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CHARACTERIZATION OF GENETIC DIVERSITY IN THREE GUAVA (*Psidium guajava* L.) POPULATIONS

Caracterización de la diversidad genética en tres poblaciones de guayabo (*Psidium guajava* L.)

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ABSTRACT. Guava (*Psidium guajava* L.) is an economically important fruit tree in several countries, where breeding programs are being developed with different objectives. Evaluations on the genetic variability of crop germplasm collections have been performed in some of these countries; however, the variability present in guava populations had not been evaluated so far. Ten quantitative morphoagronomic traits were assessed for three years in parents and progenies of three guava populations, with the aim of characterizing the genetic diversity of such populations derived from controlled crossings. Main component analysis clusters and discriminant factorials were made in order to determine the highest variability characters that allow making up diversity groups and confirming if there are differences among them. Significant differences were also determined among populations for the characters: leaf length and width, plant height, fruit length and width, external and internal pulp thickness, and seed number per fruit. Fruit characters were the greatest contributors to the variability observed. Regarding dendrograms obtained, four diversity groups were formed in each population, mainly based on fruit mass, length and width, seed number and its total mass per fruit. All the results allowed detecting high population variability for the traits evaluated.

Key words: genetic variability, genetic breeding, tropical fruit trees, diversity groups

RESUMEN. El guayabo (*Psidium guajava* L.), es un frutal de gran importancia económica en diversos países, en los cuales se están desarrollando programas de mejoramiento genético, con distintos objetivos. En varios de estos países, se han realizado evaluaciones de la variabilidad genética presente en colecciones de germoplasma del cultivo; sin embargo, hasta la fecha no se había realizado ninguna evaluación de la variabilidad presente en poblaciones del cultivo. Con el objetivo de caracterizar la diversidad genética presente en tres poblaciones de guayabo, obtenidas a partir de cruzamientos controlados, se evaluaron diez caracteres morfoagronómicos cuantitativos durante tres años, en los progenitores y los descendientes de las poblaciones. Se realizaron análisis de componentes principales, de agrupamientos y factoriales discriminantes, para determinar los caracteres de mayor variabilidad que permiten la formación de grupos de diversidad en las poblaciones y corroborar si hay diferencias entre los grupos formados. También se determinó que existían marcadas diferencias entre las tres poblaciones para los caracteres: largo y ancho de la hoja, altura de la planta, largo y ancho del fruto, espesor externo e interno de la pulpa y número de semillas por fruto; los caracteres del fruto son los de mayor contribución a la variabilidad detectada. En los dendrogramas obtenidos se observó la formación de cuatro grupos de diversidad, en cada una de las poblaciones, atendiendo principalmente a los caracteres: masa, largo, ancho del fruto, número y masa total de las semillas por fruto. La integración de los resultados permitió detectar una alta variabilidad en las tres poblaciones, para los caracteres evaluados.

Palabras clave: variabilidad genética, mejoramiento genético, frutales tropicales, grupos de diversidad

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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 (1). It belongs to Myrtaceae family that includes from 130 to 150 genera[A], with more than 5000 species, and just a few have edible fruits (2). This fruit tree is significant from a commercial viewpoint, mainly due to the high nutritional value of its fruits, with great contents of vitamins A, B and C, dietary fiber and folic acid (3). Its fruits are not only used for fresh consumption, but also as an important source of raw materials for juice, nectar, ice cream, jelly and candy industry.

Despite its significance, the germplasm preservation of this fruit tree is still restricted, so that its sustainability is involved. There are more than 67 % genotypes of the planet collections in Latin America and the Caribbean. Thus, countries such as Brazil, Cuba, Costa Rica, India, Mexico, Puerto Rico and Venezuela make great efforts to preserve this germplasm in several research and teaching institutions (4).

Although the selective breeding of guava cultivars started almost a century ago, its available seed dispersion and high heterozygosity level prevent to conserve improved cultivars without significant attribute changes. There are probably more than 400 guava cultivars in the world, but only a few of them are commercially grown (5).

In Cuba, this fruit tree has become very important in recent decades, since it is a profitable crop with high internal demand and export potentialities. Its yields have been enhanced by seeding highly productive potential cultivars, such as 'Enana Roja Cubana' ('EEA 18-40'), whose yields exceed 70 t ha^{-1} with a steady production throughout the whole year and two periods of top production.

'Enana Roja Cubana' is the main commercially exploited cultivar and the pattern to be improved by crop growers and specialists, due to its distinctive morphoagronomic characteristics of low plant erection and high yields (6). Therefore, it has been used as female parent in several crossing programs aimed to obtain and evaluate new genotypes with interesting characteristics for breeding, such as low plant erection, high productivity and large, rounded shape, homogeneous fruits with high contents in vitamin C, acidity and total soluble solids, increased external pulp thickness, low seed number and mass, which can be considered as good quality for industry and fresh consumption.

With this background information, the objective of this study was to characterize genetic diversity of populations resulting from crosses between the following guava (*Psidium guajava* L.) cultivars: 'Enana Roja Cubana' as female parent with 'N6', 'Suprema Roja' and 'Belic L-207' as male parents, based on quantitative morphoagronomic traits.

MATERIALS AND METHODS

Planting material

Three guava (*Psidium guajava* L.) populations, derived from intraspecific crosses performed by controlled pollination, were used as planting material in the Scientific-Technological Base Unit (STBU) of Alquízar, Artemisa province, belonging to the Research Institute of Tropical Fruit Culture (RITFC) of Cuba, in 2001. The STBU is located at 22° 47' north latitude and 82° 31› west longitude, 11 m above sea level, on an eutric Ferralsol with a flat topography of zero slope (7).

To carry out crossings, three plants from 'Enana Roja Cubana' ('EEA 18-40') cultivar were used as female parents whereas 'N6', 'Red Supreme' and 'Belic L-207' cultivars as male parents. These cultivars were selected as parents because of their great genotypic and phenotypic variability.

