sustainability

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# Evaluation of Indonesian Butterfly Pea (*Clitoria ternatea* L.) Using Stability Analysis and Sustainability Index

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**Abstract:** Yield and yield attributes are important components in genotypic evaluation. The butterfly pea is a native plant of Indonesia, and it is considered an underutilized crop. The goals of this study were to evaluate genotypes using environment (year) interactions (GEIs) with yield and yield attributes, and evaluate butterfly pea genotypes based on stability measurements and sustainability index (SI). The study was conducted at the Ciparanje Experimental Field, Faculty of Agriculture, Universitas Padjadjaran using 35 butterfly pea genotypes in a randomized complete block design with two replications. The field trial was conducted over three years (2018–2020). The results showed that the yield and yield attributes were influenced by GEIs. Additive main effects and multiplicative interaction (AMMI) selected 11 stable genotypes (31.43%); genotype plus genotype by environment interaction (GGE) biplot, AMMI stability value (ASV), and genotype stability index (GSI), each selected six genotypes (17.14%) that were stable and high-yielding, and SI selected 18 genotypes (51.43%) that were stable and high-yielding. There were three genotypes identified by all measurements, namely G2, G14, and G16. These three genotypes can be selected as the superior genotypes of the butterfly pea for flower production, and can be used as material for crosses in plant-breeding prog.

**Keywords:** AMMI; butterfly pea; *Clitoria ternatea*; evaluation; flower production; genotypes; GGE biplot; sustainability

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## 1. Introduction

Indonesia is a tropical country that is considered to have the highest biodiversity in the world. One of Indonesia's biodiversity resources is the butterfly pea (*Clitoria ternatea* L.) Butterfly pea belongs to the Fabaceae plant family. Butterfly pea is often found in tropical Southeast Asia [1,2]. This plant is known to be tolerant of excess rain and drought [3]. In Indonesia, it is easily found in home gardens, forest edges or in the wild.

Butterfly pea is one of Indonesia's original local crops that has the potential to be further developed [4]. The wide genetic diversity of the Indonesian butterfly pea, based on morphological characteristics, provides opportunities for research and development [3,5]. In addition, the butterfly pea has many uses, including as a natural dye [6], food coloring [7], and cancer prevention because of its high antioxidant content [8], and also as an ornamental crop [9]. During the COVID-19 pandemic, the use of natural ingredients rich in healthy nutrients, such as anthocyanin, to increase body resistance was highly recommended to avoid the transmission of COVID-19 [10]. Since the butterfly pea contains anthocyanins, it is often associated with increased body resistance and cancer prevention [8]. Thus, the development of the butterfly pea has a great potential to support food, health, and industrial needs [4].

The butterfly pea has an important role for the people of Indonesia. In some parts of Indonesia, the butterfly pea was used as an eye medicine [11], as food coloring [7], and has its own cultural value for the community [12]. The name 'ternatea' was taken from one of the islands in Indonesia, namely Ternate [7]. In our previous studies, the genetic diversity of the butterfly peas from Indonesia was broad and it had varied patterns and number of petals [3,13]. This implies that the origin of the Indonesian butterfly pea is an important genetic resource that must be utilized and preserved properly. Currently, testing of GEIs on yield and yield attributes regarding the origin of the Indonesian butterfly pea is still very limited. Therefore, testing in different planting seasons to evaluate GEIs on yield and yield attributes, as well as the selection of high-yielding and stable genotypes, are very valuable.

Extreme seasonal changes have an impact on the development of plant varieties. Several studies reported that the growing seasons affect yields and yield attributes [14–16]. In addition, the interaction between genotypes and growing seasons have also been reported to greatly affect crop yields and make research prog inefficient [17–20]. Currently, studies on the effects that genotypes by environment interactions have on the butterfly pea are still very limited. Since the butterfly pea is an underutilized crop, the research and development of this plant is still quite rare. Therefore, it is very important to evaluate the genotype using the way the growing seasons interact with the yield and yield attributes of the butterfly pea.

The sustainability index (SI) is one of the genotypic selection indices used in diverse seasons. The use of the SI to select or evaluate the genotypes of some crops that have a greater potential regarding change during growing seasons has been reported [21–25]. This study aimed to evaluate the butterfly pea's genotype using environment (growing seasons) interactions (GEIs) with yield and yield attributes, and selecting superior genotypes (stable and high-yielding) across three different growing season (years) using stability analysis and the sustainability index (SI).

## 2. Materials and Methods

### 2.1. Plant Materials

There were 35 butterfly pea genotypes, collected from around Indonesia, that were used in this study. These genotypes had diverse genetic backgrounds (Table 1) and high genetic diversity [3]. The butterfly pea (BFP) is a perennial crop, and hence, it grows during the whole year. The data were obtained by three planting seasons, and hence, there was a three-year observation period involving wet and dry seasons.

