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GENETIC DIVERGENCE OF GUAVA (*Psidium guajava* L.) GENOTYPES IN BANGLADESH

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ABSTRACT

A noticeable variation is present among the guava (*Psidium guajava* L.) genotypes available in Bangladesh. Thirty-three (25 indigenous, 5 released, and 3 exotic) genotypes of guava were used in *ex-situ* conditions from different locations of Chattagram, Brahmanbaria, Pirojpur, and Gazipur districts and assessed based on 10 traits to know their genetic diversity. The measured traits were number of flowers, fruits, harvested fruits per plant, single fruit weight (g), number of seeds/fruits, thousand seed weight (g), vitamin C, total sugar content, and fruit yield/plant (kg). Twenty-one genotypes showed 100-400 g of single fruit weight, and 12 showed 20-100 g. The genotype G14 (BARI Peyara-1) produced the highest fruit yield/plant (131.04 kg) followed by G24 (PG Muk-005) and G23 (PG Muk-005) yielded 65.49 kg and 64.62 kg, respectively. Twenty-one genotypes showed above 250 mg/100g vitamin C content. Above 42% (14 genotypes) contained total sugar content of over 5%. The first two axes accounted 58.8% of the total variation among 10 traits. Based on the heatmap analysis, cluster-IV represents a high value containing the number of flowers, fruits, and harvested fruits per plant. The genotypes G14, G17 (BARI Peyara-4), G21 (PG Sit-003), G23, G24, and G29 (Thai Peyara-3) might be considered the best based on the morpho-biochemical characteristics. Many traits are of significant economic importance and could be used as breeding targets to increase yield and quality. Therefore, variation among guava genotypes will be an excellent source for future crop improvements.

Keywords: *Psidium guajava,* Genetic variability, Quality traits, Germplasm, Bi-plot analysis, Heatmap

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INTRODUCTION

Guava (*Psidium guajava* L.) is one of the most economically important tropical and subtropical fruit trees, which is commercially grown in over 60 countries. It belongs to Myrtaceae family that includes from 130 to 150 genera, with more than 5000 species and among them few are edible. India, Pakistan, Mexico, Brazil, Egypt, Thailand, Columbia, and Indonesia are the top producers of guava (Pommer and Murakami, 2009). The common guava is found in the moist tropics, primarily in South America, Australia, and tropical Asia, although it can also be found in Africa and even South Europe (Grattapaglia et al., 2012). Bangladesh is one of the world's most important guava producers. In Bangladesh it is a major fruit crop with an estimated area of 2,68,220 ha and production of 36,67,890 MT (BBS, 2021). Generally, guava is grown in homestead areas and is commercially grown in Barisal, Sylhet and Chattogram areas. In recent year, commercial cultivation has been extended throughout the north- western region of Bangladesh. One of the important reasons of this increasing trend is the development of some high-yielding, high-quality cultivars, particularly BARI Peyara-1 (Kazi Peyara). Bangladesh Agricultural Research Institute (BARI) has been released four varieties these are BARI Peyara-1, BARI Peyara-2, BARI Peyara-3 and BARI Peyara-4. In the farmer's field, two BARI variety (BARI Peyara-1 and BARI Peyara-2) and Bangabandu Sheikh Mujibur Rahman Agricultural University has been released one variety (IPSA Peyara-1) are being grown extensively. A mature guava tree produces 54 to 100 kg of fruits per year, with two seasons of production - one in which there is a major crop and another with a minor second crop (Nyambo et al., 2005). Most research efforts are focused on important fruit crops such as mango, citrus etc. Minor fruit crops are often overlooked probably due to lack of information about their potential and maximum utilization of natural resources. Therefore, to maintain health and nutrition, it is also important to carry out investigation on such minor crop such as guava. Guava fruit is mostly consumed fresh and has been reported to be rich in several important nutrients. Recent studies have reported appreciable amount of vitamin C and other antioxidants, calcium, potassium and phosphorus, as well as dietary fibres (Youssef and Ibrahim, 2016; Singh, 2005). It is a fruit of great nutritional value, in which its high content of vitamin C. stands (Gil, 2010).