Thus, 100 seeds out of those obtained from each crossing were selected per each one and sown in seedbeds. Afterwards, they were transplanted to 26x46-cm individual bags containing eutric Ferralsol and organic matter (filter cake) in the ratio of 3:1. When plants reached from 50 to 60 cm high, they were planted in the STBU, following a 6x5-m planting frame. The three populations were planted next to each other, making up a compact block in the same lot together with parents.

Plants were watered by drip irrigation using RAM spreaders of 2,3 L h^{-1}, at a spacing of 0,65 m within a 20-mm-diameter side. They were irrigated at fixed doses or fixed intervals (every other day), interrupting during heavy rainfall events. Cultural practices, fertilization and phytosanitary control followed Crop Technical Instruction (8).

[A] Faruk, O. *Morphological characterization of guava germplasm*. Tesis de Maestría, Universidad Agrícola de Bangladesh, 2012, 54 p.

Evaluation of quantitative traits in three guava (*Psidium guajava* L.) populations

Ten quantitative characters of those proposed by the International Union for Plant Protection of New Varieties (UPOV) (9) were evaluated in the three populations obtained, as well as those considered descriptors in Cuban guava germplasm collection (10). The characters are as follows: leaf blade length and width; plant height; fruit mass, length and width; external and internal pulp thickness; seed number and its total mass per fruit. They were selected according to their degree of importance for breeding and marketing this species, which were also used by other researchers (11) to characterize Cuban crop germplasm collection. Measurements considered crop descriptor recommendations published by UPOV (9).

Five-year-old plants started to be evaluated in 2006 and measurements were recorded for three consecutive years (2006-2008) in the three populations. All traits were assessed in parents and progenies from each crossing, whereas vegetative characters within the period between March and April in equivalent plant regions and fruit characters over the period from August to September, which is summer harvest peak. Fruits were harvested at its physiological maturity and evaluated in full maturation, two or three days after harvest.

Genetic diversity characterization in three guava populations through quantitative traits

Firstly, a discriminant factorial analysis was performed with data recorded when measuring quantitative characters in the three progenies, excluding parent values. Subsequently, a main component analysis was done for each population based on Pearson's correlation matrix. Then, those values that were greater than half of the largest absolute value in each component were considered significant.

Afterwards, cluster analyses were made with the traits selected in each population, based on Euclidean distance matrix and Ward's clustering method of minimum variance for building dendrogram. Diversity groups were determined by taking into account 70 % similarity in each population. Furthermore, the K-means clustering method was performed to find the highest contributing characters to group formation. Once the groups were formed, discriminant factorial analyses were made with the purpose of corroborating such groups and detecting the traits that allow distinguishing such groups. Statistical analyses were made in the STATISTICA program version 8.0 (12).

RESULTS AND DISCUSSION

Discriminant factorial analysis enabled to detect the existence of marked differences between populations for the quantitative characters evaluated, since a significant Lambda de Wilks' statistical value was recorded. The groups were formed with 74,07 % reliability, which is not very high because plants of the same cultivar ('EEA 18-40') were used as female parents in the three crossings, that is, they had a common mother. However, it is considered an acceptable reliability percentage value, since the purpose of this analysis was to determine if there were differences between the three progenies obtained, regarding the quantitative traits evaluated, which could be verified by discriminant analysis results, despite they were half-sib progenies. Each group of analysis represents the progeny obtained in each crossing, which are recognized by a different color in Figure 1.

In addition, it was determined that leaf length and width, plant height, fruit length and width, external and internal pulp thickness, and seed number per fruit were the most distinguishing traits for the three progenies; therefore, they presented the greatest variability among progenies. Based on these results, a genetic diversity study was conducted in each population separately, in order to determine the highest contributing characters to the variability observed within each population, as well as to group genotypes and characterize groups based on diversity.

After the main component analyses were made with 10 quantitative traits assessed, it was possible to explain 59,35; 58,06 and 61,17 % of total variability with the first two components in populations 1, 2 and 3, respectively (Table). Similar results were observed by other authors (13) when evaluating *Psidium* accessions through using morphological and biochemical characters, so that 58,4 % variability could be explained with the first two main components.

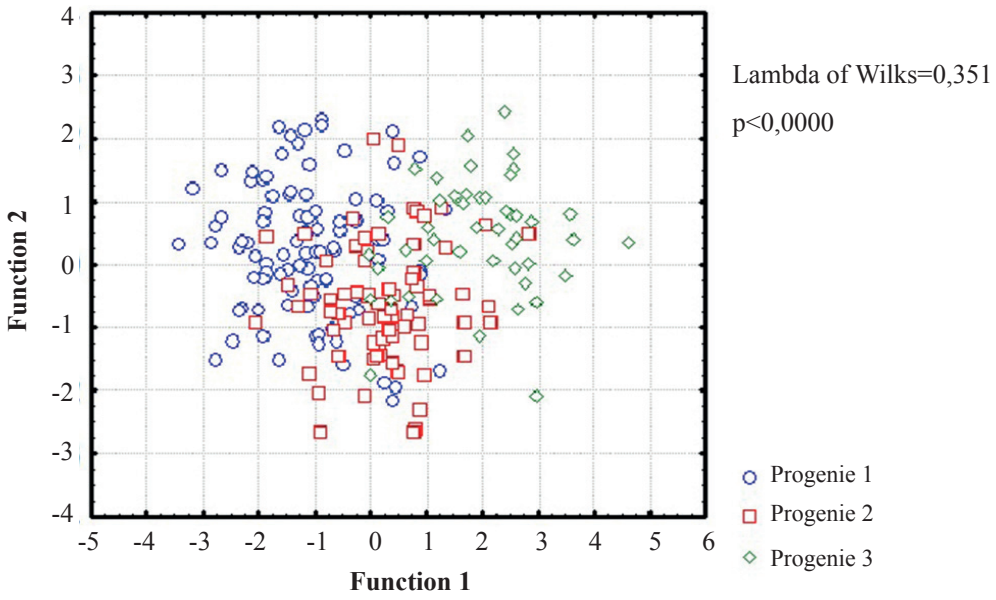


Figure 1. Distribution of three guava progenies at the level of the first two discriminant functions for the quantitative traits evaluated

