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## Hierarchical and optimization methods for the characterization of tomato genotypes

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**ABSTRACT:** The correct characterization of germplasm banks is fundamental for breeders to succeed in breeding programs. Several studies have sought to obtain genotypes with resistance to pests. However, there is no consensus about which methodology is the most appropriate to characterize a germplasm bank of tomato with different levels of resistance to pests. The objective of this study was to compare methods of multivariate analysis for the evaluation of genetic diversity in tomato genotypes with different levels of resistance to pests. The experiments were conducted at the Vegetable Experimental Station of the Federal University of Uberlândia - Monte Carmelo campus (18° 42' 43.19" South latitude and 47° 29' 55.8" West longitude, 873 m altitude), in the period from April 2013 to November 2016. Sixteen genotypes were evaluated from the interspecific cross between LA-716 (*S. pennellii*) versus pre-commercial line (UFU-057) followed by backcrossing and self-fertilization, along with the pre-commercial line UFU-057 (recurrent parent) Santa Clara and the wild accession *S. pennellii* (donor genitor). The contents of acylsugar, foliar trichomes, South American tomato pinworm and leaf miner repellency tests were analyzed. The experimental design was the randomized block design totaling 76 plots (19 genotypes x 4 blocks). It was concluded that there was genetic variability among the evaluated genotypes. The method of graphic dispersion by principal components revealed a greater power of discrimination. Genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 and UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 contain the highest levels of acylsugar, resistance to *Liriomyza* spp. and *T. absoluta*.

**Key words:** tomato, insect resistance, multivariate analysis

## Métodos hierárquicos e de otimização na caracterização de genótipos de tomateiro

**RESUMO:** Uma correta caracterização de bancos de germoplasma é fundamental para melhoristas obterem sucesso em programas de melhoramento. Várias pesquisas têm buscado obtenção de genótipos com resistência a pragas. No entanto, não há um consenso em relação a qual metodologia é a mais adequada para caracterizar um banco de germoplasma de tomateiro com diferentes níveis de resistência a pragas. O trabalho foi realizado com o objetivo de comparar métodos de análise multivariada para avaliação da diversidade genética em genótipos de tomateiro com diferentes níveis de resistência a pragas. Os experimentos foram conduzidos na Estação Experimental de Hortaliças da Universidade Federal de Uberlândia - campus Monte Carmelo (18° 42' 43,19" latitude Sul e 47° 29' 55,8" longitude Oeste, 873 m de altitude), no período de abril de 2013 a novembro de 2016. Foram avaliados dezesseis genótipos provenientes do cruzamento interespecífico entre LA-716 (*S. pennellii*) versus linhagem pré-comercial (UFU-057) seguido de um retrocruzamento e uma autofecundação, juntamente com a linhagem pré-comercial UFU-057 (genitor recorrente), Santa Clara e o acesso selvagem *S. pennellii* (genitor doador). Foram analisados os teores de acilaçúcares, tricomas foliares, teste de repelência a traça-do-tomateiro e a larva-minadora. O delineamento experimental foi em blocos ao acaso totalizando 76 parcelas (19 genótipos x 4 blocos). Conclui-se que houve variabilidade genética entre os genótipos avaliados. O método de dispersão gráfica por componentes principais revelou maior poder de discriminação. Os genótipos UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 e UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 contêm os maiores teores de acilaçúcares, resistência a *Liriomyza* spp. e a *T. absoluta*.

**Palavras-chave:** tomate, resistência a insetos, análise multivariada



## INTRODUCTION

The South American tomato pinworm (*Tuta absoluta*) and the leaf miner (*Liriomyza* spp.) are important pests of tomato cultivated in Brazil (Maciel et al., 2011; Guimarães et al., 2015). The control of these pests is carried out mainly by the application of insecticides. An alternative to this problem is the breeding for resistance of plants to arthropods (Broekgaarden et al., 2011; Gruber, 2017).

It is important to know the genetic variability associated with tolerance and susceptibility to insect pests of the samples present in the germplasm bank. The genetic divergence between the accessions can be determined from biometric models estimated by Euclidean distance and hierarchical grouping methods (Cruz et al., 2012).

