

Genetic gain and relationship of yield and yield attributes of mutant and cross-bred stevia (*Stevia rebaudiana*) genotypes

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Abstract. Amien S, Maulana H, Ruswandi D, Nurjanah S. 2021. Genetic gain and relationship of yield and yield attributes of mutant and cross-bred stevia (*Stevia rebaudiana*) genotypes. *Biodiversitas* 22: 3119-3126. Plant breeding programs involved many traits and genetic parameters in the selection process. The information on genetic parameters on yield and other related traits provided an overview for breeders and farmers in selecting new superior genotypes. The purpose of this study was to estimate genetic parameters including heritability and genetic gains in yield and other traits, to determine the relationship between various traits, and to select superior stevia (*Stevia rebaudiana* Bertoni) genotypes for each trait. Field experiments were carried out in two planting environments, namely, the highlands and the medium plains employing a randomized completed block design and each genotype was three replicates. The results showed that the yield had high heritability and genetic gains in mutant populations, whereas cross-bred populations had moderate heritability and low genetic gains. Stem weight (SW) and number of leaves (NoL) traits were identified as having high heritability and genetic gains in both populations. The GT biplot measurement showed that the yield was identified to have a significant and positive correlation with SW ($p < 0.05$). H4 was correlated with Number of branches (NoB), Yield, SW, and chlorophyll content (Chl) traits in the cross-bred populations. H9 excelled on and was correlated with NoL and plant height (PH). M11 was identified to be highly correlated with NoL, PH, NoB, and Chl traits in the mutant populations, while M15 excelled on and was correlated with yield and SW. The results of this study revealed that there was a potential for improvement in the traits tested of stevia through cross-bred and mutant populations in different environmental conditions. The selected genotypes can be developed in a suitable environment and used for further stevia plant breeding programs.

Keywords: GT biplot, heritability, selection, stevia, traits, West Java

INTRODUCTION

Stevia (*Stevia rebaudiana* Bertoni) is one of the potential sweetener plants. Stevia leaf have a higher sweetness than sugar (glucose) (Zhang and Bell 2017). In addition, the sweetness of stevia leaf also provides no side effects, so it is safe for consumption. Stevia leaf extract also has antibacterial, antifungal, antimicrobial, and antiviral properties (Kumar et al. 2014). Stevia has a yield potential of up to 60-80 tons ha⁻¹ annually. Stevia yields were influenced by altitude, temperature, day length, and photoperiod intensity (Benhmimou et al. 2017). In addition, pinching treatment has also been reported to increase stevia yields (Kumar et al. 2014). The description shows that stevia has the potential to be used as a source of natural sweetener that is safe for health with a fairly high yield and profit potential.

Selection is an important stage in plant breeding programs in determining superior genotypes. Several researchers have selected several characters including Yan and Frégeau-reid (2018) on oat yield, agronomic and quality traits, and Karuniawan et al. (2021) on the yield and sweetness traits of sweet potatoes. Selection on multiple traits allows researchers and farmers to select genotypes that excel at multiple traits. Therefore, this process will

determine whether the genotype is further employed in the plant breeding program or not.

In developing new varieties, the genetic parameters including heritability and genetic gains are very important to determine the effect of additive genes. According to Annicchiarico et al. (2010), high heritability showed that the effect of additive genes in these traits was more dominant, so that the selection process for these traits can be carried out based on their phenotypic traits. Atnaf et al. (2017) added that if the heritability and genetic gains were low, then the environment influence was greater than the effect of additive genes. So that the selection process becomes less efficient. This suggests that high heritability and genetic gains were desirable in the plant selection process.

The development of superior plants with high yielding and other important traits is difficult and complicated. Many external factors influence it, including the emergence of the GE interactions (Maulana et al. 2020; Mustamu et al. 2018). The use of multiple traits can increase the efficiency of plant breeding programs. However, it is very difficult to do considering the large interaction between each trait against environmental factors. Currently, there is a genotype by traits (GT) biplot analysis to assess genotypes based on several traits and to identify superior genotypes based on several traits tested. Researchers used this

measurement to understand the effect of genotype and environment on the relationship between yield and other traits (Yan and Frégeau-reid 2018). However, this measurement can only see the relationship between each trait and the yield, but cannot determine the effect of the combined yield on the other traits under different environmental conditions. Therefore, this measurement is very suitable for selecting genotypes that were superior to certain traits.