Table I. Self-values (%), cumulative percentages and values of their own vectors obtained at the main component analysis performed with quantitative traits in the three guava populations

Components	Population 1		Population 2		Population 3	
	MC_1	MC_2	MC_1	MC_2	MC_1	MC_2
Self-values %	3,865	2,070	3,314	2,495	3,416	2,702
Cumulative %	38,65	20,70	33,14	24,95	34,16	27,02
	38,65	**59,35**	33,14	**58,09**	34,16	**61,17**
Own vectors	MC_1	MC_2	MC_1	MC_2	MC_1	MC_2
Vegetative traits						
Leaf length	-0,0237	-0,0880	0,0652	0,2032	-0,1189	-0,1589
Leaf width	-0,0627	0,0603	0,0624	0,2260	-0,1580	-0,1802
Plant height	0,0500	0,2480	0,0449	-0,0992	0,0107	-0,1771
Fruit traits						
Fruit mass	**-0,5013**	-0,0898	**-0,5049**	0,2098	**-0,5149**	-0,0772
Fruit length	**-0,4200**	-0,2395	-0,3164	**0,3637**	**-0,3325**	-0,2985
Fruit width	**-0,4936**	-0,0147	**-0,4905**	0,0556	**-0,4879**	0,1065
External pulp thickness	**-0,3838**	-0,3825	-0,2626	**0,5046**	**-0,3987**	-0,2699
Internal pulp thickness	-0,3196	**0,4002**	-0,3570	**-0,3965**	-0,2595	**0,4223**
Seed number	-0,1103	**0,5586**	-0,2657	**-0,4284**	-0,1823	**0,3622**
Total seed mass	-0,2450	**0,4930**	**-0,3566**	-0,2692	-0,2960	**0,4013**

MC: Main component

The greatest contributors in each component are highlighted in bold

In Brazil, the main component analysis was also used to select the most important quantitative traits of leaves and fruits, when a study was done on genetic differences in guava cultivars (2). These authors were able to explain 75,60 % variability only with the first two main components.

Results from the main component analysis enabled to select the greatest contributors to variability, which were fruit size and shape in the three populations (Table). Some of these characters, such as fruit width, pulp thickness, seed number per fruit and its mass were among the ones selected[B] to characterize guava (*Psidium guajava* L.) accessions at the genebank of Cuba and to evaluate cultivars in Brazil (2).

Variability percentage explained with only two components was higher than the one found by other authors that included some of the quantitative traits evaluated in this study, when characterizing guava accessions in Mexico (14), Colombia (15), Pakistan (16) and Cuba[B], which required more than four components to account for about 60 % variability. Results also differ from those presented by several Serbian authors when assessing genetic diversity in peach (*Prunus persica* spp. *vulgaris* Mill.) genotypes (17) and apple (*Malus* sp.) cultivars (18). They evaluated genetic diversity in accessions or cultivars of the crop involved; however, there was not any study designed to estimate genetic diversity in populations derived from controlled crosses, prior to this work.

Based on the results from the main component analysis, cluster analyses were performed with fruit characters, which were the largest contributors to variability in the three populations. The analysis allowed making up four diversity groups in each population, mainly considering fruit mass, length and width, seed number and its total mass per fruit. Similar results were obtained in a morphological characterization of wild guava accessions in Colombia (15). These authors also got four diversity groups when performing cluster analysis with the quantitative traits assessed and found that fruit mass, length and width, internal pulp thickness, total soluble solid and acidity contents were the largest contributing characters to diversity group formation.

In Pakistan, genetic diversity was also assessed in guava accessions through employing quantitative and qualitative traits (16); many of them match those used in this study. Three diversity groups were obtained in this evaluation by means of cluster analysis, besides using Ward's clustering method and Euclidean distances. Meanwhile in Indonesia, crop germplasm collections were evaluated by qualitative and quantitative traits, also vegetative and fruit characters to obtain two groups formed with 70 % similarity, just like this work (19).

In general, when analyzing results of the above mentioned studies and this one, it can be observed that fruit characters showed greater variability than vegetative traits, so that they are more useful to differentiate and characterize crop genotypes.

The dendrogram obtained in population 1 is shown in Figure 2, where the formation of four groups is clearly observed.

Group 1 consisted of genotypes: 1, 15, 17, 18, 39, 44, 58, 64, 71, 92 and 106, which presented medium-sized fruits with weight values from 126.2 to 248.0 g, rounded shape with similar values of length (57,1-80,0 mm) and width (59,3-79,6 mm), as well as the highest values of seed number (385-487) and its total mass (3.23-5.38 g) per fruit in the population.

Group 2 consisted of genotypes: 20, 21, 24, 27, 29, 36, 48, 53, 54, 59, 70, 85, 88, 93, 95, 97, 103 and 104, which presented the smallest fruits (90,6-160,0 g) in the population, rounded shape (length: 55,7-81,6 mm; width: 56,3-79,7 mm) and high values of seed number (275-390) and its total mass (2,51 and 5,22 g) per fruit.

Group 3 consisted of genotypes: 2, 3, 4, 5, 6, 12, 13, 14, 16, 19, 22, 25, 28, 31, 32, 33, 34, 35, 37, 38, 40, 41, 43, 45, 46, 47, 49, 52, 55, 60, 65, 66, 67, 76, 78, 79, 81, 89, 94, 105, 108 and 'EEA 18-40', which had the largest fruits in the population, with mass values between 175,8 and 266,4 g, the highest fruit length (70,6-88,2 mm) and width (65,2-77,1 mm), long shape (higher fruit length than width), medium-sized seeds (2,54-4,33 g) and medium to high seed number (210-343); these genotypes are more like the mother, which is included in the group.