The Euclidean distance is estimated by average data, disregarding the residual variances and covariance between the measured attributes. The hierarchical method Unweighted Pair-Group Method Using Arithmetic Averages (UPGMA) and the Tocher optimization method are routinely used in tomato for the estimation of genetic divergence (Mattedi et al., 2014; Araújo et al., 2016).

The principal component analysis (PCA) is used to identify the variable that contributed the most and contributed the least to the differentiation of the genotypes (Cruz et al., 2012). However, there is no consensus as to the best grouping method for evaluating tomato germplasm with different levels of pest resistance (Luz et al., 2016).

The objective of this present study was to compare different methods of multivariate analysis for the evaluation of genetic diversity in tomato genotypes with different levels of pest resistance.

## MATERIAL AND METHODS

The experiments were conducted at the Experimental Station of Vegetables (18° 42' 43.19" S and 47° 29' 55.8" W, 873 m altitude) and at LAGEN (Genetic Resources Laboratory), of Federal University of Uberlândia - UFU, Monte Carmelo campus, in the period from April 2013 to September 2016.

Sixteen genotypes were evaluated from the interspecific cross between LA-716 (*S. pennellii*) versus pre-commercial line (UFU-057) followed by backcrossing and self-fertilization (UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7, UFU-057F<sub>2</sub>RC<sub>2</sub>7#7.1, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.1, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.3, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.4, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.9, UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.6, UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9, UFU-057F<sub>2</sub>RC<sub>2</sub>10#8.7, UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.1, UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.5, UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.1, UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.2, UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.4), together with the pre-commercial line UFU-057 (recurrent parent), Santa Clara and the wild accession *S. pennellii* (donor genitor).

The genotype UFU-057 (recurrent parent) belongs to the germplasm bank of the Federal University of Uberlândia. It has good agronomic characteristics: large fruits (340 g), salad type, determinate growth habit (homozygous recessive: sp/sp), low levels of acylsugar and susceptibility to pests. The wild accession LA-716 [*(S. pennellii)*, donor genitor] does not have

satisfactory agronomic potential; however, it is rich in acylsugar and has a broad spectrum of pest resistance (Maluf et al., 2010; Maciel et al., 2011).

The sowing was carried out in 200-cell polystyrene trays filled with commercial coconut fiber substrate. The transplanting was carried out at 35 days after sowing (DAS) to 5-L pots with commercial coconut fiber substrate. The experiment was carried out in an arched greenhouse, with dimensions of 7 x 21 m and ceiling height of 4 m, covered with transparent 150-micron polyethylene film, with additives against UV light, and side curtains made of white anti-aphid screen.

The experimental design was in randomized block design (RBD) totalizing 76 plots (19 genotypes x 4 blocks). Each plot was composed of three plants. The same plants were used to quantify the levels of acylsugar, foliar trichomes and the performance of the South American tomato pinworm and tomato leaf miner repellency test. The mean temperature and the relative humidity of the air, between the beginning and the end of the evaluations, were of 18.7 to 34 °C and 72 to 95%, respectively. The quantification of the acylsugar contents, quantification of the trichomes in the leaflets, and the South American tomato pinworm and tomato leaf miner repellency test were performed.

The quantification of acylsugar contents in leaflets was done 30 days after transplanting. A sample composed of six leaf discs (equivalent to 4.2 cm<sup>2</sup>) was collected in the upper third of each plant of the plot in order to quantify the acylsugar content, according to the methodology proposed by Resende et al. (2002) and adapted by Maciel & Silva (2014).

The quantification of glandular trichomes (types I, IV, VI and VII) in leaflets was done according to Glas et al. (2012), being performed after 30, 45, 60, 75 and 90 days of sowing. Five young and expanded leaflets were collected from the upper third of each plant and the number of epidermal glandular trichomes per cm<sup>2</sup> was evaluated on the abaxial and adaxial surfaces. The evaluation was performed using a stereoscopic microscope (40X), with micrometric scale of 1 cm<sup>2</sup> area.

