Phenotypic Diversity Assessment of Guava (*Psidium guajava* L.) Collection in Vietnam

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**ABSTRACT**

**Background:** Guava (*Psidium guajava* L.) is an important cultivated fruit crop in Vietnam due to its commercial value for fresh consumption and especially for fruit processing industry. A large number of diverse guava accessions, both indigenous and exotic, are available in Vietnam but their characterization, which is needed to identify targeted guava accessions for breeding programs, is still limited.

**Methods:** The phenotypic variation and relationship among 40 guava accessions collected across Vietnam were assessed employing leaf and fruit morphological and physiological characterizations.

**Result:** Range of variation for different leaf and fruit parameters were recorded. Significant correlations between leaf and fruit traits relating to yield and fruit quality were also observed implying a possibility of their simultaneous or interchangeable use in selection. Furthermore, the dendrogram generated from agglomeration hierarchical clustering grouped the 40 guava accessions into four major clusters which are highly associated with their origins. The result indicated that existing guava accessions are an important source of genetic diversity and can be used in the guava improvement program in Vietnam.

**Key words:** Clustering analysis, Principal component analysis, Phenotypic diversity, *Psidium guajava*.

**INTRODUCTION**

Guava (*Psidium guajava* L.) is the most important and popular species of the genus *Psidium* which has been widely cultivated for fruit and medicinal purposes in tropical and subtropical regions (Gutiérrez et al. 2008). Along with its dispersal, selective breeding of guava has been performed through the identification of outstanding plants which were propagated by seeds or vegetative cloning method (Pommer and Murakami 2009, Boora 2012). In this context, understanding the available guava germplasm's genetic variation and relationships is a key step for any selective breeding program. Morphological characterization is the easiest approach to assess the genetic variation of a population because of its simplicity, cost-effectiveness and usefulness in determining the relatedness and other parameters among the different varieties/accessions. For guava, besides leaf characteristic, fruit is an important component of production that differs in shape, size, color, and weight and hence is one of the important morphological characters used to determine the relatedness and genetic clustering analysis (Nasution and Hadiati 2014).

In Vietnam, guava is widely used for both fresh consumption and processing. Formerly, only some local varieties such as Oi Bo, Oi Dong Du, Oi Dao… (in those “Oi” means “guava”) mostly bearing small and/or aromatic fruits were commercially grown (Pham et al. 1993). However, their adverse attributes i.e., low productivity and uneven quality have hindered the production and market value of guava in Vietnam. For decades, various guava cultivars from Taiwan, Thailand and India with promising fruit characteristics and adaptability have been introduced and cultivated extensively across the country. Nevertheless, because of the diversification of fruit morphology and quality, especially the plenty-of-seed characteristic, the domesticated accessions have not yet become the preferable choices as elite cultivars for guava production in Vietnam. Even so, they together with available local varieties provide valuable germplasm for guava improvement research. In this presented study, the phenotypic diversity of guava accessions collected across the country were evaluated using morphological/physiological traits. It would further help in the identification of potential parents for effective utilization in future selective breeding programs of superior guava varieties which are still lacking in Vietnam.

**MATERIALS AND METHODS**

**Plant materials and experimental sites**

The 40 guava accessions collected from different regions of Vietnam and used in this study are sub-classified into...
two groups: 10 indigenous and 30 exotic accessions (Table 1). The indigenous accessions were propagated by air-layering method while the exotic accessions were grafted on rootstocks of the local accessions “DongDu”. All studied accessions were grown in the experimental orchard of the Fruit and Vegetable Research Institute (FAVRI) with 4 x 4 m space between plants in spring 2017. The soil was alluvial-based and typical for the old Red River Delta of Vietnam. It was light to medium texture soil, fertile, well-drained with soil pH ranging from 6.1 to 7.1 and the amount of organic carbon, total N, available P and available K were 0.99-1.94%, 5.73-22.36 mg/100 g and 2.49-10.19 mg/100 g of the soil sample, respectively. Common agronomic and management practices were applied to all studied accessions in that, the amount of fertilizer applied annually per tree was 50 kg decomposed manure, 0.5 kg CO(NH$_2$)$_2$, 0.6 kg P$_2$O$_5$ and 0.55 kg KCL.