**Table 1.** Butterfly pea genotypes used in experiments.

| No. | Code | Accessions | Origin | | |
|---|---|---|---|---|---|
| | | | Island | Province | District |
| 1 | G1 | CT 1.1 | Sumatera | Aceh | Banda Aceh |
| 2 | G2 | CT 1.2 | Sumatera | Aceh | Banda Aceh |
| 3 | G3 | CT 1.3 | Sumatera | Aceh | Banda Aceh |
| 4 | G4 | CT 1.4 | Sumatera | Aceh | Banda Aceh |
| 5 | G5 | CT 1.5 | Sumatera | Aceh | Banda Aceh |
| 6 | G6 | CT 2.1 | Sumatera | Aceh | Banda Aceh |
| 7 | G7 | CT 2.2 | Sumatera | Aceh | Banda Aceh |
| 8 | G8 | CT 2.3 | Sumatera | Aceh | Banda Aceh |
| 9 | G9 | CT 2.4 | Sumatera | Aceh | Banda Aceh |
| 10 | G10 | CT 2.5 | Sumatera | Aceh | Banda Aceh |
| 11 | G11 | CT 3.1 | Sumatera | Aceh | Banda Aceh |
| 12 | G12 | CT 3.2 | Sumatera | Aceh | Banda Aceh |
| 13 | G13 | CT 3.3 | Sumatera | Aceh | Banda Aceh |
| 14 | G14 | CT 3.4 | Sumatera | Aceh | Banda Aceh |
| 15 | G15 | CT 3.5 | Sumatera | Aceh | Banda Aceh |
| 16 | G16 | CT 4.1 | Java | West Java | Bandung |

**Table 1.** *Cont.*

| No. | Code | Accessions | Origin | | |
|---|---|---|---|---|---|
| | | | **Island** | **Province** | **District** |
| 17 | G17 | CT 4.2 | Java | West Java | Bandung |
| 18 | G18 | CT 4.3 | Java | West Java | Bandung |
| 19 | G19 | CT 4.4 | Java | West Java | Bandung |
| 20 | G20 | CT 4.5 | Java | West Java | Bandung |
| 21 | G21 | CT 5.4 | Java | West Java | Kuningan |
| 22 | G22 | CT 6.1 | Java | Jakarta | Jakarta |
| 23 | G23 | CT 6.2 | Java | Jakarta | Jakarta |
| 24 | G24 | CT 6.3 | Java | Jakarta | Jakarta |
| 25 | G25 | CT 6.5 | Java | Jakarta | Jakarta |
| 26 | G26 | CT 9.1 | Java | West Java | Kuningan |
| 27 | G27 | CT 10.1 | Java | East Java | Madura |
| 28 | G28 | CT 10.2 | Java | East Java | Madura |
| 29 | G29 | CT 10.3 | Java | East Java | Madura |
| 30 | G30 | CT 10.4 | Java | East Java | Madura |
| 31 | G31 | CT 10.5 | Java | East Java | Madura |
| 32 | G32 | CT12.1 | Bali | Bali | Bali |
| 33 | G33 | CT12.2 | Bali | Bali | Bali |
| 34 | G34 | CT12.3 | Bali | Bali | Bali |
| 35 | G35 | CT12.4 | Bali | Bali | Bali |

### 2.2. Field Experiments and Data Collection

Field experiments were conducted at the Ciparanje Field Research Station (6°54′58.4″ S 107°46′17.3″ E; altitude 721 meters above sea level), Faculty of Agriculture, Universitas Padjadjaran (UNPAD), Jatinangor, Sumedang, West Java, Indonesia during a three-year period (Table 2). Information about the environment is presented in Table 2. The field experiment trials used a randomized completed block design with two replications per year. Each genotype was planted at a spacing of 100 cm × 50 cm. The number of plants of each replicate was 20 plants. The first year it was planted in January–November 2019. The second year it was planted in February–December 2020. The third year it was planted in January–November 2021. The land was loosened, the bunds were 25 cm tall, the length of each bund was 5 meters. The initial fertilization was performed one week before planting, using chicken manure at a dose of 5 tons/ha. The second fertilization was performed eight weeks after planting, using an NPK fertilizer at a dose of 120 kg/ha. Six weeks after planting (WAP), the plants were wrapped around a bamboo stake. The observed traits include fresh flower yield (gram), flower length (FL in cm), flower width (FW in cm), and calix length (CL in cm). The yield and yield attributes were measured and collected at harvest time.

**Table 2.** Trial growing seasons information.

| Seasons | Temperature (°C) | | Rainfall (mm Month$^{-1}$) | | Humidity | | Soil Conditions | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Min–Max** | **Mean ± SD** | **Min–Max** | **Mean ± SD** | **Min–Max** | **Mean ± SD** | **pH** | **K** | **P** | **N** | **C-O** |
| Season-1 (2018) | 18.02–31.83 | 23.60 ± 0.32 | 0.2–313.5 | 169.3 ± 122.1 | 90–97 | 93.50 ± 3.50 | 5.5 | 13.96 | 31.48 | 0.13 | 1.32 |
| Season-2 (2019) | 17.71–32.64 | 26.10 ± 0.74 | 30.0–337.0 | 201.6 ± 115.0 | 70–87 | 74.72 ± 7.16 | 5.6 | 16.66 | 31.29 | 0.13 | 1.41 |
| Season-3 (2020) | 18.48–31.27 | 31.27 ± 0.70 | 33.2–454.3 | 180.9 ± 114.2 | 67–80 | 73.50 ± 6.50 | 5.5 | 12.43 | 31.20 | 0.22 | 1.11 |

Note : SD = standard deviation; Min = minimum value; Max = maximum value; K = potassium (%); P = phosphor (%); N = nitrogen (%); C-O = carbon organic (%).