Information regarding yield and other traits of stevia genotypes is considerable. So far, some researchers have focused on growth and yield (Gomes et al. 2018; Kumar et al. 2014). However, some have identified other traits such as stevioside (Zhang and Bell 2017; Sieminska et al. 2020) and yield attributes (Benhmimou et al. 2017). Meanwhile, testing and selection of new stevia varieties for multi-traits are still very limited. The use of the GT biplot in this study was expected to add information about superior stevia genotypes in yields and other traits and estimate the relationship between each trait tested to be used for future stevia development and plant breeding programs.

MATERIALS AND METHODS

Field trial and samples collection

Field experiments were carried out in the highlands (Ciwidey, Bandung, Indonesia) and the medium plains (Jatinangor, Sumedang, Indonesia) using a randomized completed block design and three replicates. Ciwidey is at a coordinate of 7°05'34.8 "South latitude, 107°29'07.8" East longitude, an altitude of 1100 m asl, an average temperature of 22°C, average monthly rainfall 369.80 mm, and average humidity during the experiment was 69%. Jatinangor is at a coordinate of 6°54'59.6 " South latitude 107°46'14.5" East longitude, an altitude of 530 m asl, an average temperature of 25.00°C, an average monthly rainfall of 275.30 mm, and average humidity during the experiment of 64%. Each stevia genotype was planted at a distance of 50 cm x 50 cm. Each genotype was planted in three rows with 10 plants in each row. Information about the genotypes used was presented in Table 1. The traits observed in this study were yield, chlorophyll content (Chl), number of leaves (NoL), number of branches (NoB), plant height (PH), and stem weight (SW).

Table 1. New stevia genotypes used in the experiments

Population	Codes	Genotypes	Information of the population
Mutant	M1	GR 3,5 B	Garut gama ray radiation 3,5 no. B
	M2	TEA	Tawangmangu EMS no. A
	M3	GR 7,5 A	Garut gama ray radiation 7,5 no. A
	M4	TR 3,5 B	Tawangmangu gama ray radiation 3,5 no. B
	M5	BEB	Bogor EMS no. B
	M6	GR 5 B	Garut gama ray radiation 5 no. B
	M7	BR 5 B	Bogor gama ray radiation 5 no. B
	M8	GEA	Garut EMS no. A
	M9	BED	Bogor EMS no. D
	M10	TR 3,5 C	Tawangmangu gama ray radiation 3,5 no. C
	M11	BR 5 C	Bogor gama ray radiation 5 no. C
	M12	GR 3,5 C	Garut gama ray radiation 3,5 no. C
	M13	GR 7,5 B	Garut gama ray radiation 7,5 no. B
	M14	TED	Tawangmangu EMS no. D
	M15	BR 5 D	Bogor gama ray radiation 5 no. D
	M16	BR 5 A	Bogor gama ray radiation 5 no. A
Cross-bred	H1	STG 1	Tawangmangu x Garut 1
	H2	STG 7	Tawangmangu x Garut 7
	H3	STG 8	Tawangmangu x Garut 8
	H4	STG 10	Tawangmangu x Garut 10
	H5	SBG 3	Bogor x Garut 3
	H6	SBG 4	Bogor x Garut4
	H7	SBG 5	Bogor x Garut 5
	H8	SBG 7	Bogor x Garut 7
	H9	SBG 10	Bogor x Garut 10
	H10	SGB 2	Garut x Bogor 2
	H11	SGB 3	Garut x Bogor 3
	H12	SBT 11	Bogor x Tawangmangu 11
Check	C1	BK	Bogor (Check)
	C2	TK	Tawangmangu (check)
	C3	GKA	Garut control (check) no. A