Mature leaves and fruits were randomly collected in spring 2020 from the three-year-old guava trees with three replicates for this study.

**Phenotypic assessment and data collection**

In total, nine quantitative and eleven qualitative traits for leaf and fruit were employed (Table 2). Characteristics viz. LL, LW, FL, FW, MT were measured by a digital caliper. The

### Table 1: Detail of guava collection used in the study.

| Accessions name  | Collection location                  | Type    |
|------------------|--------------------------------------|---------|
| Alahabed Safeda  | Chau Thanh dist., Tien Giang province| exotic  |
| BaTu             | Chau Thanh dist., Tien Giang province| exotic  |
| Beaumont         | Chau Thanh dist., Tien Giang province| exotic  |
| BoCam            | Thai Binh city, Thai Binh province   | indigenous |
| BoDen            | Thanh Ha dist., Hai Duong province   | indigenous |
| BoRuotDo         | Dong Hy dist., Thai Nguyen province  | indigenous |
| BoXanh           | Thanh Ha dist., Hai Duong province   | indigenous |
| BomDaiLoan       | Chau Thanh dist., Tien Giang province| exotic  |
| Bom              | Chau Thanh dist., Tien Giang province| exotic  |
| DaiLoan1         | Gia Lam dist., Hanoi City            | exotic  |
| DaiLoan2         | Gia Lam dist., Hanoi City            | exotic  |
| DaiLoan3         | Gia Lam dist., Hanoi City            | exotic  |
| DongDu           | Gia Lam dist., Hanoi City            | indigenous |
| Florida          | Chau Thanh dist., Ben Tre province   | exotic  |
| KhongHatDai      | Hochiminh City                       | exotic  |
| KhongHatThaiLan  | Chau Thanh dist., Tien Giang province| exotic  |
| KhongHatTron     | Chau Thanh dist., Tien Giang province| exotic  |
| KhongHat         | Gia Lam dist., Hanoi City            | exotic  |
| KimChu           | Gia Lam dist., Hanoi City            | exotic  |
| LeDaiLoan        | Chau Thanh dist., Tien Giang province| exotic  |
| LeHongDaiLoan    | Cho Lach dist., Ben Tre province     | exotic  |
| America          | Chau Thanh dist., Tien Giang province| exotic  |
| NuHoang          | Long Ho dist., Vinh Long province    | exotic  |
| OiDai            | Thanh Ha dist., Hai Duong province   | indigenous |
| Paxithong        | Chau Thanh dist., Tien Giang province| exotic  |
| RuotHongDaLang   | Chau Thanh dist., Tien Giang province| exotic  |
| RuotHongDaSan    | Chau Thanh dist., Tien Giang province| exotic  |
| RuotHong         | Chau Thanh dist., Tien Giang province| exotic  |
| RuotTrang        | Chau Thanh dist., Tien Giang province| exotic  |
| RuotVang         | Chau Thanh dist., Tien Giang province| exotic  |
| ThaiLanLai1      | Cho Lach dist., Ben Tre province     | exotic  |
| ThaiLanLai2      | Cho Lach dist., Ben Tre province     | exotic  |
| ThaiLanXaLiNghe  | Chau Thanh dist., Tien Giang province| exotic  |
| ThaiLan          | Thanh Ha dist., Hai Duong province   | exotic  |
| TimMaLai         | Cho Lach dist., Ben Tre province     | exotic  |
| TrangSo1         | Gia Loc dist., Hai Duong province    | exotic  |
| XaLiNghe         | Chau Thanh dist., Tien Giang province| indigenous |
| XaLiSNG          | Chau Thanh dist., Tien Giang province| indigenous |
| XaLiTron         | Chau Thanh dist., Tien Giang province| indigenous |
| Xu               | Thanh Ha dist., Hai Duong province   | indigenous |
SN per fruit was manually counted and classified as modification from UPOV’s guideline. The FW was measured by digital balance with 0.01 g precision whereas the MP was calculated using the formula:

$$MP \text{ (\%)} = \frac{SFW - \text{Total seeds weight}}{SFW} \times 100\%$$

The FA and SSC were determined by titration using 0.1M sodium hydroxide and a simple digital refractometer, respectively. Other qualitative traits of leaf and fruit were scored according to the UPOV’s guidelines for guava (UPOV 1987).