### 2.3. Statistical Analysis

The combined ANOVA statistical model to estimate GEIs follows this equation:

$$Y_{opqr} = \mu + G_o + E_p + GE_{op} + R_{q(p)} + B_{r(q)} + \varepsilon_{opqr} \tag{1}$$

where $Y_{opqr}$ is the value of the butterfly pea $o$ in plot $r$, and the value in year $p$ of each replication is $q$; $\mu$ is the grand mean of yield; $G_o$ is the effect of butterfly pea o; $E_p$ is the effect of year p; $GE_{op}$ is the effect of GEIs on butterfly pea o and year p; $R_{q(p)}$ is the effect of replicate q on year p; $B_{r(q)}$ is the effect of replication q on plot r; and $\varepsilon_{opqr}$ is the error effects from butterfly pea o in plot r and repeat q of year p, respectively. In the case of multi-environment testing (location or season), GEIs information was needed to find out whether further testing was necessary using stability analysis. If GEIs have a significant effect, then researchers must carry out further analysis using stability measurements to determine which genotypes are stable (the genotype response to GEIs is small) and which ones are adaptive to certain environments (genotype response to GEIs is large). Genstat 12th is used to calculate the combined ANOVA.

AMMI is used to estimate the stability of the butterfly pea yields, following [26]:

$$Y_{ef} = \mu + Ge + E_f + \sum_{k=1}^{n} \left( \lambda_g \, \alpha_{eg} \gamma_{fg} \right) + \rho_{ef} \tag{2}$$

where: $Y_{ef}$ is the yield performance of the genotype $e^{th}$ in the year $f^{th}$, $\mu$ is the average of all yield performances from the genotypes used, $G_e$ is the mean deviation of genotype $e^{th}$, $E_f$ is the mean deviation of year $f^{th}$, $\lambda_k$ is the square root of the eigenvalue of the PCA axis $g$, $\alpha_{eg}$ and $\gamma_{fg}$ were the PC scores for the PCA axis, $g$, of genotype $i^{th}$ and year $f^{th}$, respectively, $\rho_{ef}$ is the residual. According to the AMMI measurement, genotypes was considered stable if they are within the radius of the circle and close to the axis (0.0). In contrast, the adaptive genotypes are far from the axis and close to the environment line vector. AMMI was analyzed using the PBStat online software [27].

The AMMI stability value (ASV) was used to estimate the stability of the butterfly pea yields, following the formula [28]

$$\mathrm{ASV} = \sqrt{\frac{ss\ IPCA\ 1}{ss\ IPCA\ 2}(IPCA\ 1\ score)^2 + (IPCA\ 2\ score)^2} \tag{3}$$

where *ss IPCA* 1 and *ss IPCA* 2 were the wight given to the *IPCA* 1 and *IPCA* 2 scores by dividing *ss IPCA* 1 and ss *IPCA* 2. The *IPCA* 1 score and *IPCA* 2 score were the first and second IPCA scores for each genotype from the AMMI analysis. Genotypes that were stable across the years were indicated by a small ASV value and vice versa.

The genotype stability index (GSI) for butterfly pea genotypes was calculated based on the ASV rank (RASV) from the genotypes tested in three environments (years) and the yield performance rank (RGM) of genotypes tested during those three years using Equation (4). Genotypes that were stable across the years were indicated by a small GSI value and vice versa.

$$\mathrm{GSI} = \mathrm{RASV} + \mathrm{RGM} \tag{4}$$

The model for the GGE biplot following [29] was this formula

$$\bar{Y}_{mn} - \mu_m = \beta_n + \sum_{k=1}^{t} \lambda_o \alpha_{mo} \gamma_{no} + \varepsilon_{mn} \tag{5}$$

where $\bar{Y}_{mn}$; $\mu_m$; $\beta_n$; $k$; $\lambda_o$; $\alpha_{mo}$; $\gamma_{no}$; $\varepsilon_{mn}$ are the performance in year '*n*' of the butterfly pea '*m*'; overall average yield; the influence of year '*n*'; number of primer components; the singular value of the primer component '*o*'; the value of butterfly pea '*m*' and year '*n*' for primer component '*o*'; and the error of the butterfly pea '*m*' in year '*n*', respectively. The GGE biplot was analyzed using the R program.

The sustainability index (SI) was estimated by the following formula used by [22]

$$SI = \left[ \frac{(Y - \sigma n)}{YM} \right] \times 100 \tag{6}$$

where $Y$ is the mean performance of a butterfly pea, σn is the standard deviation, and $YM$ is the best performance of a butterfly pea in any year. The $SI$ values were classified arbitrarily into five groups, i.e., very low (up to 20%), low (21% to 40%), moderate (41% to 60%), high (61% to 80%), and very high (above 80%) [30]. SI was calculated using Microsoft Excel 2013.

## 3. Results

### 3.1. GEIs Estimation of the Yield and Yield Attributes of the Butterfly Pea Genotypes

The yield and yield attributes of 35 butterfly pea genotypes during the three-year period were evaluated. The results of the combined ANOVA showed that genotype, environment, and GEIs had a significant effect on the variation in the yield and yield attributes of each genotype tested (Table 3). Yields are in the range of 4.70–151.70 g, where the highest yields is in the second year (2019). The FL trait is in the range of 1.45–7.87 cm, where the highest values are in 2019 and the lowest values in 2020. The FW trait is in the range of 1.36–5.80 cm, where the highest values are in 2019 and the lowest values in 2020. The CL trait is in the range of 0.63–4.60 cm, where the highest value is in 2019 and the lowest in 2020. The coefficient of variation (CV) value for the traits tested show a low value for the yield, moderate for the CL, and high for the FL and FW traits. In this test, all the traits tested showed the influence of GEIs. However, in general, genetic influences are greater than GEIs for all traits, so that the variations that occur in the traits tested may be due to the origin of each genotype.