Group 4 had the remaining genotypes: 7, 8, 9, 10, 11, 23, 26, 50, 51, 56, 57, 68, 69, 73, 77, 80, 83, 86, 87, 90, 91, 98, 99, 100, 101, 110 and 'N6', with medium-sized fruits (121,2-207,1 g), long shape (length: 58,8-81,8 mm; width: 59,5-73,7 mm) with the lowest seed number (116-249) and its total mass (1,55-3,15 g) per fruit in the population.

[B] Valdés-Infante, J. *Utilización de caracteres morfoagronómicos y de marcadores de ADN para el desarrollo de una metodología que contribuya al mejoramiento genético del guayabo (Psidium guajava L.) en Cuba*. Tesis de Doctorado, Universidad de La Habana, Cuba, 2009, 131 p.

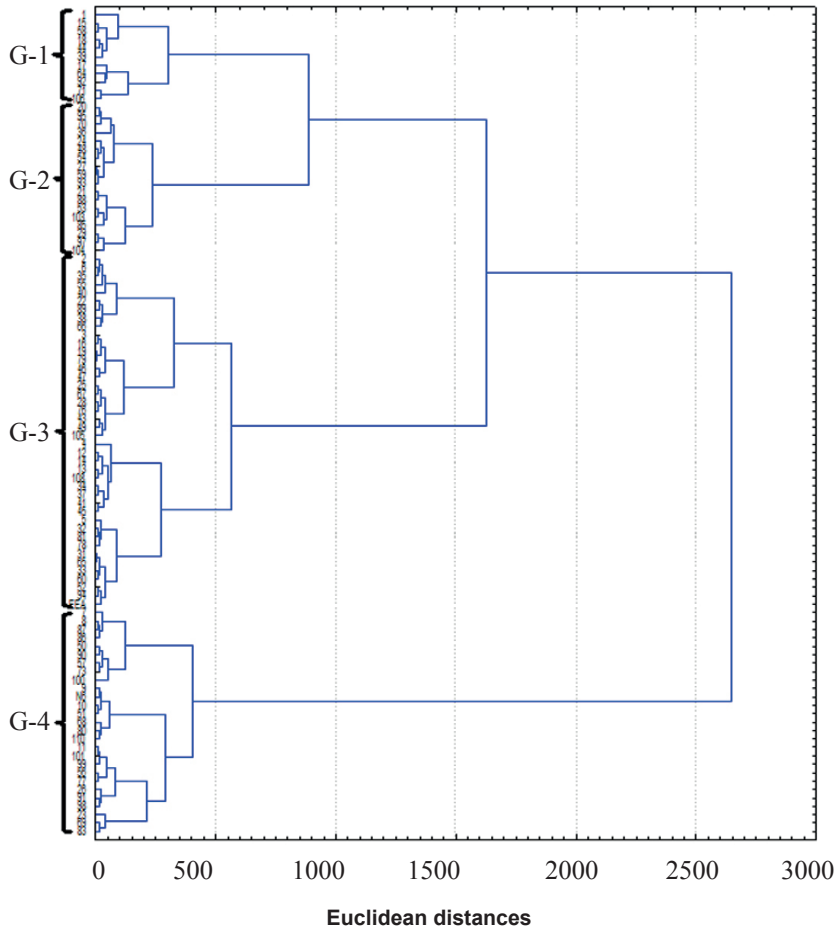


Figure 2. Dendrogram obtained with seven quantitative traits selected in guava population 1 ('EEA 18-40'x'N6'), based on Euclidean distances and Ward's clustering method

The dendrogram obtained for population 2 is shown in Figure 3. The following genotypes were gathered in group 1: 111, 113, 115, 117, 120, 125, 128, 129, 132, 145, 147, 151, 152, 153, 156, 158, 159, 162, 163, 164, 166, 185, 197, 214, 215, 220 and 'Red Supreme' with medium-sized fruits (weight: 118,9-179,5 g), rounded shape (length: 59,8-71,4 mm; width: 60,2-70,8), with the lowest values of external pulp thickness (10,9 and 15,5 mm) and medium to high seed number per fruit (189-275); these genotypes are more like the father.

The following genotypes were gathered in group 2: 116, 121, 127, 136, 137, 139, 141, 144, 148, 165, 170, 171, 173, 188, 203, 205, 206, 212, 224 and 'EEA 18-40' with the largest fruits (weight: 192,3-269,7 g), long shape (length: 71,1-88,7 mm; width: 67,1-72,6 mm) and the highest external pulp thickness (13,5-17,8 mm), medium to high seed number per fruit (188-271); these genotypes are more like the mother.

Group 3 consisted of genotypes: 112, 119, 124, 131, 134, 135, 138, 140, 143, 169, 172, 176, 177, 186 and 218, with medium-sized fruits (126,4-196,8 g), long shape (length: 64,6-95,8 mm; width: 55,7-70,3 mm), with mean values of external pulp thickness (12,1-18,7 mm) and the lowest values of seed number per fruit (73-183) in the population.

Group 4 consisted of genotypes: 123, 126, 130, 149, 161, 168, 181, 183, 187, 193, 208, 209 and 217, with medium to large fruits (142,7-256,1 g), long shape (length: 63,5-91,1 mm; width: 62,7-78,1 mm), mean values of external pulp thickness (12,1-16,5 mm) and the highest values of seed number (282-359).