Analysis of heritability and genetic gains

Phenotypic and genotypic variance coefficients, heritability, genetic gains as percent of mean, were estimated following the formula by Fehr (1991):

$$\text{Phenotypic variance coefficient} = \frac{\sqrt{\sigma_p^2}}{x} \times 100 \quad (1)$$

$$\text{Genotypic variance coefficient} = \frac{\sqrt{\sigma_g^2}}{x} \times 100 \quad (2)$$

$$\sigma_p = \sqrt{\sigma_p^2} \quad (3)$$

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \quad (4)$$

$$\text{Genetic gains} = h^2 \cdot i \cdot \sigma_p$$

Where, σ_p^2 is phenotypic variance, σ_g^2 is genotypic variance, x is the grand mean; h^2 is the broad-sense heritability; σ_p is phenotypic standard deviation; and i is the selection intensity (20% = 1.74). The heritability values were categorized as follows : 0 - 0.3 as low, 0.3 - 0.6 as moderate, and > 0.6 as high. The values of genetic gains were categorized as follows: 0 - 10% as low, 10 - 20% as moderate, and >20% as high (Johnson et al. 1955).

Analysis of genotype by traits (GT) biplot

The GT biplot analysis was used to determine each trait's relationship and select the best stevia genotypes based on each trait. The equations used to follow (Yan and Rajcan 2002):

$$\frac{T_{ij} - T_j}{s_j} = \lambda_1 \zeta_{i1} \tau_{j1} + \lambda_2 \zeta_{i2} \tau_{j2} + \varepsilon_{ij} \quad (6)$$

Where, T_{ij} is the average of i^{th} genotype for j^{th} trait, T_j is the average of j^{th} trait in all genotypes, s_j is the standard deviation of j^{th} trait among the genotype averages; ζ_{i1} and ζ_{i2} were the first and second principal component (PC1 and

PC2) scores for i^{th} genotype, τ_{j1} and τ_{j2} were the PC1 and PC2 scores for j^{th} trait, respectively, and ε_{ij} is the error of the model associated with the i^{th} genotype and j^{th} trait.

The relationship analysis between each trait

The relationship between each tested trait was calculated based on the Pearson correlation. The equations used was as follows:

$$r_{xy} = \frac{\sum_{i=1}^n x_i y_i - \sum_{i=1}^n x_i \sum_{i=1}^n y_i}{\sqrt{\sum_{i=1}^n x_i^2 - (\sum_{i=1}^n x_i)^2} \sqrt{\sum_{i=1}^n y_i^2 - (\sum_{i=1}^n y_i)^2}} \quad (7)$$

where r_{xy} is the correlation coefficient. x is the variable (trait) x , and y is the variable (trait) y . If the value is 1 or -1, then the relationship is very strong. Meanwhile, if the value is close to 0.0, then the relationship of the two variables is getting weaker.

GT biplot was analyzed using Genstat 12th software, while the correlation between each trait was analyzed using Ms. Excel 2013.

RESULTS AND DISCUSSION

Estimate of variance component, heritability, and genetic gains

The coefficient of phenotypic variance (σ_p^2) was higher than the coefficient of genotypic variance (σ_g^2) for all traits studied in the two populations (Table 2). The difference between σ_p^2 and σ_g^2 was taken into account in the environmental conditions in which the genotype grows. The wide difference between σ_p^2 and σ_g^2 indicates a high degree of environmental influence on these traits. In the mutants, the differences ranged from 2.27 at SW to 15.56 at NoL, indicated that environmental influences were significant on the expression of NoL; the same result was also shown by cross-bred population (cross-breeds).

Table 2. Coefficient of variance, heritability, and genetic gain on new stevia genotypes