The evaluation of oviposition of the South American tomato pinworm was carried out twenty-four days after the infestation, every three days. It was done by counting the number of eggs in 2 cm<sup>2</sup> of leaf area with the aid of a binocular stereoscopic microscope with magnification of 20 to 80 times. The counts were made on both sides (adaxial and abaxial) of 30 leaflets located in the upper third of the plant. The average of the plot was equivalent to the average number of eggs per 2 cm<sup>2</sup> of leaf area.

The injury levels of *T. absoluta* to the plants were evaluated from 36 days after infestation through scales ranging from 0 (absence of damage); 1 (up to 5% damage); 2 (damage between 5-20%); 3 (damage between 20-50%); 4 (damage between 50-80%); 5 (damage between 80-100%) according to Maluf et al. (1997) for plant damage and leaf damage. The percentage of leaflets attacked was evaluated according to the grades 0 (absence of damage); 1 (rare injuries); 2 (medium injuries and the rare presence towards the edges); 3 (lesions of medium to large size); 4 (large lesions that coalesce and deform the leaves); 5 (leaf surface having 100% lesions). Two evaluations

were made regarding the injury level, with a difference of one week between two weeks.

The leaf miner repellency test was carried out by counting the area damaged by the insect after infestation and performed from the moment when the presence of lesion onset was observed. The same scale used in the characterization of South American tomato pinworm injuries was used for the damage caused by the leaf miner in the leaf, and the walking done by the insect on the leaves allowed to quantify the percentage of attack.

For the infestation of both *T. absoluta* and *Liriomyza* spp., a tomato-moth and leaf miner breeding was previously established in an arched greenhouse, with dimensions of 6 x 4 m and ceiling height of 2 m, covered with transparent 150-micron polyethylene film and side curtains made of white anti-aphid screen. Infestation in the greenhouse was carried out with visibly attacked plants of the susceptible cultivar Santa Clara. Every ten days new plants of the cultivar Santa Clara were placed in the breeding so as to maintain high populations of the insects.

In order to test the residual normality, homogeneity of variances and block additivity, the Kolmogorov-Smirnov, Levene and Tukey Additive tests were used. The analysis of variance (ANOVA) was performed applying the F test at 0.05 probability level. The comparison of means was done by applying the Scott-Knott's test at 0.05 probability.

The data were submitted to multivariate analyses with the objective of determining the genetic dissimilarity between the genotypes. The dissimilarity matrix was obtained by the Euclidean distance and from this matrix the genetic divergence was represented by dendrogram obtained by the hierarchical method Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and by the Tocher optimization method.

The relative contribution of the evaluated traits was calculated according to Singh (1981). The genetic divergence through Principal Component Analysis (PCA) was

demonstrated by the dispersion of the scores in graphs, with the axes represented by the first major components. All analyses were performed using the Genes software v. 2015.5.0 (Cruz, 2013).

## RESULTS AND DISCUSSION

The genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3 and *S. pennellii* had plants with lower insect injuries, while the accessions UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2, UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9 and Santa Clara had the most injured plants. No injuries were observed on leaf and leaflet in *S. pennellii*. In contrast, the greatest damage caused by *Tuta absoluta* on tomato leaf was characterized in UFU-057F<sub>2</sub>RC<sub>2</sub>8 # 2.2. On the other hand, the greatest damages in leaflets were observed in the genotypes Santa Clara, UFU-057F<sub>2</sub>RC<sub>2</sub>10 # 3.9 and UFU-057 (Table 1).

Dias et al. (2013), evaluating tomato genotypes with high and low levels of acylsugar, reported that the smallest injuries in the plants, leaflets and the smallest number of leaves injured by *T. absoluta* were obtained in plants with high content of this allelochemical. In contrast, the highest values for plant, leaflet and leaf injuries were observed in plants with low acylsugar content. The results observed in the present study confirm those obtained by these authors.

The amount of injuries caused by *Liriomyza* spp. in tomato leaves was higher in UFU-057, Santa Clara, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.1 and UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9 and smaller in the genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2, UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 and *S. pennellii*. A higher number of South American tomato pinworm eggs was reported in Santa Clara and UFU-057 and smaller numbers in UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 and *S. pennellii* (Table 1). The genotypes Santa Clara and UFU-057 are considered susceptible to pest attack. This explains the greater amount of leaf miner, South American tomato pinworm egg and leaflet injury of these plants.