For population 3, the following genotypes were gathered in group 1: 229, 250, 253, 255, 261, 265, 272, 299, 305, 307 and 335, with medium to large fruits (weight: 147,8-225,3 g), mean values of internal pulp thickness (32,4-40,1 mm), seed number (157-195) and its total mass (1,99-2,81 g) per fruit. The genotypes were gathered in group 2: 236, 264, 288, 298, 300, 302, 306, 309, 340, 347, 348 and 'Belic L-207', with small fruits (97,0-172,2 g) and the lowest values of internal pulp thickness (25,8-37,5 mm), seed number (113-182) and its total mass (1,41-2,62 g) per fruit; these genotypes are more like the father.

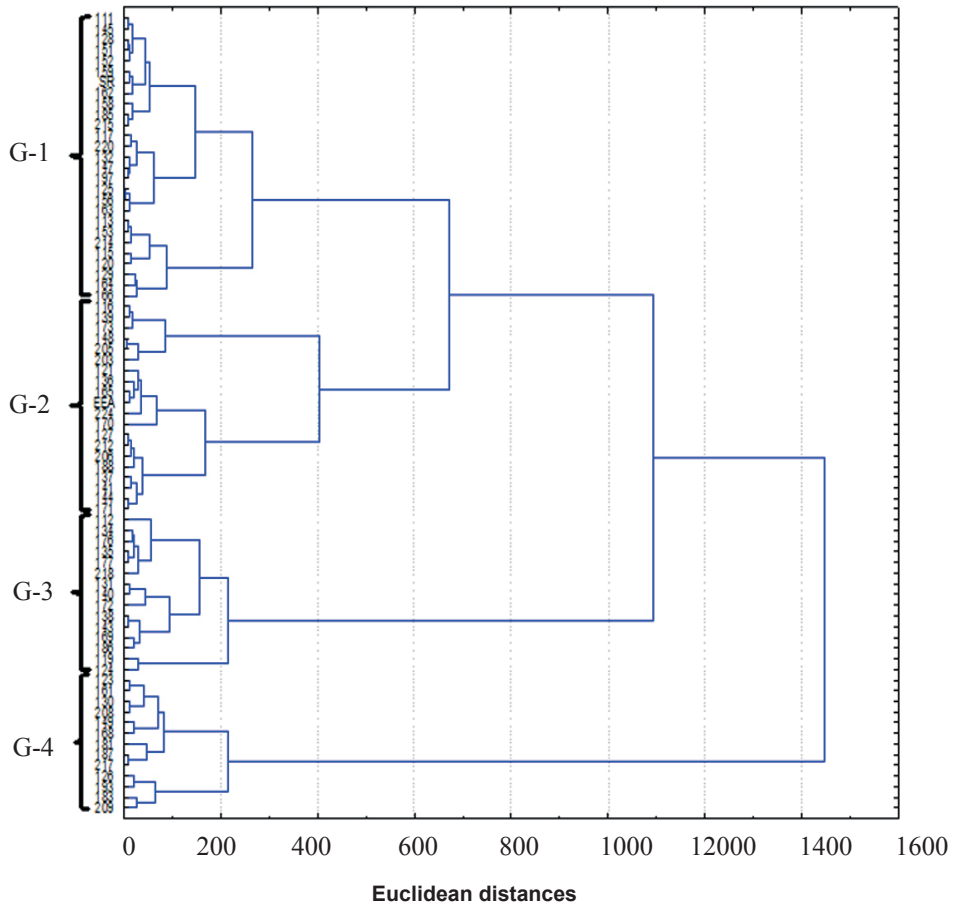


Figure 3. Dendrogram obtained with seven quantitative traits selected in guava population 2 ('EEA 18-40'x'Red Supreme'), based on Euclidean distances and Ward's clustering method

Group 3 had the remaining genotypes: 230, 231, 233, 256, 267, 284, 304, 336, 346 and 'EAA 18-40', with the largest fruits (157,5-244,3 g) and the highest values of internal pulp thickness (34,2-43,0 mm), seed number (247-332) and its total mass (2,59-6,53 g) per fruit in the population.

Group 4 consisted of genotypes: 262, 273, 277, 278, 280, 282, 287, 291, 293, 294, 301, 308, 313, 316, 322 and 329, with small fruits (118,6-171,9 g), similar to those in group 2, but with higher values of internal pulp thickness (32,9-40,1 mm), seed number (204-283) and its total mass (2,29-3,40 g) per fruit (Figure 4).

K-means cluster analysis was made with fruit traits in the three populations, which proved to be the largest contributors to variability in previous analysis. From the variance analysis of this procedure, it was determined that the seven characters included in the analysis contributed significantly to four diversity group formation in each population. Fruit mass and seed number per fruit were the best characters for discriminating groups in the three populations. These results can be seen in Figures 5, 6 and 7, which represented the mean values of fruit characters in each of the four diversity groups formed in populations 1, 2 and 3, respectively.

As shown in Figures 5, 6 and 7, the mean values of groups have higher differences from each other, with regard to fruit mass and seed number per fruit, in the three populations, as the dashed lines linking the mean values of characters in each group are more separated in such traits, indicating that their mean values have greater differences between groups.

The characters of fruit mass and seed number per fruit are among the Mexican guava accessions of greater variability for group formation by cluster analysis (16).