**Data analysis**

The mean of the evaluated traits was calculated and used for statistical analysis using the XLSTAT 2016 package. For descriptive statistics, the minimum value, maximum value, standard deviation (SD) and coefficient of variation (CV%) were calculated. Parametric Pearson’s and polychoric correlation coefficients were used to measure the degree of pairwise association between quantitative and qualitative traits, respectively. The degrees of correlation were interpreted as negligible (0.00 to ±0.30), low (±0.30 to ±0.50), moderate (±0.50 to ±0.70), high (±0.70 to ±0.90) and very high (±0.90 to ±1.00). The relationships between the accessions were determined using principal component analysis (PCA). For better elucidation of variation patterns among studied accessions, the combined data from the quantitative and qualitative traits were used to estimate the Euclidean genetic distance matrix which was then subjected to cluster analysis using the agglomerative hierarchical clustering (AHC). Data of each character was normalized before proceeding to PCA and cluster analysis to avoid erroneous effects due to scaling differences. Statistical significance was set at $p < 0.05$ for all analyses.

**RESULTS AND DISCUSSION**

**Morphological characteristics of guava accessions**

Morphological characterization is the first and highly recommended step before further attempts utilizing biochemical or the currently most popular, molecular approaches in genetic diversity assessment and preservation studies (Sun et al. 2019). In this study, the morphological characteristics of the most abundant guava

| Character | Character code | Phenotype and descriptive value |
|-----------|----------------|---------------------------------|
| Leaf blade length | LL | In centimeters |
| Leaf blade width | LW | In centimeters |
| Fruit length | FL | In centimeters |
| Fruit width | FW | In centimeters |
| Single fruit weight | SFW | In grams |
| Mesocarp thickness | MT | In centimeters |
| Mesocarp percentage | MP | In percentages |
| Fruit acidity | FA | In percentages |
| Soluble solid content | SSC | In percentages |
| **Leaf color** | LC | 1 (yellow green), 2 (grey green), 3 (green), 4 (dark green) |
| **Leaf shape** | LS | 1 (round), 2 (ovate), 3 (obovate), 4 (trullate), 5 (obtrullate), 6 (oblong) |
| **Degree of leaf margin undulation** | LMU | 1 (none), 3 (weak), 5 (medium), 7 (strong) |
| **Shape of leaf tip** | LT | 1 (attenuate), 2 (apiculate), 3 (acute), 4 (obtuse), 5 (rounded) |
| **Fruit shape** | FS | 1 (round), 2 (ovoid), 3 (pear-shape), 4 (elongate) |
| **Fruit skin color** | FSC | 1 (pale yellow-green), 2 (pale green), 3 (dark yellow), 4 (orange), 5 (orange green), 6 (dark green), 7 (red) |
| **Fruit skin surface** | FSS | 3 (smooth), 5 (rough), 7 (bumpy) |
| **Mesocarp color** | MC | 1 (white), 2 (cream), 3 (pale pink), 4 (pink), 5 (dark pink), 6 (orange pink), 7 (orange) |
| **Seed number** | SN | 1 (none), 2 (very few), 3 (few), 5 (medium), 7 (many), 9 (very many) |
| **Fruit brittleness** | FB | 3 (low), 5 (medium), 7 (high) |
| **Fruit muskiness (flavor)** | FM | 1 (absent), 9 (present) |
collection in Vietnam were assessed for the first time. Descriptive statistics results of all 20 assessed morphological traits are presented (Table 3).