**Table 1.** Mean content of acylsugar (nmols cm<sup>-2</sup> leaf area) and average percentage of injuries on plant, leaf and leaflet of tomato genotypes submitted to *Liriomyza* spp. and *Tuta absoluta* infestation

ID	Genotype	<i>Tuta absoluta</i> <sup>1</sup>				<i>Liriomyza</i> spp. <sup>1</sup>		Content of acylsugar (nmol cm <sup>-2</sup> of leaf area) <sup>1</sup>	Number of trichomes <sup>1</sup>	
		Injuries on the plants	Injuries on the leaves	Injuries on the leaflets	Number of eggs	Injuries on the leaves	Adaxial		Abaxial	
T1	UFU-057F <sub>2</sub> RC <sub>2</sub> 8#2.2	4.6 a	4.6 f	2.6 d	0.2 a	0.0 a	31.50 c	4.4 d	1.5 c	
T2	UFU-057F <sub>2</sub> RC <sub>2</sub> 10#3.9	3.5 b	3.2 e	3.5 e	2.0 c	2.2 d	18.25 h	1.5 f	1.9 c	
T3	UFU-057F <sub>2</sub> RC <sub>2</sub> 13#4.1	2.8 c	1.2 b	1.2 c	0.7 b	1.7 c	21.64 f	4.7 d	1.2 c	
T4	UFU-057F <sub>2</sub> RC <sub>2</sub> 8#2.3	2.5 c	3.0 e	2.7 d	2.0 c	1.9 c	17.96 h	2.5 f	2.5 b	
T5	UFU-057F <sub>2</sub> RC <sub>2</sub> 8#2.9	2.0 d	2.4 d	2.2 d	1.8 c	1.7 c	16.07 j	3.0 e	1.9 c	
T6	UFU-057F <sub>2</sub> RC <sub>2</sub> 7#4.7	1.5 d	2.0 c	1.8 c	0.7 b	0.5 a	33.80 b	20.5 b	3.7 b	
T7	UFU-057F <sub>2</sub> RC <sub>2</sub> 10#8.7	1.7 d	1.9 c	1.5 c	2.2 c	1.7 c	17.98 h	1.3 f	1.8 c	
T8	UFU-057F <sub>2</sub> RC <sub>2</sub> 8#2.1	1.5 d	1.9 c	1.4 c	1.7 c	2.2 d	18.15 h	2.0 f	0.7 c	
T9	UFU-057F <sub>2</sub> RC <sub>2</sub> 10#3.6	1.5 d	2.0 c	1.7 c	0.9 b	1.7 c	19.74 g	2.6 f	3.5 b	
T10	UFU-057F <sub>2</sub> RC <sub>2</sub> 7#7.1	1.0 e	1.7 c	1.9 c	1.9 c	1.5 c	13.55 k	1.0 f	0.4 c	
T11	UFU-057F <sub>2</sub> RC <sub>2</sub> 13#4.2	0.8 e	0.8 b	0.7 b	1.5 c	1.0 b	25.44 d	15.6 c	3.2 b	
T12	UFU-057F <sub>2</sub> RC <sub>2</sub> 13#2.1	0.8 e	1.0 b	1.7 c	0.9 b	1.2 c	25.93 d	3.2 e	1.9 c	
T13	UFU-057F <sub>2</sub> RC <sub>2</sub> 13#2.5	0.7 e	1.1 b	1.5 c	2.1 c	1.5 c	23.13 e	2.1 f	1.5 c	
T14	UFU-057F <sub>2</sub> RC <sub>2</sub> 13#4.4	0.6 e	0.7 b	1.6 c	1.1 b	1.7 c	20.66 g	1.5 f	0.7 c	
T15	UFU-057F <sub>2</sub> RC <sub>2</sub> 8#2.4	0.6 e	2.0c	1.4 c	2.0 c	1.5 c	16.85 i	1.7 f	1.2 c	
T16	UFU-057F <sub>2</sub> RC <sub>2</sub> 7#4.3	0.6 f	1.0 b	1.7 b	0.7 b	1.0 c	30.47 c	1.7 f	2.9 b	
T17	<i>Solanum pennellii</i>	0.0 f	0.0 a	0.0 a	0.0 a	0.0 a	35.30 a	63.0 a	78.7 a	
T18	UFU-057	3.0 c	3.0 e	3.4 e	2.5 d	2.5 d	16.47 i	1.1 f	1.0 c	
T19	Santa Clara	3.3 c	3.3 e	3.7 e	2.9 d	2.2 d	15.28 j	0.8 f	1.4 c	
CV (%)		24.38	17.84	23.08	25.71	25.68	4.65	11.67	23.46	