In guava, self-pollination is possible; however, insect cross-pollination results in larger yields (Crane and Balerdi, 2005). Guava is a highly heterozygous allogamous fruit crop. In Bangladesh guava has a wide range of variability (Chandra and Mishra, 2007). Study on the field performance is necessary to select superior genotypes based on different characters but such study on guava has remained neglected in this region. There is a large range of diversity among cultivated guava types, which can be used in crop improvement programme. A breeder's goal is to develop high-yielding varieties by selecting superior genotypes that already exist. As a result, the genetic information on yield and its contributing features must be thoroughly evaluated in order to improve production. Genetic and environmental variables influence the expression of numerous plant characteristics. The proportion of heritable and environmental differences is often difficult to determine. The size, type, and interaction of genotypic and environmental changes in plant traits influence breeding progress. Therefore, genetic parameter research is required which will provide useful information on the inheritance of various features and will aid in the selection of plants with acceptable characteristics for the development of new guava varieties. The present investigation aims to generate information on genetic diversity for morphological, yield and quality parameters of guava genotypes available in Bangladesh.

MATERIALS AND METHODS

Materials and Experimental Design

In this study a total of 33 guava genotypes including 25 local genotypes, four released varieties from Bangladesh Agricultural Research Institute (BARI), one from Bangabandhu Sheikh Mujibur Rahman Agricultural University and three exotic genotypes were used as experimental materials (Table 1). All 33 genotypes of guava were evaluated *ex-situ* condition at farmer's field and/or in the fruit garden of the respective institutes during the year of 2019. The genotypes were arranged in an augmented randomized complete block design (augmented RCBD) with five check varieties.

Table 1: Thirty three genotypes of guava with their source of collection

Sl. No.	Code	Genotype/variety	Source/origin
1	G 1	PG Hat 004	Kanchannagor, Chandonaish, Chattagram.
2	G 2	PG Hat 009	
3	G 3	PG Hat 010	
4	G 4	PG Hat 011	
5	G 5	PG Hat 012	
6	G 6	PG Hat 013	
7	G 7	PG Hat 014	
8	G 8	PG Hat 015	
9	G 9	PG Hat 016	
10	G 10	PG Hat 017	
11	G 11	PG Hat 018	
12	G 12	PG Hat 019	
13	G 13	PG Hat 020	
14	G 14	BARI Peyara -1	BARI, Gazipur.
15	G 15	BARI Peyara -2	Agricultural Research Station, BARI[1],

Sl. No.	Code	Genotype/variety	Source/origin
16	G 16	BARI Peyara -3	Khulshi, Pahartoli, Chattgram.
17	G 17	BARI Peyara -4	
18	G 18	IPSA Peyara-1	BSMRAU, Salna, Gazipur.
19	G 19	PG Sit-001	Chowdhuripara, Sitakundo pouroshova, Sitakundo, Chattagram.
20	G 20	PG Sit-002	
21	G 21	PG Sit-003	
22	G 22	PG Sit-004	
23	G 23	PG Muk-004	Vil: Shejamora, Po: Mukundopur Bijounagor, Brahmabaria.
24	G 24	PG Muk-005	
25	G 25	Lata	Vil: Adabari, Po: Kuriana, Th: Nesarabad, Pirojpur.
26	G 26	Poltola	
27	G 27	Purnamandali	
28	G 28	Swarupkathi-1	Horticulture Research Centre, BARI[1], Gazipur.
29	G 29	Thai Peyara-3	
30	G 30	Thai Peyara -5	
31	G 31	Thai Special	
32	G 32	Swarupkathi-3	
33	G 33	Poly-Peyara	

Data collection

Data on different morpho-biochemical traits were recorded from the guava plants of each location during the course of experiment. Data were recorded on number of flowers per plant (FPP), number of fruits per plant (NFP), number of harvested fruits per plant (HFP), single fruit weight (SFW), number of seeds per fruit (NSF), thousand seed weight (TSW), vitamin C (VTC), total sugar (TSU), reducing sugar (RSU), fruit yield per plant (FYP).