Traits	Minimum	Mean	Maximum	σ_p^2	σ_g^2	h^2	Genetic gain (%)
Mutant populations							
Yield	10.58	20.88	33.78	11.48	8.39	0.73	21.54
Stem weight (SW)	4.90	15.72	36.35	10.85	8.58	0.79	22.66
Number of leaves (NoL)	10.17	38.61	89.17	102.31	86.75	0.85	74.62
Number of branches (NoB)	0.83	7.10	17.33	5.79	2.92	0.50	10.55
Plant height (PH)	6.63	18.55	29.47	11.62	6.78	0.58	17.29
Chlorophyll content (Chl)	11.51	24.20	35.87	9.78	5.99	0.61	16.66
Cross-bred populations							
Yield	7.77	20.24	29.20	5.12	2.02	0.40	9.73
Stem weight (SW)	6.34	15.90	27.33	7.90	5.63	0.71	21.78
Number of leaves (NoL)	17.00	45.63	89.17	65.44	49.89	0.76	67.06
Number of branches (NoB)	1.83	8.47	17.33	3.38	0.51	0.15	3.03
Plant height (PH)	9.67	20.18	30.12	10.02	5.17	0.52	17.77
Chlorophyll content (Chl)	11.54	23.61	35.28	9.04	5.25	0.58	18.99

Note: σ_p^2 : coefficient of phenotypic variance; σ_g^2 : coefficient of genotypic variance; h^2 : broad-sense heritability

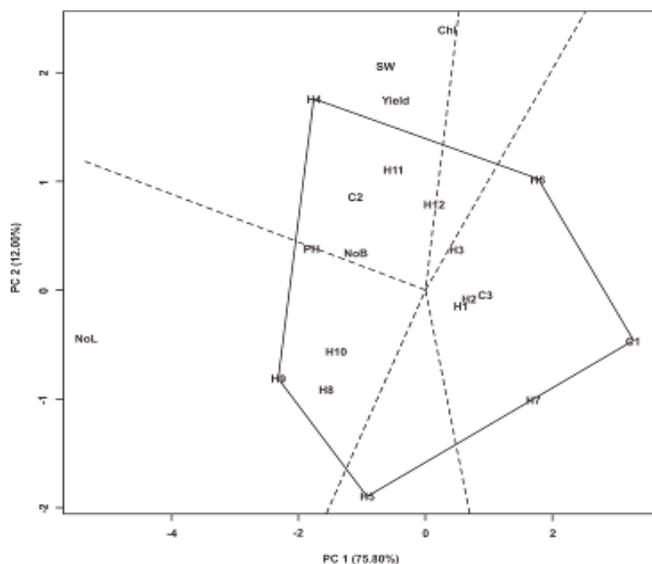


Figure 1. GT biplot “which, won, where” on the cross-bred populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

Based on Table 2, heritability estimates ranged from 0.50 for PH to 0.85 for yield in the mutant population. In the cross-bred population, it ranged from 0.15 for NoB to 0.76 for NoL. From the traits studied, SW and NoL consistently showed high heritability in both populations. Yield showed moderate to high heritability for both populations. NoB showed low to moderate heritability, PH showed moderate heritability in both populations, and Chl showed moderate to high heritability. The low heritability for NoB in cross-bred populations suggests that environmental factors were greater than genetic factors.

The high estimates of genetic gains were shown by the SW and NoL traits for both populations. Yield and NoB show low genetic gains in cross-bred populations and high in mutant populations. PH and Chl indicate moderate genetic gains in both populations.

Relationships between traits tested against cross-bred and mutant populations of stevia using genotype by traits (GT) biplot

Figure 1 shows the GT biplot “which won where” for cross-bred populations based on data from two planting environments. Five sectors were generated in Figure 1, with the genotypes and traits tested in different sectors. The genotypes in the same sector as the tested trait had a close relationship. H4 was in sector 1 and correlated with the NoB, Yield, SW, and Chl traits. H9 excelled in sector 2 which correlated with NoL and PH. The test results also showed that the biplot was very strong because it represents 87.80% (PC1 and PC2) of the total variation.

Figure 2 shows the GT biplot “which won where” for mutant populations based on data from two planting environments. This population also produced five sectors that divided the genotypes and observed traits in different groups. Mutant M11 correlated with the NoL, PH, NoB,