<sup>1</sup>Means followed by the same letter in the column do not differ from each other by Scott-Knott test, p < 0.05

The number of adaxial (63) and abaxial (78.75) trichomes, together with the acylsugar content (35.29 nmols cm<sup>-2</sup> leaf area) was higher in *S. pennellii*, while the other genotypes showed lower amounts of the three analyzed characters. The second genotype with the highest acylsugar content was UFU-057F<sub>2</sub>RC<sub>2</sub>7 # 4.7, followed by UFU -057F<sub>2</sub>RC<sub>2</sub>8#2.2 and UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3 (Table 1).

The acylsugar contents in the UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 and UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 accessions were the closest to the amount present in *S. pennellii* (35.29 nmols cm<sup>-2</sup> leaf area), being respectively 30.47; 31.50 and 33.80 nmols cm<sup>-2</sup> leaf area (Table 1). The accession UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 was the third genotype with the highest acylsugar content (31.50 nmols cm<sup>-2</sup> leaf area). However, this accession showed high levels of injury to the plant, leaf and leaflet (Table 1). This can be explained by the presence of other allelochemicals with an antagonistic effect similar to that caused by the acylsugar and also by the fact that this accession showed a low amount of abaxial trichomes. Maluf et al. (2010) reported that this divergence is normal due to other resistance factors other than the acylsugar present in *S. pennellii* that may not have been recovered in the selection. These results suggest that the action of the allelochemical is associated with two mechanisms of resistance, not preference for oviposition and antibiosis, which avoids proliferation and larval development.

Similar results to those obtained in this study were reported by Maciel et al. (2011) and Dias et al. (2013), who observed lower oviposition and number of *T. absoluta* larvae in tomato genotypes with higher acylsugar content. Sohrabi et al. (2017) attributed the resistance of tomato cultivars Berlina, Zaman and Golsar to *T. absoluta* to the high density of foliar trichomes. Lucatti et al. (2013) and Andrade et al. (2017) associated the lowest amount of egg and nymph and consequently the resistance of the tomato accessions evaluated to *Bemisia tabaci* with the highest amount of type IV trichomes. The differences observed in the levels of injury caused by *T. absoluta* and *Liriomyza* spp. in the different cultivars studied in this work are associated with the genetic variability between them.

The analysis of importance of characters stands out because it characterizes the total available variation of the genotypes based on the characteristics evaluated. Based on the criteria proposed by Singh (1981), it was verified that the most important characteristics for discrimination of the genotypes were: Acylsugar content (16.75%) and presence of leaf miner larvae (14.75%), and the characters of least contribution were the amount of adaxial trichomes (9.88%) and abaxial amount of trichomes (9.25%) (Table 2).

**Table 2.** Relative contribution (%) of characteristics for genetic divergence in mini tomato genotypes, estimated by the method proposed by Singh (1981)