The coefficient of variation (CV) for the assessed trait indicates its degree of dispersion. Among the 40 guava accessions, the low CV value (less than 0.20) revealed for most of the leaf and fruit morphological traits indicated that these traits remained relatively stable among accessions. Meanwhile, important indicators for guava productivity SFW and MT together with physiological traits FA and SSC, exhibited higher CV values (0.28, 0.26, 0.41 and 0.24, respectively), demonstrating the existence of a higher range of selection for those traits (Mehmood and Prasanna 2003, Mahour et al. 2012). An extensive variation, on the other hand, was revealed for most of the qualitative traits studied except FSC and FM, which exhibited lower CV values (0.17) among the collection. The tendency of introducing potential guava genotypes producing freshly-green fruit with attractive aroma to meet Vietnamese consumer preference may lead to the observed results. For each of the remaining qualitative traits, the presence of two or more phenotypic stages was the main explanation for their higher variation within the collection. Similar results were revealed in evaluating the diversity of Pakistani guava germplasm (Mehmood et al. 2014). The diversity of morphological characters in the studied guava collection in Vietnam also provides an ample scope for the selection of excellent individuals for further improvement as reported in previous studies (Purbajanti et al. 2016, Sun et al. 2019).

Correlations among quantitative and qualitative traits

Enlightening the relationship between traits related to fruit and leaf morphology and physiology can guide the selection of appropriate options for breeding programs. The pairwise Pearson correlations between nine quantitative traits were shown (Fig 1). Different statistically significant correlations were observed among quantitative variables, indicating the feasibility of improving some traits by breeding among studied guava accessions. While LL and LW showed significant negative correlations with fruit morphological and physiological characters, there were significant positive correlations among fruit morphological variables FL, FW, SFW, MT and MP. Especially, FL and MT had high correlations with SFW and MP, respectively, which imply that these traits are efficient in yield determination and possibly used either simultaneously or interchangeably in selections (Loko et al. 2018). Remarkably, all correlations between leaf traits and fruit morphological and physiological traits were negatively significant (Fig 1). This result indicates that the simultaneous selection of guava with greater leaf size would result in greater core part and lower level of fruit acidity and soluble solid content, and consequently may lead to the decrease of fruit yield and quality. However, the magnitudes of these simple correlations between leaf and fruit traits were low, precluding indirect selection for fruit yield and quality in leaf morphology.

The polychoric correlations between eleven qualitative traits were also estimated (Fig 3). Negative correlations were not found significantly between analyzed

Table 3: Description statistic of quantitative and qualitative traits recorded for 40 guava accessions.

| Statistic                  | Abbreviation | Min | Max  | Mean  | Standard deviation (n=1) | CV  |
|----------------------------|--------------|-----|------|-------|--------------------------|-----|
| Quantitative traits        |              |     |      |       |                          |     |
| Leaf blade length (cm)     | LL           | 7.85| 15.55| 11.34 | 1.96                     | 0.17|
| Leaf blade width (cm)      | LW           | 4.21| 7.35 | 5.78  | 0.82                     | 0.14|
| Fruit length (cm)          | FL           | 6.15| 11.78| 8.48  | 1.38                     | 0.16|
| Fruit width (cm)           | FW           | 5.60| 10.20| 7.49  | 1.04                     | 0.14|
| Single fruit weight (g)    | SFW          | 64.60| 446.00| 253.93| 70.67                    | 0.28|
| Mesocarp thickness (cm)    | MT           | 1.20| 3.50 | 2.14  | 0.55                     | 0.26|
| Mesocarp percentage (%)    | MP           | 60.55| 100.00| 77.31 | 9.00                     | 0.12|
| Fruit acidity (%)          | FA           | 0.15| 0.64 | 0.28  | 0.11                     | 0.41|
| Soluble solid content (%)  | SSC          | 5.50| 13.50| 8.11  | 1.96                     | 0.24|
| Qualitative traits         |              |     |      |       |                          |     |
| Leaf color                 | LC           | 1   | 4    | 3.22  | 0.97                     | 0.30|
| Leaf shape                 | LS           | 2   | 6    | 4.00  | 2.03                     | 0.51|
| Degree of leaf margin undulation | LMU    | 1   | 7    | 3.35  | 2.60                     | 0.78|
| Shape of leaf tip          | LT           | 2   | 4    | 3.50  | 0.85                     | 0.24|
| Fruit shape                | FS           | 1   | 4    | 2.47  | 1.34                     | 0.54|
| Fruit skin color           | FSC          | 1   | 6    | 1.72  | 1.11                     | 0.64|
| Fruit skin surface         | FSS          | 3   | 7    | 4.75  | 0.81                     | 0.17|
| Mesocarp color             | MC           | 1   | 4    | 1.85  | 0.89                     | 0.48|
| Seed number                | SN           | 1   | 7    | 5.82  | 2.00                     | 0.34|
| Fruit brittleness          | FB           | 3   | 7    | 6.45  | 1.11                     | 0.17|
| Fruit muskiness (flavor)   | FM           | 1   | 9    | 4.80  | 4.05                     | 0.84|
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qualitative traits. Among qualitative variables, on the other hand, only statistically-significant positive correlations were observed. The low to high positive correlations existing between leaf (LC, LS, LMU) and fruit (FSS, FB, FM) characters showed that leaf traits are feasible measures to predict some fruit qualitative traits having potential economic interest.