**Table 3.** Combined ANOVA of yield and yield attributes on butterfly pea genotypes.

| Source | df | Sum of Square | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Yield (g) | | FL (cm) | | FW (cm) | | CL (cm) | |
| Env | 2 | 18,024 | ** | 178.01 | * | 83.49 | ** | 36.12 | * |
| Rep (env) | 3 | 36 | ** | 76.11 | ** | 11.26 | ** | 27.39 | ** |
| Gen | 34 | 255,120 | ** | 46.52 | ** | 46.56 | ** | 43.54 | ** |
| Gen x Env | 62 | 63,745 | ** | 22.47 | * | 10.41 | * | 8.39 | ** |
| Error | 102 | 28 | * | 28.01 | * | 23.01 | * | 4.30 | * |
| Min | | 4.70 | | 1.45 | | 1.36 | | 0.63 | |
| Max | | 151.70 | | 7.87 | | 5.80 | | 4.60 | |
| Mean | | 65.35 | | 4.49 | | 3.51 | | 1.71 | |
| CV (%) | | 0.42 | | 24.53 | | 25.39 | | 15.66 | |

Note: df = degree freedom; Env = environment; Rep = replication; CV = coefficient of variation; FL = flower length; FW = flower width; CL = calix length; * $p < 0.05$; ** $p < 0.01$.

### 3.2. Yield Stability Using AMMI and GGE Biplot

The results of the stability analysis using the AMMI biplot are presented in Figure 1. The AMMI biplot showed that PC1 had a contribution of 96.8% to the total variation and PC2 had a contribution of 3.2%. In Figure 1, the genotypes that are close to the axis (0.0) and are on the radius of the circle are the most stable during the three years of testing. The eleven genotypes that were on the radius of the circle were identified; they were G2, G20, G14, G16, G25, G19, G8, G24, G17, G28, and G15. Those eleven genotypes were the most stable according to the AMMI biplot measurement.

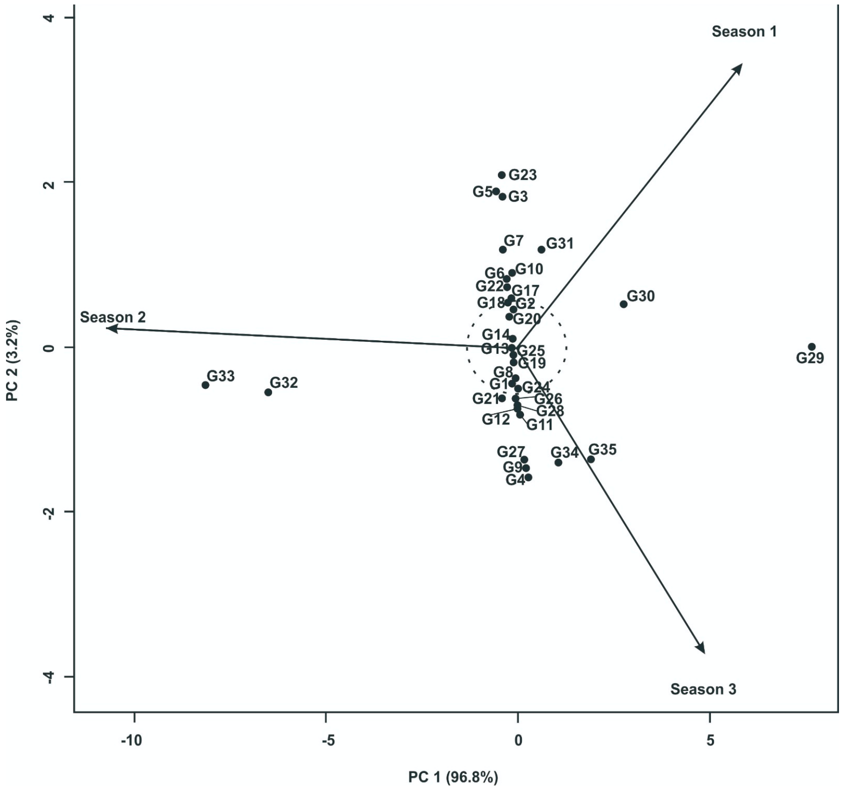
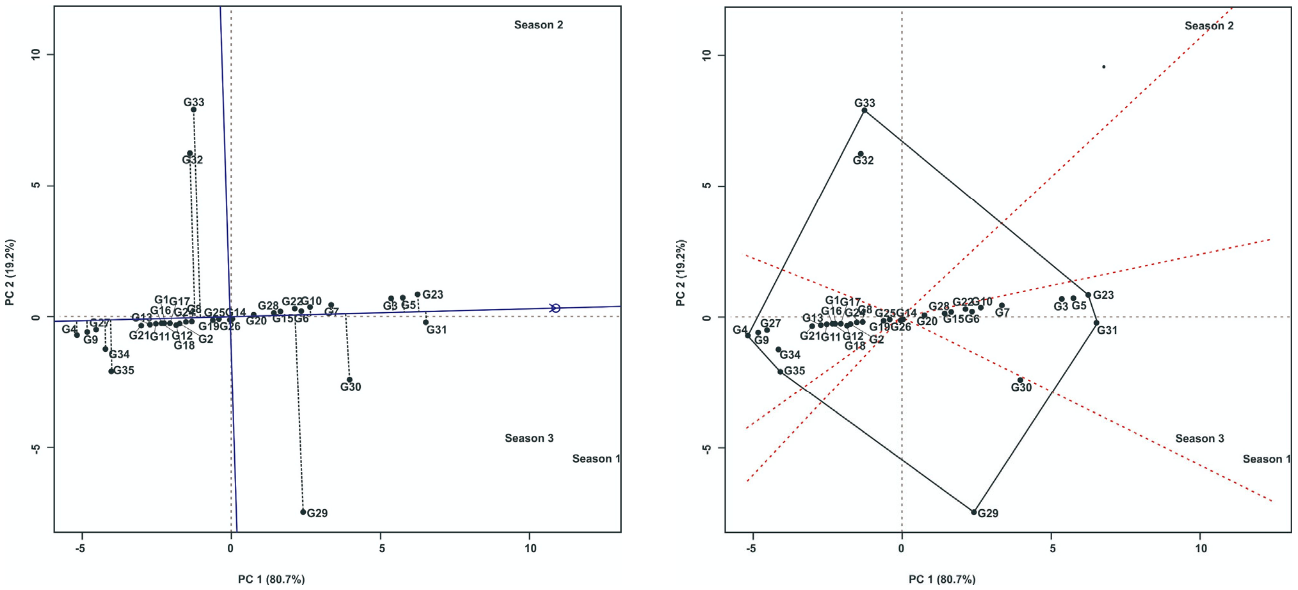