Statistical analysis

The R-statistics platform (version 4.0.2) was used to conduct the statistical studies (Pinheiro et al., 2007). The R software was used to perform analyses of variance (ANOVA) for each trait (Aravind et al., 2020). The method was used to determine phenotypic and genetic variance (PV and GV), as well as genotypic and phenotypic coefficients of variation (GCV and PCV) described by Falconer and Mackay (1983). Burton's (1952) formula for calculating heritability (h^2b) and genetic advance (GA)

RESULTS AND DISCUSSION

Analysis of variance

Table 2 furnish the analysis of variance studied for 10 traits. All of the traits showed significant variance among genotypes, demonstrating a wide range of variability among genotypes for the morpho-biochemical component traits studied in this study, indicating the possibility of effective selection (Hossain et al., 2020).

Table 2. Analysis of variance for thirty-three genotypes of guava

Sources of variation	d.f	FPP	NFP	HFP	SFW	NSF	TSW	VTC	TSU	RSU	FYP
Replication	2	43.832	84.012	86.783	284.108	2.616	0.001	5.86	0.029	0.016	33.379
Genotype	32	544305.17 **	363487.39 **	179320.59 **	25270.22 **	54225.31 **	18.28**	3479.86 **	8.26**	4.33**	2078.33 **
Error	64	5.07	5.98	13.48	80.15	113.43	0.01	3.37	0.03	0.01	16.09
CV (%)		0.26	0.39	1.06	5.97	4.52	0.55	0.72	3.97	0.96	9.98

Note: FPP = Number of flowers per plant, NFP = Number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW = Thousand seed weight (g), VTC = Vitamin C (mg/100g), TSU = Total sugar (%), RSU = Reducing sugar (%), FYP = Fruit yield per plant (kg). ** = Significant at the 1% level, d.f = Degrees of freedom.

Descriptive statistic of the traits

The descriptive statistics on morpho-biochemical traits i.e., number of flowers per plant, number of fruits per plant, number of harvested fruits per plant, single fruit weight, number of seeds per fruit, thousand seed weight, vitamin C, total sugar, reducing sugar and fruit yield per plant of the genotypes presented in the Table 3. Number of flowers per plant varied from 142.53 to 1874.66. The genotype G21(PG Sit-003) produced the maximum flower while the minimum was produced by the genotype G33 (Poly-Peyara). The average number of flowers per plant were 876.18 (Table 3).

Number of fruits per plant ranged from 80 to 1483. Average number of fruits were calculated as 620.57. The maximum number of fruits was found in G21 (PG Sit-003) genotype while the minimum was in G33 (Poly-Peyara) genotype. Rahman et al., (2006) observed the highest number of fruits per plant was 1484.00 and lowest was 135.33. Most of the genotypes (21 genotypes) showed 100 to 400 g of single fruit weight, and the remaining (12 genotypes) showed 20 to 100 g. Single fruit weight was ranged from 21 to 392 g. The heaviest fruits were observed in genotype G29 (Thai Peyara-3) while the lightest were observed in genotype G21 (PG Sit-003). Rahman et al. (2006) found the highest single fruit weight (303.67 g) while the other genotypes ranged from 31.00 g to 202.00 g. Number of seeds per fruit and thousand seed weight were ranged from 0 to 517 and 0 to 13.1 g, respectively. Maximum number of seeds per fruit and thousand seed weight were found in G7 (PG Hat 014) and G15 (BARI Peyara -2) genotype respectively while minimum was found in the genotype of G17 (BARI Peyara -4). The genotype G14 (BARI Peyara -1) (131.04 kg) followed by G24 (PG Muk-005) and G23 (PG Muk-004) yielded 65.49 kg and 64.62 kg, respectively while the lowest (4.58 kg) were produced by the genotype G33 (Poly-Peyara). Rahman et al. (2006) reported 2.01 kg to 92.02 kg yield per plant in guava. Most of the genotypes (21 genotypes) showed above 250 mg/100g vitamin C content. The highest vitamin C were found in G23 (PG Muk-004) and the lowest in G19 (PG Sit-001) genotype (Table 3). Recent studies have reported appreciable amount of vitamin C (Youssef and Ibrahim, 2016). More than 42% of the genotypes performed total sugar content of over 5% (14 genotypes).