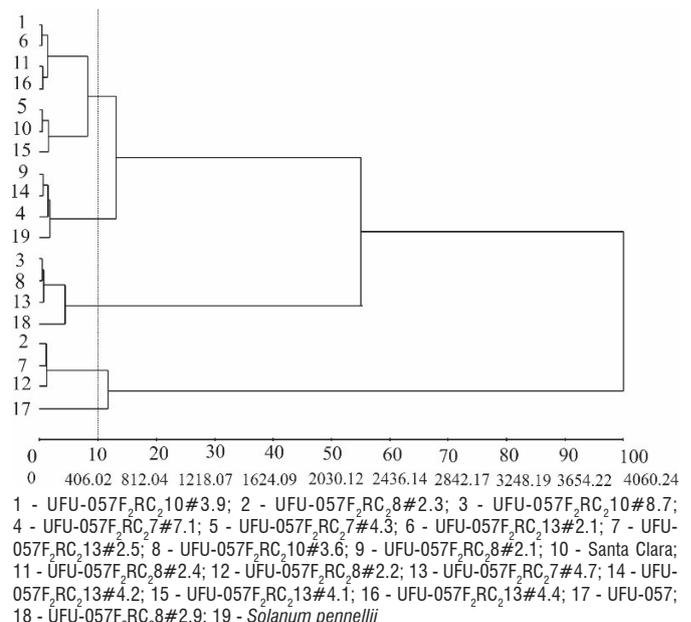
Variables analyzed	S.j (%)
Acylsugar (nmol cm <sup>-2</sup> of leaf area)	16.75
Leaf miner presence	14.75
South American tomato pinworm eggs	13.73
Plant injuries	13.31
Leaflet injuries	11.56
Leaf injuries	10.78
Number of trichomes in the adaxial part	9.88
Number of trichomes in the abaxial part	9.25

Using the dissimilarity matrix by means of the Euclidean distance to generate the dendrogram by the UPGMA method, a correlation coefficient of 0.81% with a 16.43% distortion was observed. This shows an adequate relation between the distance matrix and the generated dendrogram (Figure 1)

When a cut was made considering 10% of dissimilarity, it was possible to observe the formation of five clusters. The first group consisted of the genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9; UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.1; UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.4; UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.4; UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3; UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.1 together with the Santa Clara cultivar, which is characterized as susceptible to pest attack. This group had the highest number of genotypes (36.84%). The second group consisted of UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.1; UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.2; UFU-057F<sub>2</sub>RC<sub>2</sub>7#7.1 and *S. pennellii*, which is considered as tolerant to pest attack. The third group consisted of the genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>10#8.7; UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.6; UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 and UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.9. The fourth group included the genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.3, UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.5 and UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2, and the fifth group was formed only by the genotype UFU-057, which is susceptible to pest attack.

Using this same method, Flores-Hernández et al. (2017) detected divergence among the 45 accessions of wild tomatoes characterized as morphology and agronomic properties. The authors reported the formation of three groups. Bottega et al. (2015), when evaluating the resistance of nine tomato genotypes to the development of *T. absoluta*, observed the formation of four groups.

For the satisfactory interpretation of the variability found among the genotypes, the first two principal components need to have minimum estimates of 80% of the total variation contained in the character set (Cruz et al., 2012). In this study the first two principal components explained 80.75% of the total variance of the analyzed characters. The principal component I (adaxial trichomes) was responsible for the greater variability among



**Figure 1.** Illustrative dendrogram analysis of 19 tomato genotypes by the unweighted pair-group method with arithmetic mean (UPGMA) obtained with the average Euclidean distance generated with eight characters

the genotypes, representing 59.43%. The principal component 2 (plant injury) explained 21.32% of the variance. Thus, the manifested variability among the genotypes can be explained by means of the two-dimensional scatter plot.

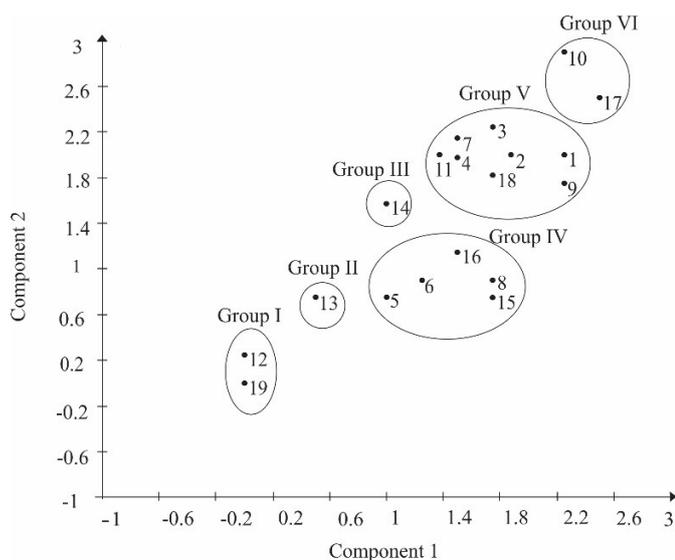
The scatter plot analysis by means of principal components allowed the identification of six groups of similarity (Figure 2), a result similar to that obtained by means of the grouping method UPGMA (five groups). However, when comparing the methods, there was a difference in the allocation of genotypes in the groups.