**Figure 1.** AMMI biplot of 35 butterfly pea genotypes across three seasons (years) in Indonesia.

The evaluation of the butterfly pea's genotypes using a GGE biplot measurement was presented in Figure 2. Based on the GGE biplot measurement, PC1 and PC2 explained 80.7% and 19.2% of the total variation, respectively. Thus, they contribute 99.9% of the total variation in the butterfly pea yield across the three growing years in Indonesia (Figure 2). The GGE biplot 'mean vs stability' graph showed that 14 genotypes of the butterfly pea were on the right side of the Y-axis and another 21 genotypes were on the left of the Y-axis (Figure 2a). The Y-axis showed the average yield of each genotype, and the X-axis showed the stability of the yield of each tested genotype. Agronomically, genotypes G2, G14, G15, G16, and G20 were the most stable and had above average yields. A genotype close to the ideal point in the GGE biplot has a high and stable yield. In this study, it was identified that G31 was close to the ideal point, which means this genotype was able to produce high yields in both optimal and marginal environments.

The graph on the GGE biplot, 'which-won-where' (Figure 2b), showed that the three years had six sectors with different winning genotypes. G33 is the top genotype in Year 2 (second year). G31 is the top genotype in Years 1(first year) and Year 3 (third year). In this study, the six genotypes of the butterfly pea that were close to the center of the sector were identified; namely, G1, G2, G6, G14, G15, and G16. These genotypes have a smaller GEIs effect than other genotypes, but do not necessarily have high yields, so other measurements are needed to be able to select stable and high-yielding genotypes.



(**a**) (**b**)

**Figure 2.** (**a**) GGE biplot 'mean vs stability' of 35 butterfly pea genotypes against average yields in three growing years; (**b**) GGE biplot 'which-won-where' of 35 butterfly pea genotypes against average yields in the three growing years.

### *3.3. Yield Stability of Butterfly Pea using AMMI Stability Value (ASV) and Genotype Stability Index (GSI)*

Information on ASV and GSI was presented in Table 4. The low value genotypes were identified as having stable yields. Based on ASV, G16 was identified as the most stable genotype, followed by G14, G25, G19, G20, and G2. The GSI measurements identified the G14 genotype as the most stable followed by G16, G2, G20, G15, and G17. Table 4 shows that ASV and GSI identified G2, G14, G16, and G20 genotypes as stable and high-yielding.

**Table 4.** IPCA on AMMI analysis, AMMI stability value (ASV), and genotype stability index (GSI).

| Genotypes | Y | IPCA [1] | IPCA [2] | RY | ASV | RASV | GSI | RGSI |
|---|---|---|---|---|---|---|---|---|
| G1 | 37.24 | 0.18 | 0.72 | 28 | 1.23 | 18 | 46 | 26 |
| G2 | 77.89 | −0.07 | −0.46 | 14 | 0.61 | 6 | 20 | 3 |
| G3 | 125.16 | −0.37 | −1.84 | 4 | 2.73 | 26 | 30 | 15 |
| G4 | 8.58 | 0.36 | 1.56 | 35 | 2.52 | 25 | 60 | 33 |
| G5 | 127.41 | −0.38 | −1.90 | 3 | 2.83 | 27 | 30 | 16 |
| G6 | 90.37 | −0.15 | −0.82 | 8 | 1.17 | 16 | 24 | 10 |
| G7 | 102.09 | −0.22 | −1.16 | 6 | 1.69 | 22 | 28 | 13 |
| G8 | 49.57 | 0.10 | 0.36 | 22 | 0.68 | 7 | 29 | 14 |
| G9 | 13.69 | 0.33 | 1.41 | 34 | 2.29 | 24 | 58 | 32 |
| G10 | 92.83 | −0.17 | −0.90 | 7 | 1.28 | 19 | 26 | 12 |
| G11 | 34.28 | 0.20 | 0.81 | 30 | 1.37 | 21 | 51 | 28 |
| G12 | 36.24 | 0.19 | 0.75 | 29 | 1.28 | 20 | 49 | 27 |
| G13 | 37.35 | 0.18 | 0.72 | 27 | 1.23 | 17 | 44 | 25 |
| G14 | 65.75 | 0.00 | −0.11 | 16 | 0.11 | 2 | 18 | 1 |
| G15 | 81.69 | −0.10 | −0.57 | 13 | 0.78 | 8 | 21 | 5 |
| G16 | 63.41 | 0.02 | −0.04 | 17 | 0.11 | 1 | 18 | 2 |
| G17 | 82.67 | −0.10 | −0.60 | 11 | 0.82 | 10 | 21 | 6 |
| G18 | 44.16 | 0.14 | 0.52 | 24 | 0.92 | 12 | 36 | 20 |
| G19 | 56.11 | 0.06 | 0.17 | 19 | 0.39 | 4 | 23 | 9 |
| G20 | 74.97 | −0.05 | −0.38 | 15 | 0.48 | 5 | 20 | 4 |
| G21 | 39.9 | 0.17 | 0.64 | 26 | 1.11 | 15 | 41 | 23 |
| G22 | 88.42 | −0.14 | −0.77 | 10 | 1.08 | 14 | 24 | 11 |