Table 3. Descriptive statistics of yield contributing traits of different guava genotypes

Traits	Average	Range		Standard deviation
		Maximum	Minimum	
FPP (no.)	876.18	1874.66	142.53	433.19
NFP (no.)	620.57	1483	79.56	354.15
HFP (no.)	347.42	1009.33	47.21	249.08
SFW (g)	150.03	392	21	93.84
NSF (no.)	235.75	517	0	136.33
TSW(g)	8.62	13.1	0	2.59
VTC (mg/100g)	253.19	299.61	185	34.24
TSU (%)	4.65	10.31	1.58	1.75
RSU (%)	3.5	8.02	1.18	1.28
FYP (kg)	40.21	131.04	4.58	27.63

Note: FPP = Number of flower per plant, NFP = Number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW = Thousand seed weight (g), VTC = Vitamin C (mg/100g), TSU = Total sugar (%), RSU = Reducing sugar (%), FYP = Fruit yield per plant (kg).

Genetic variability parameters

Table 4 summarizes the results for all 10 traits in terms of genetic parameters such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as the percent of the mean at 5% selection intensity. Harvested fruits per plant had the highest phenotypic variability (70.38%) and genotypic variability (70.37%) followed by fruit yield per plant, single fruit weight, number of seeds per fruit and number of flowers per plant. High phenotypic variability and high genotypic variability indicates that these traits are influenced by genetic control. The traits total sugar, reducing sugar and thousand seed weight were noted for moderate magnitudes of both phenotypic variability and genotypic variability, respectively. The traits low magnitudes of both phenotypic variability and genotypic variability were recorded for vitamin C content, respectively.

The high percentage of mean recorded for harvested fruits per plant, fruit yield per plant, single fruit weight, number of seeds per fruit, number of fruits per plant, and number of flowers per plant indicates that the high heritability observed is due to additive gene effects, and selection may be effective for these traits (Table 4). High genotypic variability and heritability estimates, along with higher genetic gains are indicative of additive gene effects governing the inheritance of the trait (Patel et al., 2015); thus, these characters reflect higher selective values and provide plenty of scope for selection. Patel et al. (2015), Raghava and Tiwari (2008), and Bihari and Suryanarayan (2011) reported high heritability along with genetic advance for different traits in guava. High heritability and moderate genetic advance as a percentage of the mean were observed for reducing sugar, total sugar, thousand seed weight, and Vitamin C in guava indicating the role of both additive and non-additive gene effects in controlling the traits, implying that selection is difficult or ineffective. Low to moderate heritability and genetic advanced values will prevent trait improvement due to the strong influence of the environment on genetic control. Effective selection can only be achieved by selecting higher values of genotypic variability, phenotypic variability, heritability and genetic advance at a selection intensity of 5% implying that additive gene influence is more stable than environmental influence (Uddin et al., 2021). From this study, harvested fruits per plant, fruit yield per plant, single fruit weight, number of seeds per fruit, number of fruits per plant and number of flowers per plant, high phenotypic variability and genotypic variability were observed, along with high heritability and high genetic advance as a percentage of the mean, indicating the preponderance of additive gene action and as a result, there is potential for selection to strengthen the trait.