**Multivariate relationships among quantitative and qualitative traits**

The Principal Component Analysis (PCA) showed that nine quantitative traits were integrated into nine principal components (PC), in which all analyzed traits have a significant contribution to the first three PCs explaining 74.946% of the total variability (Table 4). The bi-plot of the first two PCs representing 64.132% of cumulative variability mapped the relationship between quantitative traits and among assessed guava genotypes (Fig 2). It also showed the scatter of analyzed guava accessions which revealed the clustering trend of indigenous and exotic groups. Accessions such as “DongDu” and “TimMaLa” were unique due to their leaf and fruit quantitative characters, whereas the remains showed closer relationships due to their sharing

| Traits | LL | LW | FL | FW | SFW | MT | MP | FA | SSC |
|--------|----|----|----|----|-----|----|----|----|-----|
| LL     | 1  | 0.000 | 0.495 | 0.077 | 0.280 | 0.001 | 0.024 | 0.018 | 0.000 |
| LW     | 0.821 | 1  | 0.043 | 0.117 | 0.169 | 0.017 | 0.144 | 0.019 | 0.004 |
| FL     | 0.111 | 0.321 | 1  | 0.031 | <0.0001 | 0.010 | 0.247 | 0.082 | 0.058 |
| FW     | -0.283 | -0.252 | 0.341 | 1  | 0.010 | 0.000 | 0.032 | 0.392 | 0.670 |
| SFW    | 0.175 | 0.222 | 0.708 | 0.489 | 1  | 0.015 | 0.348 | 0.169 | 0.019 |
| MT     | 0.407 | 0.375 | 0.404 | 0.565 | 0.360 | 1  | <0.0001 | 0.514 | 0.352 |
| MP     | -0.358 | -0.255 | -0.187 | 0.358 | 0.152 | 0.659 | 1  | 0.355 | 0.081 |
| FA     | -0.373 | -0.370 | -0.024 | 0.139 | -0.222 | 0.106 | 0.150 | 1  | 0.001 |
| SSC    | -0.649 | -0.065 | 0.670 | -0.064 | -0.120 | 0.141 | 0.790 | 0.570 | 1  |

**Fig 1:** Pearson correlation coefficients among 9 quantitative traits in 40 guava accessions. Gradient color bar represents level of correlation between analyzed traits ranging from orange (negative correlation) to blue (positive correlation).