**Table 4.** *Cont.*

| Genotypes | Y | IPCA [1] | IPCA [2] | RY | ASV | RASV | GSI | RGSI |
|---|---|---|---|---|---|---|---|---|
| G23 | 133.99 | −0.42 | −2.09 | 2 | 3.13 | 28 | 30 | 17 |
| G24 | 45.36 | 0.13 | 0.49 | 23 | 0.87 | 11 | 34 | 19 |
| G25 | 59.03 | 0.05 | 0.09 | 18 | 0.27 | 3 | 21 | 7 |
| G26 | 41.19 | 0.16 | 0.61 | 25 | 1.06 | 13 | 38 | 22 |
| G27 | 15.13 | 0.32 | 1.37 | 33 | 2.23 | 23 | 56 | 31 |
| G28 | 81.84 | −0.10 | −0.58 | 12 | 0.78 | 9 | 21 | 8 |
| G29 | 89.28 | 7.63 | −0.04 | 9 | 41.87 | 34 | 43 | 24 |
| G30 | 107.54 | 2.70 | −0.51 | 5 | 14.80 | 32 | 37 | 21 |
| G31 | 136.68 | 0.67 | −1.18 | 1 | 3.84 | 29 | 30 | 18 |
| G32 | 52.46 | −6.32 | 0.54 | 21 | 34.65 | 33 | 54 | 29 |
| G33 | 54.18 | −7.98 | 0.47 | 20 | 43.76 | 35 | 55 | 30 |
| G34 | 19.35 | 1.02 | 1.37 | 32 | 5.78 | 30 | 62 | 34 |
| G35 | 21.5 | 1.95 | 1.34 | 31 | 10.80 | 31 | 62 | 35 |

Y = yield; IPCA = interaction principal component axis; RY = rank of yield; RASV = rank of ASV; RGSI = rank of GSI.

### 3.4. Sustainability Index (SI) on Yield of Butterfly Pea Genotypes

The results of the sustainability index (SI) analysis were presented in Table 5. The estimated SI value of butterfly pea yields was in the range of 1.72% (very low) to 83.08% (very high). The very low SI values were demonstrated by genotypes G32 (1.72%) and G33 (5.69%). One genotype had a low SI value (G4), three genotypes had a medium SI value (G9, G27, and G35), twenty-seven genotypes had a high SI value, while two genotypes had a very high SI value indicated by the G31 (86.49%) and G34 (83.08%).

**Table 5.** Estimation for sustainability index (SI) of the flower yield of the butterfly pea.

| Genotype | Y | σn | YM | SI | Criteria |
|---|---|---|---|---|---|
| G1 | 37.24 | 6.760 | 45.693 | 66.71 | High |
| G2 | 77.89 | 10.676 | 89.400 | 75.19 | High |
| G3 | 125.16 | 15.507 | 140.229 | 78.20 | High |
| G4 | 8.58 | 4.479 | 14.876 | 27.60 | Low |
| G5 | 127.41 | 15.740 | 142.648 | 78.29 | High |
| G6 | 90.37 | 11.934 | 102.815 | 76.29 | High |
| G7 | 102.09 | 13.130 | 115.417 | 77.08 | High |
| G8 | 49.57 | 7.902 | 58.948 | 70.69 | High |
| G9 | 13.69 | 4.824 | 20.365 | 43.53 | Moderate |
| G10 | 92.83 | 12.185 | 105.468 | 76.47 | High |
| G11 | 34.28 | 6.495 | 42.506 | 65.37 | High |
| G12 | 36.24 | 6.669 | 44.608 | 66.28 | High |
| G13 | 37.35 | 6.769 | 45.803 | 66.76 | High |
| G14 | 65.75 | 9.469 | 76.350 | 73.72 | High |
| G15 | 81.69 | 11.058 | 93.489 | 75.56 | High |
| G16 | 63.41 | 9.239 | 73.829 | 73.37 | High |
| G17 | 82.67 | 11.155 | 94.534 | 75.65 | High |
| G18 | 44.16 | 7.394 | 53.133 | 69.20 | High |
| G19 | 56.11 | 8.528 | 65.980 | 72.12 | High |
| G20 | 74.97 | 10.383 | 86.256 | 74.88 | High |
| G21 | 39.9 | 7.001 | 48.544 | 67.76 | High |
| G22 | 88.42 | 11.737 | 100.717 | 76.13 | High |
| G23 | 133.99 | 16.422 | 149.717 | 78.52 | High |
| G24 | 45.36 | 7.506 | 54.422 | 69.56 | High |
| G25 | 59.03 | 8.811 | 69.124 | 72.66 | High |
| G26 | 41.19 | 7.119 | 49.935 | 68.23 | High |
| G27 | 15.13 | 4.928 | 21.919 | 46.56 | Moderate |
| G28 | 81.84 | 11.073 | 93.649 | 75.57 | High |
| G29 | 89.28 | 51.584 | 136.095 | 27.70 | Low |

**Table 5.** *Cont.*

| Genotype | Y | σn | YM | SI | Criteria |
|---|---|---|---|---|---|
| G30 | 107.54 | 15.418 | 126.880 | 72.60 | High |
| G31 | 136.68 | 9.926 | 146.548 | 86.49 | Very high |
| G32 | 52.46 | 53.538 | 131.180 | 1.72 | Very low |
| G33 | 54.18 | 58.931 | 150.848 | 5.69 | Very low |
| G34 | 19.35 | 1.513 | 21.470 | 83.08 | Very high |
| G35 | 21.5 | 7.910 | 29.270 | 46.44 | Moderate |

Y = mean yield; σn = standard deviation; YM = the best performance of a genotype in any season; SI = sustainability index.