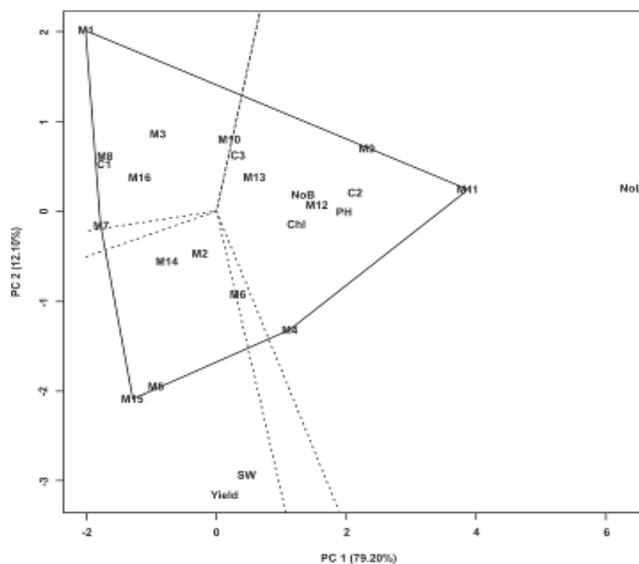


Figure 2. GT biplot “which, won, where” on the mutant populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

and Chl traits. M15 and M6 correlated with yield and SW. Figure 2 also shows that the biplot was very strong because it represents 91.30% of the total variation. In this study, both cross-bred and mutant populations, Check 1 (C1) was identified to be located apart from all traits measured. While the other two checks were still relationship to some of the observed traits. This indicates that check 1 (C1) has a relatively small value for all the traits being measured.

The relationship between the traits tested was presented in Table 3. Figure 3 and Figure 4 show the relationship between traits based on the GT biplot for cross-bred and mutant populations. Traits that have an acute angle ($<90^\circ$) were stated to be positively correlated (have a close relationship), and vice versa. In cross-bred populations, yield has a very significant and positive correlation with SW, and had no significant correlation with other traits (Figure 3). Neither were the mutant populations (Figure 4). This explanation can be seen in the correlation value for each trait (Table 3). Table 3 shows that several other traits were positively and significantly correlated ($p < 0.05$), i.e., NoL to NoB and PH; and NoB with PH in cross-bred populations. In the mutant populations, NoL was significantly and positively correlated with NoB, PH, and Chl; while NoB was correlated with PH.

Figure 3 also shows the ideal point, namely the arrow tip, which allows evaluation of the genotypes tested according to their proximity or distance to this center. The genotype that has closest to this point is the most ideal. According to Figure 3, C2 is more ideal than other genotypes because it was to closest to the “ideal center”, while C1, H5, and H7 were the least desirable genotypes because they were located farthest from the “ideal center”. In mutant populations, M4 was identified to be close to the “ideal center”, while M1 followed by M8 and C1 were the farthest from this point (Figure 4).

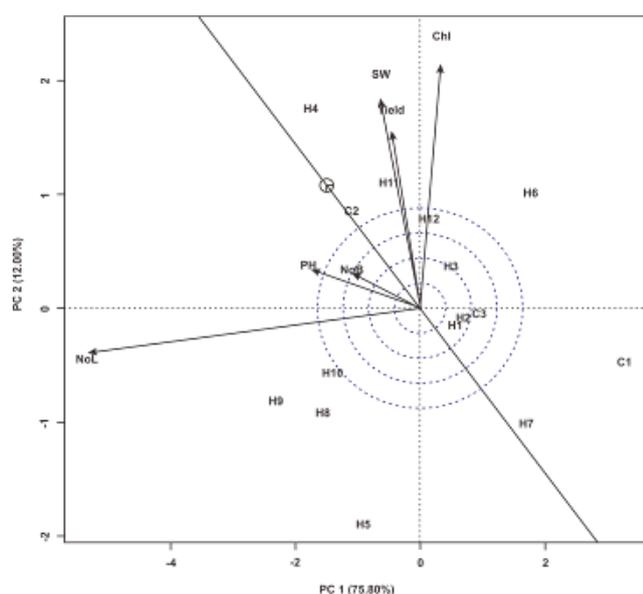


Figure 3. GT biplot “representativeness vs discriminativeness” on the cross-bred populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