Table 4. Estimation of statistical and genetic parameters of yield and its contributing traits of different guava genotypes

Traits	Mean	GCV	PCV	h^2b	GA	GAM
FPP	876.18	48.62	48.62	99.99	877.45	100.15
NFP	620.57	56.09	56.09	99.99	717.03	115.54
HFP	347.42	70.37	70.38	99.97	503.57	144.95
SFW	150.03	61.08	61.37	99.06	187.87	125.23
NSF	235.75	56.97	57.15	99.38	275.80	116.99
TSW	8.62	28.64	28.64	99.96	5.08	58.98
VTC	253.19	13.45	13.47	99.71	70.02	27.66
TSU	4.65	35.58	35.80	98.77	3.39	72.84
RSU	3.50	34.33	34.34	99.92	2.47	70.69
FYP	40.21	65.20	65.96	97.71	53.39	132.76

Note: GCV = Genotypic coefficients of variation, PCV = Phenotypic coefficients of variation, h2b = Heritability, GA = Genetic advance at 5% selection intensity, GAM = Genetic advance as the percentage of the mean at 5% selection intensity. FPP = Number of flower per plant, NFP = Number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW = Thousand seed weight (g), VTC = Vitamin C (mg/100g), TSU = Total sugar (%), RSU = Reducing sugar (%), FYP = Fruit yield per plant (kg).

Analysis of correlation matrix

The correlation matrix was developed to visualize a linear relationship between various traits using phenotypic correlation analysis (Figure 1). Fruit yield per plant had a significant positive correlation with Vitamin C, single fruit weight, number of flowers per plant and number of fruits per plant, in this study, however total sugar and reducing sugar had a negative correlation. The number of fruits per plant and harvested fruits per plant were highly and positively correlated with the number of flowers per plant and the number of flowers per plant, number of fruits per plant and harvested fruits per plant had a strong negative correlation with single fruit weight. Total sugar showed a strong positive significant correlation with reducing sugar (Figure 1). The correlation matrix is an excellent tool for determining the association between two or more variables. The correlation matrix considered as a scaling metric for higher genotype selection methods (Uddin et al., 2021; Konyak et al., 2020). A moderate to positive significant relationship can be proposed, and selection based on these traits could help increase crop yield. The findings were more or less congruent with the study of (Uddin et al., 2021; Banerjee et al., 2018).

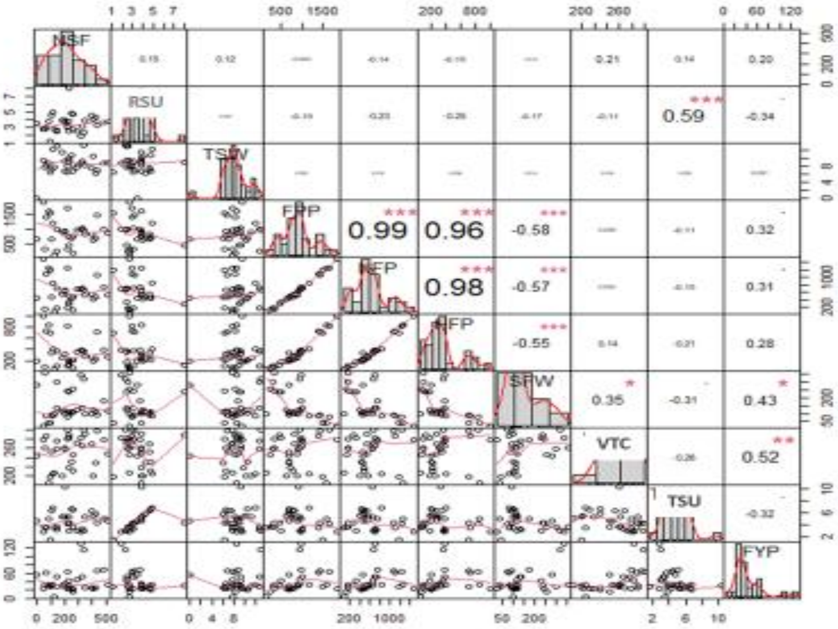

Figure 1. Correlation matrix, scatter plot and phenotypic frequency distribution of traits; *p <= 0.05; **p <= 0.01; ***p > 0.001; FPP = Number of flower per plant, NFP = Number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW= Thousand seed weight (g), VTC= Vitamin C (mg/100g), TSU= Total sugar (%), RSU= Reducing sugar (%), FYP= Fruit yield per plant (kg).