To determine the best butterfly genotype, we selected genotypes based on slices of all measurements. Table 6 presents information about the selected genotypes based on each measurement. There are three genotypes identified as the most stable with high yields; namely, G2, G14 and G16.

**Table 6.** Comparison of butterfly pea genotype selection results based on each measurement.

| Stability Measurements | Selected Genotypes | Percentage (%) |
|---|---|---|
| AMMI | G2, G20, G14, G16, G25, G19, G8, G24, G17, G28, G15 | 31.43 |
| GGE biplot | G1, G2, G6, G14, G15, G16. | 17.14 |
| ASV | G2, G14, G16, G19, G20, G25 | 17.14 |
| GSI | G2, G14, G15, G16, G17, G20 | 17.14 |
| SI | G2, G3, G5, G6, G7, G8, G10, G14, G15, G16, G17, G19, G20, G22, G23, G25, G28, G30 | 51.43 |
| Slice of all measurements | G2, G14, G16 | |

## 4. Discussion

Based on the combined ANOVA (Table 3), yield and yield attributes were influenced by GEIs. According to several researchers, yield and yield attributes are quantitative characteristics that are strongly influenced by GEIs [17,18,31]. In yield and CL traits, genotypes gave the highest contribution on the total variations. FL and FW traits, as well as environmental (year) effects gave the highest contribution on the total variations. This showed that the planting material (genotype used) has a different potential if grown in different environments (years). Ruswandi et al. (2022) [32] also revealed that differences in genotypes cause variations in crop yields in corn. In other studies, differences in the origin of the genotypes used can also be a differentiator for yields' potential on sweet potato [18]. In addition, the environment (year) also has a significant influence, which means that the growing year can also provide differences in the yield potential and traits tested for each genotype. According to Katsenios et al. (2021) [33], differences in planting environmental conditions can cause differences in yield and yield quality. The effect of GEIs also has implications for the plant selection process. The emergence of GEIs can make the selection process difficult (inefficient) [16,19,34]. In other studies, GEIs also affect yield performance, including maize hybrids in Indonesia [25], sweet potato in Tanzania [33], black soybean in Indonesia [35,36], and stevia in Indonesia [20]. The emergence of GEIs in the yield and yield attributes of the butterfly pea in multi-year testing causes breeding activities that must be continued using stability measurements. In this case, the stability test was only carried out on the yield trait. We expected a genotype with small response to seasonal changes, i.e., a stable genotype. In the latest research developments, stable and high-yielding genotypes are some of the main focuses, including the butterfly pea plant-breeding program.

The AMMI biplot showed that PC1 has a contribution of 96.8% to the total variation and PC2 has a contribution of 3.2% (Figure 1). The large contribution of PC1 to yield variation implies that the interaction of the butterfly pea genotype with the three growing years in Indonesia was predicted by the first PC from the genotype and the growing year. The same result was also expressed by Tolorunse et al., (2018) [37], which shows that PC1 plays a role in crop yield diversity by 69.9%. In AMMI biplots, genotypes that are close to the biplot axis point were stable and had low GEIs [26]. The results of this study indicate that genotypes G2, G20, G14, G16, G25, G19, G8, G24, G17, G28 and G15 were close to the biplot axis, which means that these genotypes were stable across the three years.

Based on the GGE biplot analysis, PC1 and PC2 explained 80.7% and 19.2% of the total variation, respectively. Thus, they contributed 99.9% of the total variation in butterfly pea yield across the three growing years in Indonesia (Figure 2). The GGE biplot 'mean vs stability' graph showed that 14 genotypes of the butterfly pea were on the right side of the Y-axis and another 21 genotypes were on the left of the Y-axis (Figure 2a). According to Yan and Tinker (2006) [29], the Y-axis showed the average yield of each genotype, and the X-axis showed the stability of the yield of each tested genotype. Agronomically, genotypes G2, G14, G15, G16, and G20 were the most stable and had above average yields. According to Mustamu et al. (2018) [38], a genotype close to the ideal point in the GGE biplot has a high and stable yield. In this study, it was identified that G31 was close to the ideal point, which means that this genotype was able to produce high yields in both optimal and marginal environments.

The graph on the GGE biplot, 'which-won-where' (Figure 2b), showed that the three years had six sectors with different winning genotypes. According to Maulana et al. (2022) [16], the genotype on top of the sector has the highest environmental yield in that sector. G33 is the top genotype in Year 2 (second year). G31 is the top genotype in Year1 (first year) and Year 3 (third year). Zhang et al. (2016) [39] and Karuniawan et al. (2021) [18] stated that the genotypes at the top of each sector are those that were adaptive to a particular environment. In addition, Ruswandi et al. (2021) [19] also added that genotypes located in the center of the sector (near the center of the sector), had a low effect of GEIs (stable). In this study, the four genotypes of the butterfly pea that were close to the center of the sector were identified; namely, G1, G2, G6, G14, G15 and G16. These genotypes have a smaller GEIs effect than other genotypes, but do not necessarily have high yields, so other measurements are needed to be able to select stable and high-yielding genotypes. The same idea was also expressed by Vaezi et al. (2019) [34], who reported that the selection of stable and high-yielding genotypes requires more than one stability measurement. Therefore, several yield stability measurements were needed to be able to select a stable and high-yielding butterfly pea genotype.