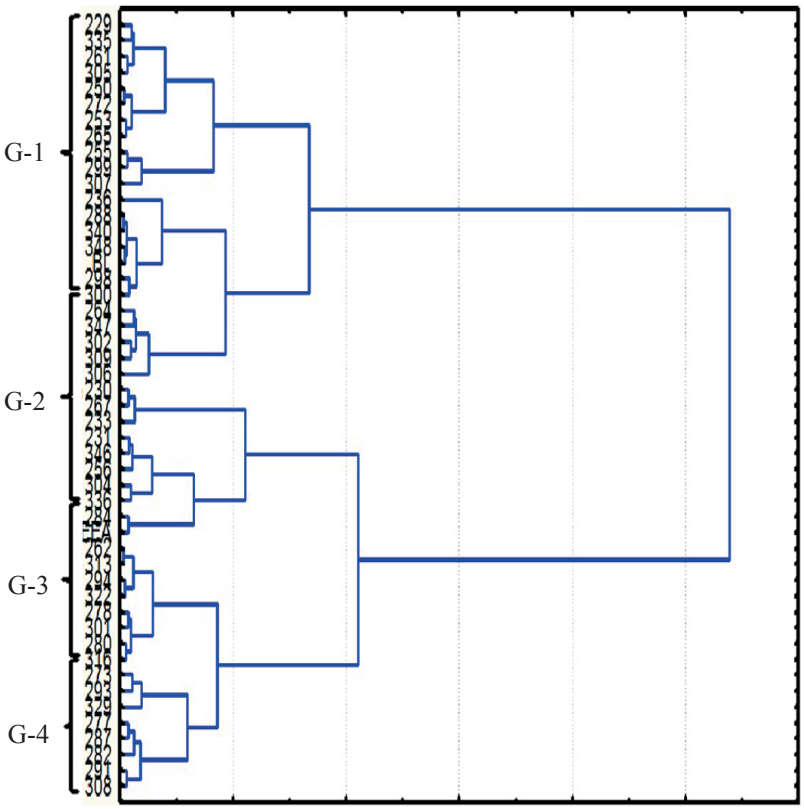
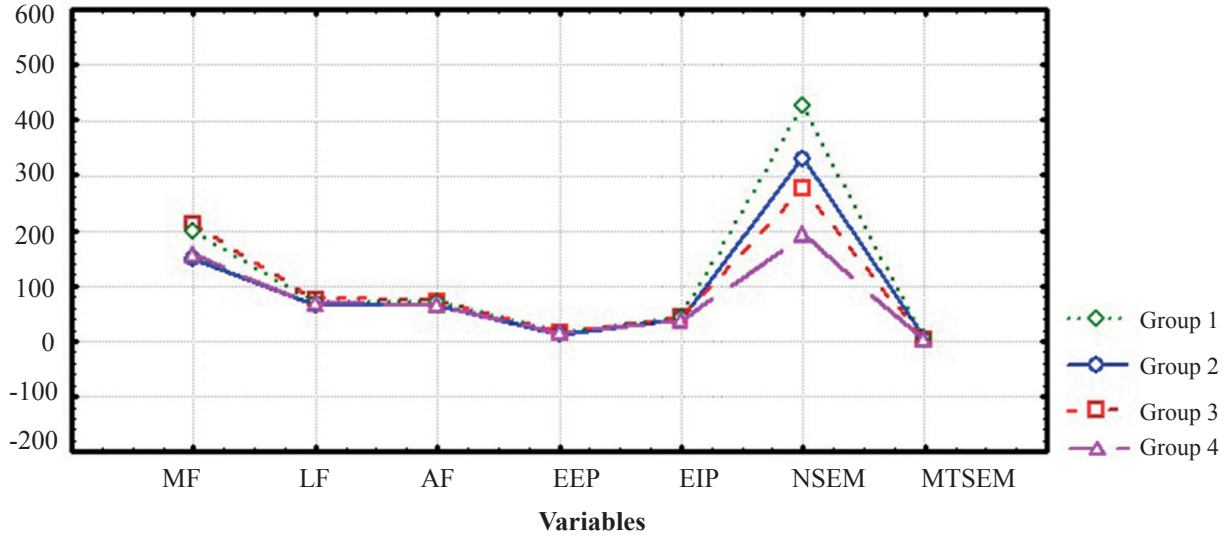
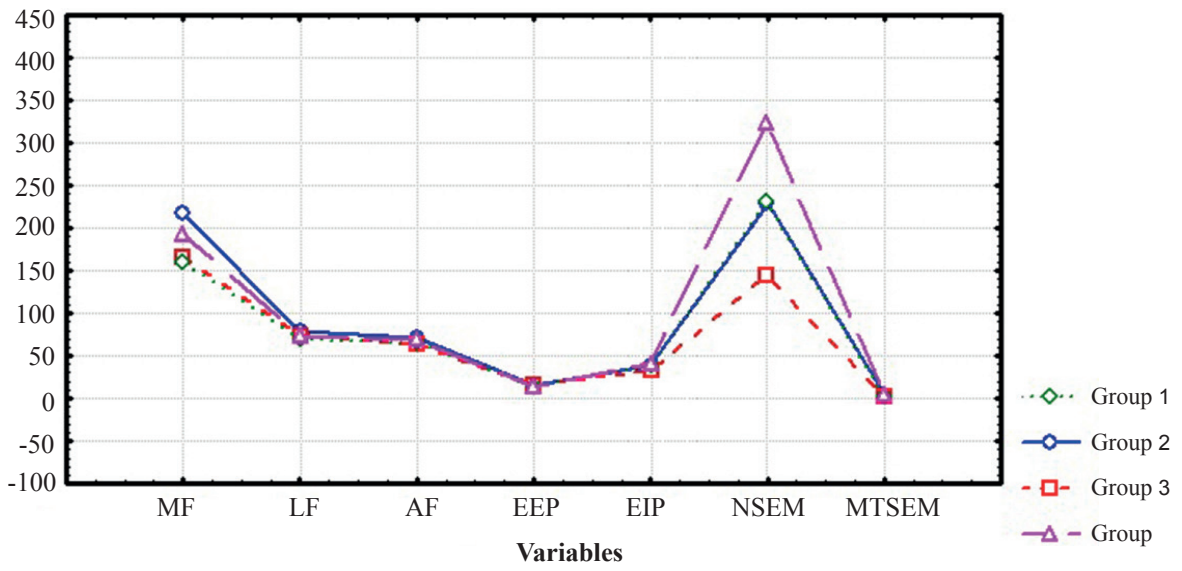