Multivariate analysis

Multivariate analysis is a tool for simultaneously identifying patterns and correlations between multiple variables. Principal component, biplot, and heatmap analysis were used to evaluate the link between guava genotypes and various morpho-biochemical parameters, revealing diverse clusters of genotypes that performed better in different aspects. The genotype by trait biplot was created using the relative value of the trait and a two-way matrix of 10 morpho-biochemical traits and 33 guava genotypes.

Principal component analysis

Eigen values of 10 principal component axis and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 5. The result revealed that the first axis largely accounted for the variation among the traits (35.4%) followed by second axis (23.4%). The first two axis accounted 58.8% of the total variation among 10 traits describing 33 genotypes. Henane et al. (2013) reported that the first three axis explained 89.86% of the observed phenotypic diversity and the first principal component explained 54.5% of the total variance.

Table 5. Eigen values and percentage of variation for corresponding 10 traits in guava genotypes

Principal component axis	Eigen values	% of Variance	Cumulative %
PC1	3.54	35.4	35.4
PC2	2.34	23.4	58.8
PC3	1.39	13.9	72.7
PC4	1.00	9.97	82.7
PC5	0.71	7.12	89.8
PC6	0.52	5.23	95.0
PC7	0.37	3.74	98.8
PC8	0.10	0.96	99.7
PC9	0.02	0.24	100
PC10	0	0.02	100

In this PCA-biplot the closeness of trait vector explains the degree of correlation between them. When the angle between trait vector within 90^0, it gives strong positive correlation, when it is above 90^0 it means negative correlation and when it 0^0, it said to be linear or perfect correlation. There was a strong correlation between the number of flowers per plant, number of fruits per plant, and harvested fruits per plant in this study. Fruit yield per plant was positively correlated with vitamin C and total sugar was positively correlated with reducing sugar in the PCA-biplot figure, but it was negatively correlated with other traits. This biplot showed that superior genotypes have higher levels of expression of positive trait combinations. The overall results suggested that the number of flowers per plant, number of fruits per plant, harvested fruits per plant, single fruit weight, fruit yield per plant, vitamin C, total sugar and reducing sugar could help in the selection of superior traits among the traits (Figure 2).