Information on ASV and GSI was presented in Table 4. According to ASV, G16 was identified as the most stable genotype, followed by G14, G25, G19, G20 and G2. According to Gauch (2013) [26], multi-environment testing using AMMI stability value (ASV) on AMMI biplot measurements can provide information on the stability rank of the genotype tested. Several researchers have also succeeded in selecting the best genotype using AMMI, including for sweet potato [18]. The use of ASV in AMMI analysis allowed researchers to identify stable and unstable genotypes in a wide range of environments. The GSI measurements identified the G14 genotype as the most stable followed by G16, G2, G20, G15, and G17. According to Maulana et al. (2020) [40] the GSI measurement can strengthen the results of genotype stability calculations. In Table 4, ASV and GSI identified G2, G14, G16 and G20 genotypes as stable and high-yielding. This shows that in this study, the two measurements gave fairly consistent results in selecting the butterfly pea genotype that was stable across three different years in Indonesia.

The results of the sustainability index (SI) analysis were presented in Table 4. Several researchers revealed that a high SI value indicates the level of stability of a genotype [22,23,30]. The distribution of SI values was based on the opinion of Atta el al. (2009) [30], which stated that the SI scores were divided into five groups; namely, very low, low, medium, high, and very high. The estimated SI values of butterfly pea yields were in the range of 1.72% (very low) to 83.08% (very high). The very low SI values were demonstrated by genotypes G32 (1.72%) and G33 (5.69%). One genotype had a low SI value (G4), three genotypes had a medium SI value (G9, G27 and G35), twenty-seven genotypes had a high SI value, while two genotypes had a very high SI value indicated by G31 ( 86.49%) and G34 (83.08%).

The estimation of variance analysis in SI for butterfly pea yields revealed significant differences in different environments (growing years), indicating genetic variability in the genotypes tested. Genotype G31 recorded an average yield of 136.68 g with a very high SI of 86.49%, indicating the best performance of this genotype (Table 5). The best performance with a very high SI value can be considered an indication of the closeness between the best performance and the average performance [41]. However, the G34 genotype showed the opposite results, where the SI value was very high (83.08%), while the yield was low (19.35 g). This showed that the result of SI in G34 show the level of yield stability only (stable low yield). The next best genotypes with high yields and SI values close to 80% were G2, G3, G5, G6, G7, G8, G10, G14, G15, G16, G17, G19, G20, G22, G23, G25, G28 and G30. Several other genotypes, such as G29, had a high average yield (89.28 g; better than the overall average) but had an SI value of 27.70%. Several other genotypes had a low average yield with a high SI value (>60%). This indicated that the performance of these genotypes were not consistent across different environments (growing years) or could have better yield performance under favorable environmental conditions, while the other two genotypes (G32 and G33) showed poor yield performance and adaptability. This was also in line with the results of the ASV and GSI measurements in Table 4, which have very low ratings (unstable and low results). In general, genotypes with high and very high SI criteria with yield performance above the overall average indicated that these genotypes were included in the ideal group (having high and stable yields). Several researchers also reported selecting high-yielding and stable genotypes using SI, including rice [23] and maize [24,25]. Thus, these results indicate that SI can be used to determine stable and high-yielding genotypes.

Overall, each stability measurement identified a different stable genotype. Table 6 presented a comparison of stable genotypes based on various analyses. AMMI identified 11 stable genotypes (31.43%); GGE biplot, ASV and GSI, each identified six genotypes (17.14%); SI identified 18 genotypes (51.43%). From the five measurements, there were three genotypes selected by all measurements; namely, G2, G14 and G16 (Table 5). The three genotypes had stable and high yields (more than the average) in three different growing years, so they could be proposed as superior local genotypes of the butterfly pea.

## 5. Conclusions

The stable and high-yielding genotypes of the butterfly pea (*Clitoria ternatea* L.) in Indonesia can be determined in this study. The yield and yield attributes of the butterfly pea were influenced by GEIs, AMMI, ASV, GSI, GGE biplot and sustainability index (SI)-selected genotypes G2, G14 and G16 as superior genotypes (stable and high-yielding), with small responses to changes during the growing year. These three genotypes can be selected as the superior genotypes of the butterfly pea for flower and seed production, and can be used as material for crosses in plant-breeding prog. The stable and high-yielding genotypes selected in this study should be broadly evaluated on-farm in order to disseminate for growers in Indonesia.

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## Abbreviations

| | |
|---|---|
| GEIs | genotype by environment interactions |
| SI | sustainability index |
| AMMI | additive main effects and multiplicative interactions |
| GGE | genotype plus genotype by environment interactions |
| ASV | aMMI stability value |
| RASV | rank of ASV |
| GSI | genotype stability index |
| RGSI | rank of GSI |
| IPCA | interaction principal component axis |
| RY | rank of yield |
| CV | coefficient of variation |
| COVID-19 | coronavirus disease 2019 |
| FL | flower length (cm) |
| FW | flower width (cm) |
| CL | calix length (cm) |
| SD | standard deviation |
| Min | Minimum value |
| Max | Maximum value |

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