The genetic variability among the genotypes evaluated in this study can be considered high, due to the differences observed between them and evidenced by the large number of groups formed by the UPGMA hierarchical method and the scatter plot. Bottega et al. (2015), when comparing the groups formed by the analysis of principal components and by the hierarchical grouping based on Euclidean distance, also found alteration of the genotypes of each group.

All the results obtained in this study confirm the inferences made by other authors (Maluf et al., 2010; Maciel et al., 2011; Dias et al., 2013; Lucatti et al., 2013; Andrade et al., 2017) that the acylsugar found in *S. pennellii* confers resistance to pests and that the indirect selection of genotypes with high content of this allelochemical promotes the production of tomato cultivars with high resistance to insects.

By the Tocher method, the formation of two distinct groups was detected, with group II being formed by only one accession. The group I was composed of 18 genotypes, approximately 94.74% (Table 3).

Therefore, it is difficult to analyze the divergence between genotypes when applying the Tocher method, since most of them are in only one group. In a study on genetic dissimilarity of 13 tomato hybrids, Luz et al. (2016) found similar results



1 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9; 2 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.3; 3 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#8.7; 4 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#7.1; 5 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3; 6 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.1; 7 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.5; 8 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.6; 9 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.1; 10 - Santa Clara; 11 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.4; 12 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2; 13 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7; 14 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.2; 15 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.1; 16 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.4; 17 - UFU-057; 18 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.9; 19 - *S. pennellii*

**Figure 2.** Scatter plot of 19 mini tomato genotypes in relation to the scores of the first two principal components - PC1 (59.42%) and PC2 (21.32%)

**Table 3.** Clustering of tomato genotypes by the Tocher optimization method, from the Euclidian distance

Group	Genotypes
I	1; 2; 3; 4; 5; 6; 7; 8; 9; 10; 11; 12; 13; 14; 15; 16; 17; and 18
II	<i>S. pennellii</i>

1 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.9, 2 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.3, 3 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#8.7, 4 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#7.1, 5 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, 6 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.1, 7 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#2.5, 8 - UFU-057F<sub>2</sub>RC<sub>2</sub>10#3.6, 9 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.1, 10 - Santa Clara; 11 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.4, 12 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2; 13 - UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7, 14 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.2, 15 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.1, 16 - UFU-057F<sub>2</sub>RC<sub>2</sub>13#4.4, 17 - UFU-057 and 18 - UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.9

when they observed the formation of four distinct groups by the same method for quantitative data. These authors report that the first group also included the great majority of the genotypes (eight genotypes, about 61.54%), in addition to identifying the formation of groups with only one genotype.

Aguilera et al. (2011), using the Tocher grouping method in a study on genetic diversity between 96 accessions of tomato and two commercial cultivars, reported the formation of two groups, the first group consisted of 98.97% of the genotypes. The results observed in the present study corroborate those obtained by these authors.

## CONCLUSIONS

1. The multivariate analysis methods indicated that the genotypes have genetic variability.
2. The method of scatter plot by principal components revealed a greater power of discrimination, allowing the identification of the largest number of groups.
3. The genotypes UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.3, UFU-057F<sub>2</sub>RC<sub>2</sub>8#2.2 and UFU-057F<sub>2</sub>RC<sub>2</sub>7#4.7 are rich in the allelochemical acylsugar, resistant to *Liriomyza* spp. and *Tuta absoluta*.

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