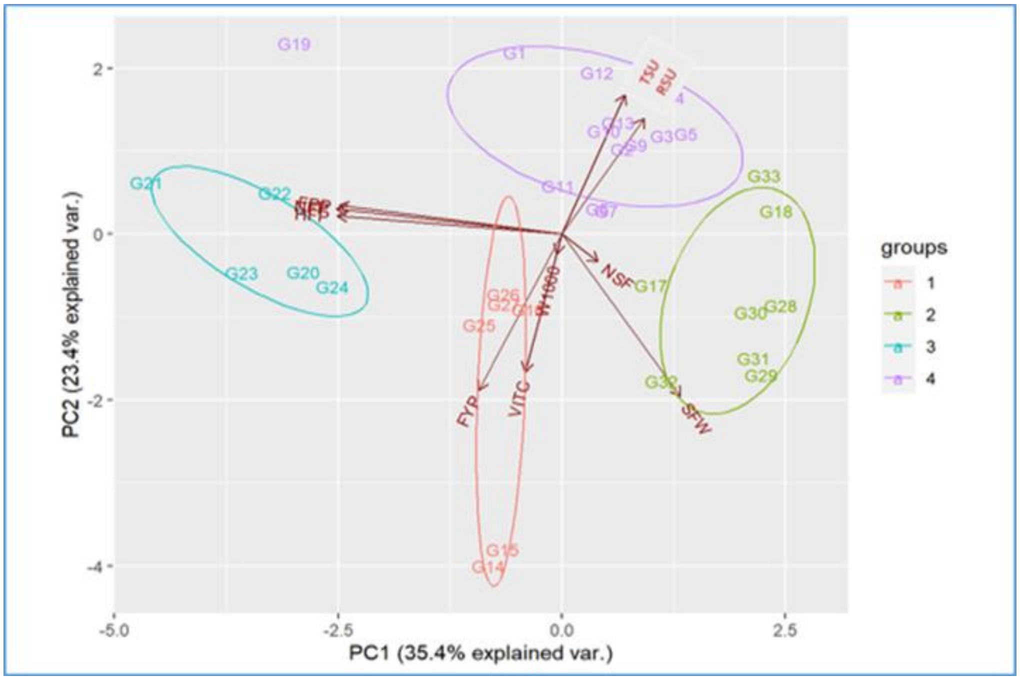

Figure 2. Genotypes by traits (G×T) biplot based on 33 genotypes and 10 traits of guava. FPP = number of flower per plant, NFP = number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW = Thousand seed weight (g), VTC = Vitamin C (mg/100g), TSU = Total sugar (%), RSU = Reducing sugar (%), FYP = Fruit yield per plant (kg).

Biplot analysis is commonly used to evaluate the component effects that result in genotypic variations. The higher values suggest that the traits have the greatest impact on overall variation. In the multi-environmental trial, biplot analysis assesses varietal stability (Uddin et al., 2021). It explains the relationship between different genotype traits. The biplot analysis revealed a relationship between morpho-biochemical traits among the 33 genotypes (Khan et al., 2021). The biplot analysis revealed trait profiles of the genotype, particularly those genotypes furthest (Figure 2) from the origin and the results revealed a correlation between traits with genotypes (Uddin et al., 2021).

Heatmap analysis

A chromatic evaluation of the genotypes was demonstrated using a heatmap analysis of features. The heatmap depicted the overall performance of 10 observable traits among the 33 guava genotypes (Figure 3). A heatmap is a two-dimensional data visualization approach that employs color to depict the magnitude of a phenomenon. The reader can see how the occurrence is grouped or varies over time by looking at color variation by hue or intensity. It shows the relative patterns of highly abundant features against a predominantly low-abundance background (Figure 3).