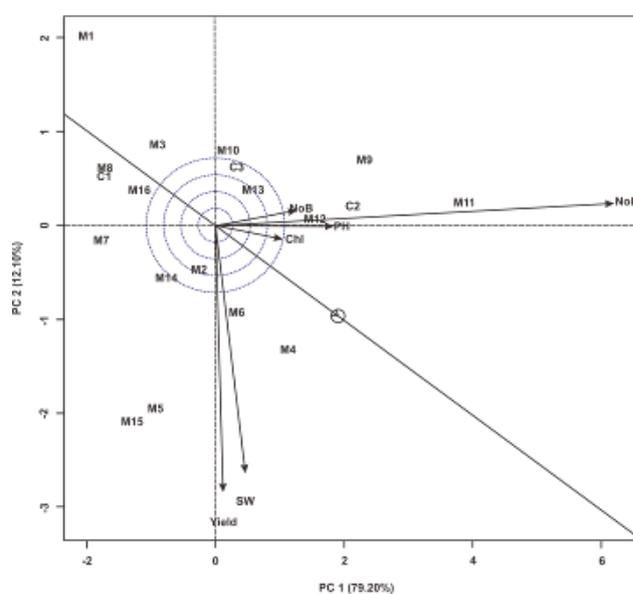


Figure 4. GT biplot “representativeness vs discriminativeness” on the mutant populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

Figures 5 and 6 show the axis of stability (Horizontal) and the average (vertical) axis based on the value of the traits tested. The genotypes that were above the vertical line (in the direction of the arrow in the small circle), are the expected genotypes. On the other hand, the genotype adjacent to the horizontal line is stable, and vice versa. In cross-bred genotypes, C2, H4, and H11 were quite stable and most preferred because they were located close to the horizontal axis, and located above the vertical axis (Figure 5). Meanwhile, M4 was identified as the most stable for all the traits tested in the mutant populations. M3 and M16 were close to the horizontal line, but they were far from the arrow in the small circle, so they have lower scores than the overall average.

Discussion

The yield and yield attributes are important traits in the breeding of new varieties. These traits were quantitative characters that are strongly influenced by the environment (Andrade et al. 2016). The study results showed that yield and Chl produced moderate to high heritability values for both populations. SW and NoL traits showed high heritability values in both populations. NoB showed low to high heritability, while PH showed moderate heritability in both populations. Some researchers also reported that yield and yield attributes have high heritability (Annicchiarico et al. 2010; Atnaf et al. 2017). The high heritability values indicated a high proportion of genetic diversity that can be passed on to the next generation. Thus, it can be used to select superior genotypes based on their phenotypic appearance (Alves et al. 2020; Annicchiarico et al. 2010; Atnaf et al. 2017). The high heritability value indicated that the genetic effects were greater than environmental effects on the observed variability.

The genetic gains measured indicated that the SW and NoL traits had high criteria for both populations. Annicchiarico et al. (2010) suggested that to predict superior genotype, considerations of heritability must be combined with genetic gains in the tested traits. High heritability coupled with high genetic gains indicated the additive gene effects, whereas high heritability coupled with low genetic gains indicated non-additive gene effects (Atnaf et al. 2017; Nehe et al. 2019; Sudrajat et al. 2018). The yield had high heritability and genetic gains in the mutant population, but the cross-bred population had moderate heritability and low genetic gains. SW and NoL had high heritability and genetic gains values in both populations. NoB had high heritability and genetic gains in the mutant population, but low value in the cross-bred population. While PH had moderate heritability and genetic gain values in all populations. Chl in the mutant population had high heritability but moderate genetic gain, while in the cross-bred population both heritability and genetic gains were moderate. Thus, the high criteria for genetic variance coefficient (σ^2g), heritability, and genetic gains of yields in the mutant population indicated that there was greater additive gene action in regulating trait expression, so that the expected genetic of yield through selection was high. Meanwhile, estimates of high or moderate heritability values and low genetic gains indicated the presence of non-additive gene action or genotypic interactions with the environment in the expression of these traits. This would make it difficult to plant selections for the improvement of the measured traits (Annicchiarico 2010). Some researchers also reported similar results for soybean mutants (Malek et al. 2014), mung beans (Payasi 2015), rice beans (Pandey et al. 2015), and white lupin (Atnaf et al. 2017).