Figure 4. Dendrogram obtained with seven quantitative traits selected in guava population 3 ('EEA 18-40' x'Belic L-207'), based on Euclidean distance matrix and Ward's clustering method



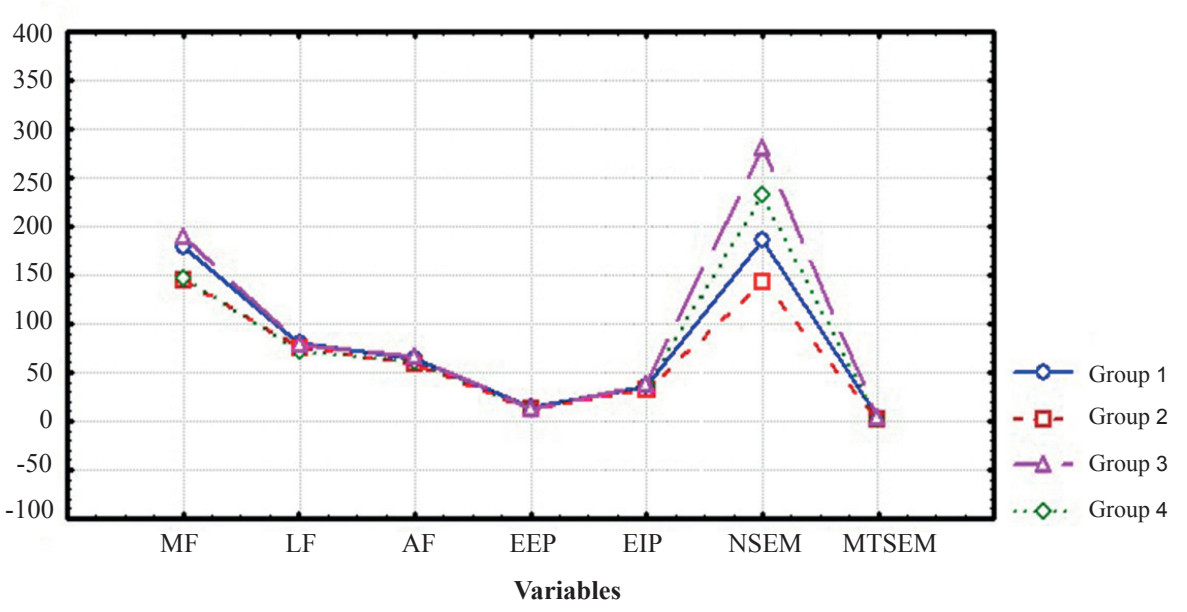
FM: fruit mass; FL: fruit length; FW: fruit width; EPT: external pulp thickness; IPT: internal pulp thickness; SNPF: seed number per fruit; TSMPF: total seed mass per fruit.

Figure 5. Mean values of seven quantitative traits in four diversity groups of guava population 1 ('EEA 18-40'x'N6')



FM: fruit mass; FL: fruit length; FW: fruit width; EPT: external pulp thickness; IPT: internal pulp thickness; SNPF: seed number per fruit; TSMPF: total seed mass per fruit

Figure 6. Mean values of seven quantitative traits in four diversity groups of guava population 2 ('EEA 18-40'x'Red Supreme')



FM: fruit mass; FL: fruit length; FW: fruit width; EPT: external pulp thickness; IPT: internal pulp thickness; SNPF: seed number per fruit; TSMPF: total seed mass per fruit

Figure 7. Mean values of seven quantitative traits in four diversity groups of guava population 3 ('EEA 18-40'x'Belic L-207')

They are also referred in the descriptors published by some researchers (11) as highly discriminants to differentiate and characterize guava accessions. In addition, they are very important traits for crop breeding, since they are among the determining fruit selecting factors either for fresh market or industry.

Seed number is a very important character in this crop, because genotypes with low seed number are considered promising to be used for breeding and marketing of this species. Seeds are generally discarded in fruit processing; however, they have 5-13 % oil rich in essential fatty acids, which could be used as salad dressing.

When the discriminant factorial analysis was done with fruit characters, it was determined that the four diversity groups formed in every population differed from each other, since they got significant Lambda de Wilks' statistical values in each analysis, which are shown in Figures 8, 9 and 10. The groups were formed with 95,92 % reliability in population 1, 93,33 % in population 2 and 97,96 % in population 3. Reliability percentage values are high, above 90 % in the three populations, indicating that the four diversity groups, previously defined in cluster and K-means analysis, actually differ from each other. In addition, it can also be concluded that the genotypes making up each group have a high probability of being present in the assigned group and not in another one.

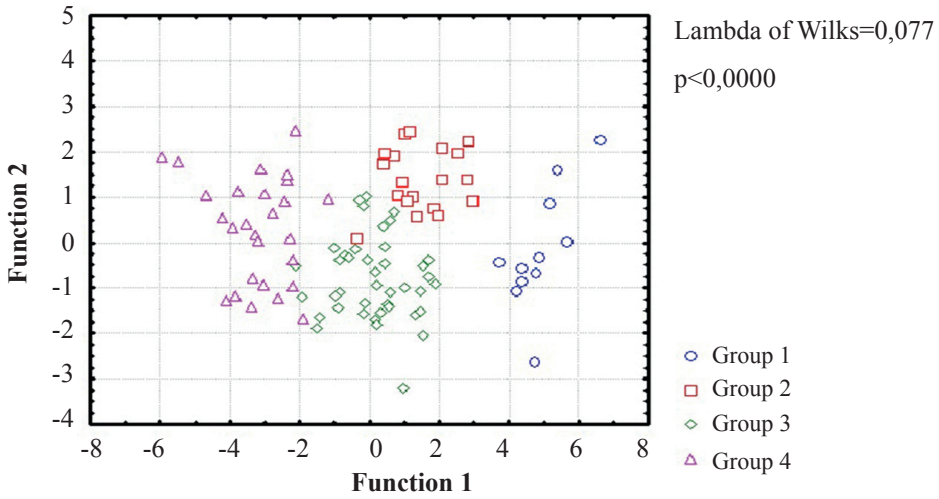


Figure 8. Distribution of diversity groups formed in guava population 1 ('EEA 18-40'x'N6') at the level of the first two discriminant functions for the quantitative traits selected