**Fig 2:** Bi-plot based on the first two principal components for 9 quantitative traits of 40 guava accessions.

| Traits | LC | LS | LMU | LT | FS | FSC | FSS | MC | SN | FB | FM |
|--------|----|----|-----|----|----|-----|-----|----|----|----|----|
| LC     | 1  | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| LS     | 0.519 | 1  | 0.550 | 0.137 | 0.416 | 0.063 | 0.049 | 0.486 | 0.068 | 0.399 | 0.004 |
| LMU    | 0.053 | 0.012 | 1  | 0.000 | 0.620 | 0.274 | 0.870 | 0.492 | 0.942 | 0.002 | 0.872 |
| LT     | 0.275 | 0.432 | 0.407 | 1  | 0.134 | 0.676 | 0.810 | 0.836 | 0.889 | 0.126 | 0.582 |
| FS     | -0.366 | -0.242 | 0.174 | 0.326 | 1  | 0.651 | 0.609 | 0.808 | 0.605 | 0.795 | 0.812 |
| MC     | 0.343 | 0.440 | -0.057 | -0.200 | 0.023 | 1  | 0.564 | 0.085 | 0.315 | 0.803 | 0.304 |
| SN     | 0.422 | 0.477 | -0.045 | -0.099 | 0.041 | 0.133 | 1  | 0.744 | 0.249 | 0.661 | 0.773 |
| FB     | 0.371 | 0.312 | 0.111 | 0.003 | 0.001 | -0.405 | -0.282 | 1  | 0.996 | 0.600 | 0.689 |
| FM     | 0.048 | 0.481 | -0.004 | -0.071 | -0.210 | 0.198 | 0.216 | 0.000 | 1  | 0.323 | 0.251 |

**Fig 3:** Polychoric correlations among 11 qualitative traits in 40 guava accessions. Gradient color bar represents level of correlation between analyzed traits ranging from orange (negative correlation) to blue (positive correlation).
of common morphological attributes. Eleven qualitative traits had the largest contributions to the first five PCs in the PCA which accounted for 79.022% of the total variability (Table 5). Relationships of assessed qualitative traits were showed in the bi-plot of the first two PCs accounting for 46.846% of the total variability. The 40 evaluated guava accessions could easily be differentiated by its qualitative traits (Fig 4).

Principal component analysis (PCA) was employed to reduce the complexity of the data set while retaining the variation within the data set as far as possible (Jolliffe and Cadima 2016). In this study, PCA showed that leaf traits of LW and LL and two fruit traits of FL and SFW had strong positive associations with the group of introduced guava genotypes. On the other hand, fruit quality traits of FA and SSC had strong positive linkages with the group of local guava accessions together with other fruit traits of MP, MT and FW which showed as indicators for the local group. Other fruit morphologies FL and SFW showed neutral or insignificant effects in indicating either group. Among qualitative traits, the leaf traits LS, LC and fruit traits FM, SN, FSC, FSS were visualized by PCA in a high association with the group of introduced guava accessions, whereas LT, LMU, FB and especially MC had linkage with local guava accessions. The expression of phenotypic characters is defined as the results of genetic and environmental factors (Purbajanti et al. 2016). In the presented study, all of the guava accessions were planted in the same cultivation condition, therefore the genetic factors are mainly responsible for the observed phenotypic diversity.

Relationships between quantitative and qualitative traits exposed by PCA analysis might correspond to a genetic linkage between loci of controlling characteristics or a pleiotropic effect (Khadivi 2018) and can be utilized as useful indicators for differentiation and evaluation of local and introduced guava accessions.

Variation between quantitative and qualitative traits and cluster analysis

The Euclidean distance matrix for the 40 guava accessions was calculated based on 20 analyzed traits. The most closed relationship was detected between “LeDaiLoan” and “DaiLoan1” accessions with a distance of 1.961, while the two local accessions “Xu” and “DongDu” had the highest distance of 11.000. Ward’s clustering method clustered the assessed guava accessions into four distinct groups with within-group variance accounting for 70.25% total variability (Fig 5a). This supports the findings in the PCA and indicates notable genetic divergence in terms of morphological traits exhibited by the studied accessions.

Histograms of means (in z-score transformation) of leaf traits, fruit morphological traits and fruit quality traits were shown in Fig 5b. Quantitatively, group I was identified by the lowest values of FW and MT. While group II was differentiated by the highest values of LL, LW and SFW, guava accessions of group III had the lowest values of LL, LW and the highest values of FA, SSC. Group IV was characterized by the highest levels of MT and MP. By qualitative traits, group I was identified by dark green leaf color. Group II was differentiated by oblong-shaped leaf, rough fruit skin surface, and the presence of aroma. On the other hand, group III and IV were characterized by the presence of aroma and smooth fruit skin surface, respectively.