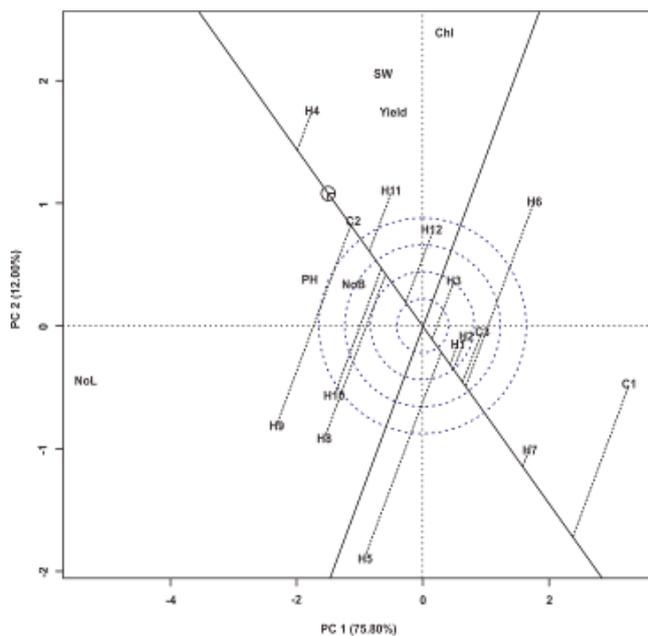


Figure 5. GT biplot “mean vs stability” on the cross-bred populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

The results showed that chlorophyll content is one of the properties that were influenced by the environmental factor. Chlorophyll content is one of the main components in the plant photosynthesis process. Chlorophyll content had a positive relationship with the rate of photosynthesis (Yeganehpour et al. 2016). According to some researchers, the change of chlorophyll content in leaves was one of plant response to drought, to minimize light absorption by chloroplasts (Anjum et al. 2011; Ucar et al. 2018; Abrar et al. 2020). In addition, the other research stated that chlorophyll content changed can be also caused by increased environmental pressure, especially drought and salinity (Taïbi et al. 2016; Bertoldo et al. 2018; Ma et al. 2020). Anjum et al. (2011) added that decreased chlorophyll content under drought stress was a type of symptom of oxidative stress and chlorophyll degradation. In this study, there was no drought stress from the two environments, and the average rainfall was relatively high and uniform, so there was no significant decrease or increase in chlorophyll content.

The genotype by traits (GT) biplot analysis assesses the genotypes tested based on several traits and can identify superior genotypes based on the traits tested. The GT biplot was used to compare genotypes based on the trait tested. This technique can only estimate the relationship between each trait and yield, but can't determine the effect of combined yields on other traits under different environmental conditions (Yan and Frégeau-reid 2018;

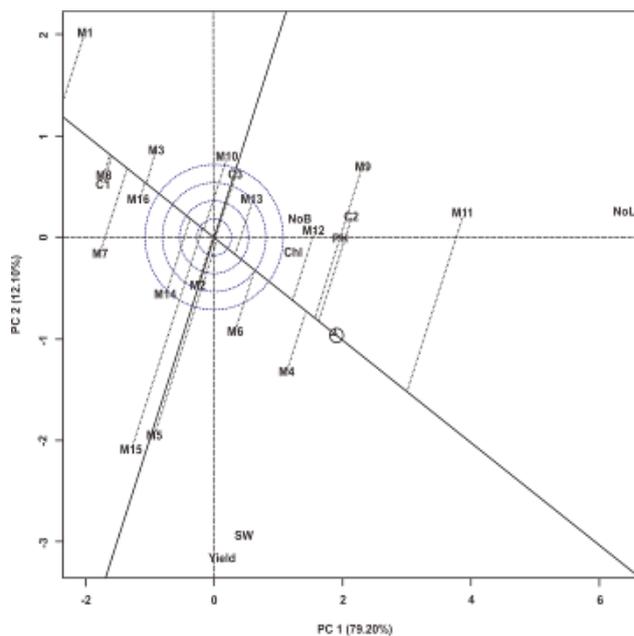


Figure 6. GT biplot “mean vs stability” on the mutant populations into six traits. SW: stem weight; NoL: number of leaves; NoB: number of branches; PH: plant height; Chl: chlorophyll content

Kendal 2019). The GT biplot analysis of the stevia genotypes showed very strong results as they were represented 87.80% for hybrids and 91.30% for mutants of the total variation. Kendal (2019) reported that the GT biplot analysis on wheat resulted in 61.50% of the total variation (quite strong). This showed that the results of the GT biplot on yields and other traits in the stevia genotypes in West Java are very good.