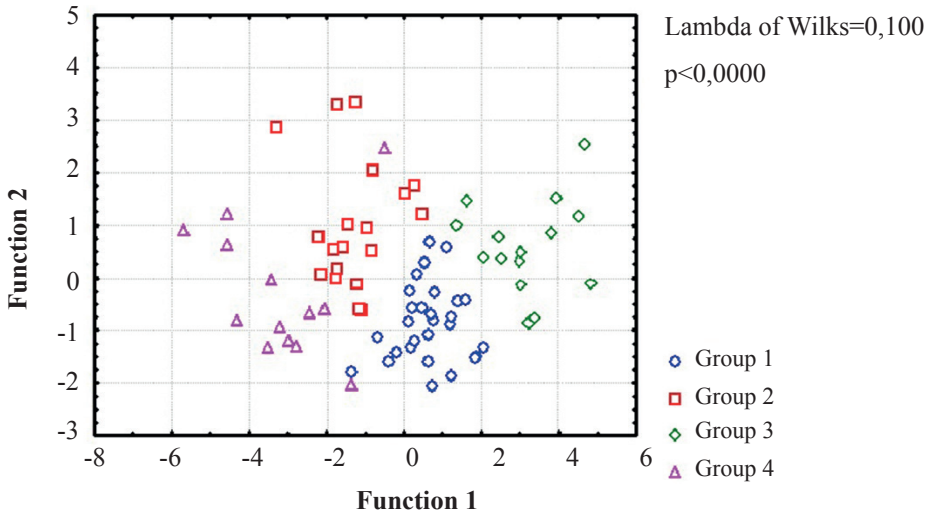


Figure 9. Distribution of diversity groups formed in guava population 2 ('EEA 18-40'x'Red Supreme') at the level of the first two discriminant functions for the quantitative traits selected

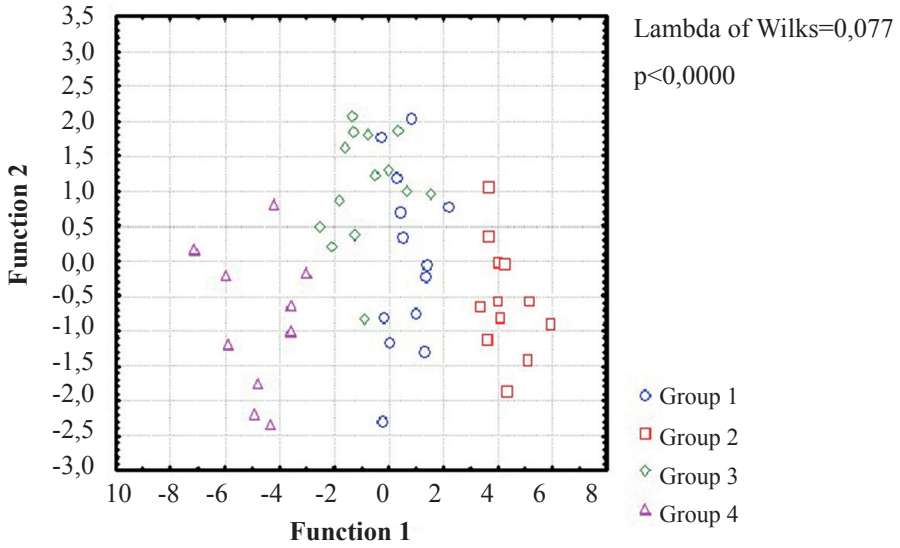


Figure 10. Distribution of diversity groups formed in guava population 3 ('EEA 18-40'x'Belic L-207') at the level of the first two discriminant functions for the quantitative traits selected

Moreover, the analysis showed that fruit mass and seed number per fruit were the largest contributors to differentiate diversity groups in populations 2 and 3, as well as seed number in population 1.

These results agree with those obtained by K-means clustering analysis, confirming the usefulness of evaluating both traits to characterize and differentiate guava genotypes. Figures 8, 9 and 10 show the distributions of four diversity groups at the level of the first two discriminant functions in the three populations respectively. Each group is represented by a different color.

As shown in these figures, there is very little overlapping between genotypes forming different groups, which confirm the high reliability percentage values in the group formation previously mentioned. This result supports the marked differences between groups in each population, for fruit traits evaluated, which were the largest contributors to variability in the three populations.

Results from this study indicate that quantitative and qualitative traits are very helpful to identify and characterize new cultivars, as it was shown in previous studies (16, 20, 21).

All the results from multivariate analyses allowed detecting a high variability in guava populations for the quantitative traits assessed, the identification of the greatest contributing characters and diversity group formation in each population. Many of these characters are very important not only for economy but also for crop breeding. These results will enable to make a more efficient genotypic selection for conservation and breeding purposes, as well as to meet market demands for fresh fruits and industry.

CONCLUSIONS

- The characters of fruit size and shape proved to have the highest genetic variability in the populations studied; thus, they should be used to evaluate new crop genotypes.
- The characters of fruit mass, length and width, external and internal pulp thickness, seed number and its total mass per fruit allowed diversity group formation in the three guava populations, suggesting that they should be used to characterize genetic diversity in other crop populations.
- In the three guava populations analyzed, there is great genotypic diversity for the vegetative traits and agronomically important fruit characters, which can be employed in future breeding programs and marketing.

RECOMMENDATIONS

To determine statistical-genetic parameters in the populations evaluated and to study genotype-environment interaction, that will contribute to select promising genotypes to be used in breeding programs and crop marketing.

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