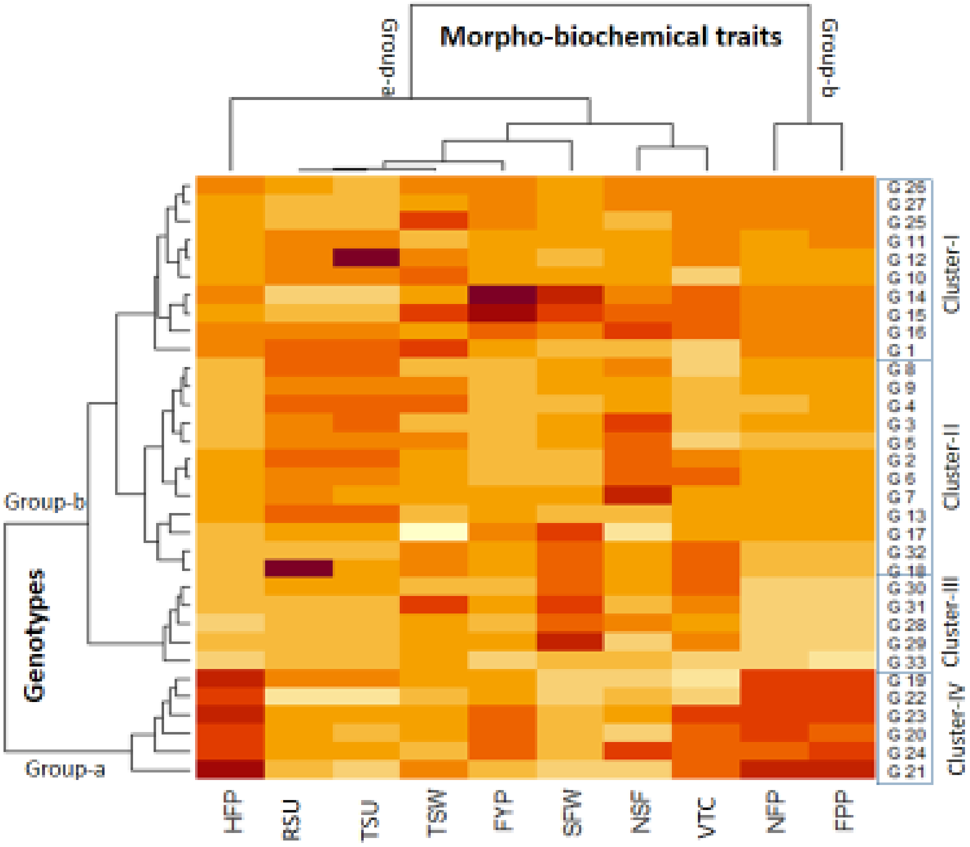

Figure 3. The grouping pattern of 33 guava genotypes with 10 morpho-biochemical traits is depicted in this heatmap. The red diagonal shows a perfect relationship of each accession with itself. Clusters of closely related genotypes can be seen in the white of warmer colors on the diagonal. FPP = number of flower per plant, NFP = number of fruits per plant, HFP = Number of harvested fruits per plant, SFW = Single fruit weight (g), NSF = Number of seeds per fruit, TSW = Thousand seed weight (g), VTC = Vitamin C (mg/100g), TSU = Total sugar (%), RSU = Reducing sugar (%), FYP = Fruit yield per plant (kg).

The heatmap analysis produced two dendrograms: one depicting the genotypes (vertical direction) and the other reflecting the traits (horizontal direction) that triggered the diffusion. Each accession's complete link to itself is depicted by the red diagonal. The symmetric off-diagonal elements indicate the relationship measures for pairs of genotypes. Through hierarchical clustering, four groupings emerged based on the morpho-biochemical features of the genotypes investigated (Figure 3). Group (a) included 6 genotypes from cluster-IV while group (b) included the remaining 27 genotypes from other three clusters. Out of a total of 33 genotypes cluster-I received 10, cluster-II received 12, cluster-III received 5, and cluster-IV received 6 (Figure 3). Dendrogram two also revealed two significant groups: group (a) is linked to eight traits, including harvested fruits per plant, single fruit weight, number of seeds per fruit, thousand seed weight, vitamin C, total sugar, reducing sugar, and fruit yield per plant, and group (b) is linked to two traits, number of flowers per plant and number of fruits per plant. The heatmap compares all of the traits and displays the high and lowest values of each genotype in distinct colors. The degree of high or low of the qualities is indicated by the color intensity. Four clusters emerged from hierarchical clustering of the researched germplasm's morpho-biochemical traits. Cluster-IV represents high value of the traits containing number of flowers per plant, number of fruits per plant and harvested fruits per plant (Fig. 3). It could be concluded that the genotype of the cluster-IV gave higher number of fruits per plant. Virga et al. (2020) used the heatmap analysis to show the degree of connection among the morpho-biochemical traits examined in guava genotypes

CONCLUSION

Wide range of variation was observed for harvested fruits per plant followed by fruit yield per plant, single fruit weight, number of seeds per fruit and number of flowers per plant. The results reflected from the magnitude of the genetic parameters such as GCV, PCV, h^2b, and GAM of guava fruit yield and related traits. The first two axis accounted 58.8% of the total variation among 10 traits describing 33 genotypes. It can also be observed the data and additional analyses of heatmap, correlation matrix, PCA analysis. Therefore, the traits flowers per plant, fruits per plant and single fruit per plant can be used as selection criteria for the improvement of guava. On the other hand, the genotypes G14 (BARI Peyara-1), G17 (BARI Peyara-4), G21 (PG Sit-003), G23 (PG Muk-004), G24 (PG Muk-005) and G29 (Thai Peyara-3) might be considered as the best genotypes based on the performance of morpho-biochemical characteristics.

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