In cross-bred populations (Figure 1), H4 was the highest and correlated with the NoB, Yield, SW, and Chl traits. H9 had the highest and was correlated with NoL and PH as compared to other genotypes. In mutant populations (Figure 2), M11 was identified as the best genotypes for NoL, PH, NoB, and Chl traits. M15 and M6 were correlated with and identified as the best genotypes for yield and SW. The genotypes that were at the top of the sector were the best in the sector (Yan and Frégeau-reid 2018; Mohammadi 2019). Some studies revealed that quantitative traits are very difficult to predict because they were strongly influenced by environmental factors (Andrade et al. 2016; Ruswandi et al. 2020). In addition, genotype testing in more diverse environmental conditions was also needed to predict the favorable environments for each genotype, both mutant and cross-bred. So that testing of genotypes in a variety of environments and different seasons was needed to predict the adaptability of each genotype.

Table 3. Pearson correlation between traits tested in stevia genotypes

Traits	Yield	SW	NoL	NoB	PH	Chl
Cross-bred populations						
Yield	1					
SW	0.61 *	1				
NoL	0.26	0.28	1			
NoB	0.40	0.37	0.88 *	1		
PH	0.29	0.39	0.80 *	0.80 *	1	
Chl	0.30	0.14	-0.17	0.01	-0.12	1
Mutant populations						
Yield	1					
SW	0.67*	1				
NoL	0.04	0.19	1			
NoB	-0.05	0.18	0.86 *	1		
PH	-0.01	0.27	0.90 *	0.82 *	1	
Chl	0.04	0.17	0.59 *	0.44	0.49	1

Note: *significantly correlated at 5% ($p < 0.05$); SW: stem weight; NoL: number of leaf; NoB: number of branch; PH: plant height; Chl: chlorophyll content

In the GT biplot, yields were significantly correlated with SW because they had very sharp angles and were close to each other. In addition, the correlation analysis of the two traits was also strong (0.61 in cross-bred and 0.67 in mutants). This indicates that these two traits have a quite strong relationship. Meanwhile, other traits were correlated with each other (Figure 3 and Figure 4). Yan and Frégeau-reid (2018) revealed that vector lines that have an angle of $< 90^\circ$ show a significant and positive correlation. In addition, in Figure 5 and Figure 6 the tested genotypes were divided by vertical (average) and horizontal (stability) lines. The expected genotypes were above the vertical line and adjacent to the horizontal line, and the ideal genotypes were close to the ideal point (Abakemal et al. 2016; Kendal 2019). Currently, plant breeding program doesn't just refer to high yields. However, it has other advantages such as high and stable yields (Maulana et al. 2020), and has other good qualities and agronomic traits (Kendal 2019). In the study, C2 (in cross-bred populations) and M4 (in mutant populations) were identified to be close to the ideal point. So that the genotypes have yields and also traits that exceed the average value for each of the traits tested.

In conclusion, heritability and genetic gains of yield and other traits showed varied values. Yields have high heritability and genetic gains in mutant populations, whereas cross-bred populations have moderate heritability and low genetic gains. SW and NoL traits were identified as having high heritability and genetic gains in both populations. The results of the GT biplot measurement showed that the yield was identified to have a significant and positive correlation with SW. In the cross-bred populations, H4 was correlated with and superior for the NoB, Yield, SW, and Chl traits. H9 excelled on and was correlated with NoL and PH. In the mutant populations, M11 was identified to be more correlated with NoL, PH, NoB, and Chl traits, while M15 excelled on and was correlated with yield and SW. The genotypes selected based on each trait can be used in future development and

plant breeding programs. In addition, it was necessary to carry out tests on more varied environmental conditions to estimate the relationship and yield stability and other traits into environmental changes.

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