(P), and P1 were stable and had relatively high results compared to the average of all genotypes in the three environments. Genotypes that showed instability were L3, H2, and P2, and they had low seed yields compared to the average of all genotypes in the three environments.

CONCLUSIONS

The effect of environment, genotype, and genotype by environment interaction was significant on grain yield were highly significant ($p < 0.01$). Genotypes L4, H4(P), L1 and L2 showed higher grain yield per hectare. According to parametric methods, genotypes H1(P), L2, and H4(P) were classified as stable. Therefore, those genotypes may be deployed in those specific locations.

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