Table 4: Principal component analysis (PCA) for 9 quantitative traits of 40 guava accessions.

|          | PC1    | PC2    | PC3    |
|----------|--------|--------|--------|
| Eigenvalue| 3.201  | 2.571  | 0.973  |
| Variability (%)| 35.566 | 28.566 | 10.815 |
| Cumulative (%)| 35.566 | 64.132 | 74.946 |
| Factor loading |
| LL     | 0.851  | 0.251  | 0.189  |
| LW     | 0.768  | 0.368  | 0.340  |
| FL     | -0.093 | 0.798  | 0.462  |
| FW     | -0.518 | 0.538  | -0.202 |
| SFW    | -0.001 | 0.882  | 0.039  |
| MT     | -0.744 | 0.516  | -0.136 |
| MP     | -0.655 | 0.303  | 0.006  |
| FA     | -0.523 | -0.320 | 0.568  |
| SSC    | -0.596 | -0.456 | 0.475  |

Values in bold correspond for each variable to the principal component for which the contribution is the largest.

Fig 4: Bi-plot based on the first two principal components for 11 qualitative traits of 40 guava accessions.
Figure 5: (a) Agglomerative hierarchical clustering based on morphological traits using Euclidean distance. Guava accessions in bold are indigenous. (b) Histograms of the transformed z-score related to leaf traits, fruit traits, and fruit quality of four clusters.

Table 5: Principal component analysis (PCA) for 11 qualitative traits of 40 guava accessions.

|                  | PC1   | PC2   | PC3   | PC4   | PC5   |
|------------------|-------|-------|-------|-------|-------|
| Eigenvalue       | 3.286 | 1.867 | 1.421 | 1.164 | 0.954 |
| Variability (%)  | 29.874| 16.973| 12.918| 10.584| 8.674 |
| Cumulative (%)   | 29.874| 46.846| 59.764| 70.349| 79.022|
| Factor loading   |       |       |       |       |       |
| LC               | 0.689 | 0.139 | -0.372| -0.170| -0.261|
| LS               | 0.839 | 0.245 | 0.173 | -0.261| 0.322 |
| LMU              | -0.437| 0.696 | 0.276 | -0.367| -0.044|
| LT               | -0.588| 0.370 | 0.129 | 0.203 | -0.078|
| FS               | -0.387| 0.234 | -0.066| 0.583 | 0.587 |
| FSC              | 0.564 | 0.418 | 0.087 | 0.362 | -0.099|
| FSS              | 0.341 | 0.411 | -0.619| -0.268| 0.386 |
| MC               | -0.353| -0.483| 0.206 | -0.477| 0.474 |
| SN               | 0.403 | -0.072| 0.742 | -0.078| -0.020|
| FB               | -0.806| 0.650 | 0.033 | -0.302| -0.109|
| FM               | 0.576 | 0.326 | 0.414 | 0.154 | 0.184 |

Values in bold correspond for each variable to the principal component for which the contribution is the largest.
other hand, most guava accessions of group III shared pale yellow-green fruit skin and high fruit brittleness. Group IV was characterized by rough fruit skin surface and especially by lower seed number in comparison with other groups. Grouping pattern not only discriminated the state of origin of guava accessions but also helped to identify candidates for further breeding programs in Vietnam which may target separately or simultaneously higher fruit weight, less seed number and aromatic trait. Similar recommendations were reported in previous studies employing morphological traits as measures to estimate the diversity and explore the possibility of exploiting the desirable variability in guava accessions worldwide (Rajan and Yadava 2012, Mehmood et al. 2014, Pérez Pelea et al. 2016, Kareem et al. 2018).

CONCLUSION
The phenotypical diversity among 40 accessions of guava Psidium guajava collected across Vietnam related to morphological and physiological characteristics are presented in this study. Principal component analysis revealed that leaf and fruit traits had a great contribution to the principal components. Additionally, the correlation analysis revealed a significant association between evaluated leaf and fruit traits. All accessions were clustered into four groups, basically distinguishing their different origins. Results suggested that phenotypic assessment could be a useful measure to understand the potential genetic variation of guava germplasm for their future utilization in improvement programs in Vietnam.

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