

Genetic divergence among processing tomato hybrids and formation of new segregating populations

Divergência genética entre híbridos de tomate industrial e formação de novas populações segregantes

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ABSTRACT

Tomato is the most important vegetable species and has a strong bottleneck effect in its domestication and evolution. In exploring the existing genetic variability in commercial germplasm, germplasm has been proven to be an excellent alternative to obtain inbred lines in order to provide superior new hybrids in the future. In this sense, the objective of this study was to estimate the genetic distance among commercial processing tomato hybrids via agronomical and quality postharvest fruit traits with the aim of suggesting promising crosses for the formation of base populations for tomato breeding. Ten hybrids of processing tomato were evaluated in a complete randomized block design with three replicates. In total, eleven agronomic and postharvest fruit quality traits were evaluated. The genetic distances were estimated between the hybrids using the generalized Mahalanobis (D_H^2) and Gower (S_{I_k}) distances. The genetic distance among tomato hybrids was determined using a graphic projection of the first two canonical variables. The presence of significant genetic variability among the hybrids ($P < 0.05$) was demonstrated and was sufficient for the selection of the best hybrids before the breeding process. The hybrid Laura stood out for its postharvest characteristics and was the most divergent genotype compared to the others evaluated. The most promising crossings for the formation of segregating populations with superior genetic merit are Kátia x Laura, Vênus x Laura, Fascínio x Laura, AP-533 x Laura, Tinto x Laura, AP-529 x Laura, Supera x Laura, Granadero x Laura, Granadero x AP533, Granadero x AP529 and Granadero x Kátia.

Index terms: *Solanum lycopersicum*; genetic distance; pre-breeding; breeding populations; transgressive segregate.

RESUMO

O tomateiro é a cultura hortaliça mais importante e sofreu um forte estreitamento de sua base genética ao longo da sua evolução e domesticação. Explorar a variabilidade genética existente em germoplasma comercial têm se mostrado uma excelente alternativa para obtenção de novas linhagens que proporcionará novos híbridos no futuro. Neste sentido, o objetivo deste trabalho foi estimar a distância genética entre híbridos de tomateiro para processamento industrial por meio de variáveis agrônomicas e de qualidade pós-colheita dos frutos, com intuito de sugerir cruzamentos promissores para a formação de populações-base para o melhoramento do tomateiro. Foi conduzido um experimento com dez híbridos de tomateiro para processamento em delineamento experimental de blocos completos casualizados com três repetições. Ao todo foram avaliadas onze características de natureza agrônômica e de qualidade pós-colheita dos frutos. As distâncias genéticas entre os híbridos foram estimadas por meio da distância generalizada de Mahalanobis (D_H^2) e Gower (S_{I_k}). A divergência genética entre os híbridos foi estudada por meio da projeção gráfica dos genótipos utilizando-se as duas primeiras variáveis canônicas. Foi comprovada a presença de variabilidade genética significativa ($P < 0,05$) entre os híbridos, viabilizando a realização da seleção dos melhores híbridos para os objetivos do melhoramento. O híbrido Laura se destacou para características pós-colheita e foi o genótipo mais divergente perante aos demais avaliados. Pensando-se em formar populações-base com ampla variabilidade genética as combinações de híbridos simples mais recomendadas é Kátia x Laura, Vênus x Laura, Fascínio x Laura, AP-533 x Laura, Tinto x Laura, AP-529 x Laura, Supera x Laura e Granadero x Laura.

Termos para indexação: *Solanum lycopersicum*; distância genética; pré-melhoramento; melhoramento de populações; transgressivos segregantes.

INTRODUCTION

The cultivated tomato (*Solanum lycopersicum*) is a naturally self-pollinated species whose hybrid utilization is widely practiced in trade (Maluf, 2001). In the global

ranking of tomato producers for processing purposes, Brazil ranks ninth for fruit production and second for fruit yield in the world; in highly technical crops, yields can be over 100 tons of fruit per hectare (Vilela et al., 2012). The prominent

position of Brazil in tomato production is due in large part to the adoption of hybrids at the expense of open pollinated cultivars (Figueiredo et al., 2016a; Santos et al., 2011).

Throughout its evolution, the domestication and spread of tomato has seriously narrowed the genetic base (*bottleneck*), losing alleles that were very important for breeding. However, as a consequence, there has been a low genetic gain obtained with intrapopulational breeding strategies (Gonçalves et al., 2008; Figueiredo et al., 2016a), which have opted for strategies that seek to recombine existing genetic variability in order to form segregating populations of wide genetic variability and to encourage the selection of transgressive genotypes (Figueiredo et al., 2016b).

The formation of base populations is a very important step in a breeding program. Breeding programs whose objective is to obtain superior hybrids chose to use germplasm with a narrow genetic base for the formation of their base population [Hallauer, Carena and Miranda Filho (2010), Oliboni et al. (2013), Souza Neto et al. (2015) and Senhorinho et al. (2015)]; studies report that commercial single cross hybrids have been used by breeders of outcrossed plants for the formation of segregating populations and is due to the advanced breeding process that these genotypes already utilize. Similarly, this can be an important strategy to generate base populations of autogamous plants such as tomato.

One of the most important prerequisites to plant breeding is the presence of sufficient genetic variability for the selection process (Shah et al., 2015). Genetically divergent individuals tend to share few alleles with each other, and when combined, they can provide the F_2 generation wide genetic variability (Mulge; Mahendrakar; Prashanth, 2012). Thus, the use of homozygous selfed generations can promote the fixation of alleles in inbred lines, which are then selected for their genetic merit and utilized in future hybrid formation. There are several studies portraying the use of genetic divergence in predicting tomato crossings (Karasawa et al., 2005; Gonçalves et al., 2008; Rocha et al., 2009; Figueiredo et al., 2016b). However, none of the current work explores the germplasm of commercial tomato hybrids.

A large section of tomato hybrids grown for processing in Brazil have originated in programs conducted out of Brazil (Aragão et al., 2004). In this sense, the creation of new breeding programs for processing tomato crops, aimed that improving germplasm and better adaptations to the soil and climate conditions of Brazil, can provide elite inbred lines and superior tomato hybrids for the processing industry (Figueiredo et al., 2016a; b). The genetic variability availability in commercial processing hybrids can be

utilized in the formation of new segregating populations with adequate genetic variability for the selection of new elite inbred lines. Therefore, this study estimated the genetic divergence between commercial processing tomato hybrids using agronomic and fruit post-harvest quality traits best suited for processing, with the aim of predicting the most promising crosses for the formation of elite base populations for the improvement of the processing tomato.

MATERIAL AND METHODS

The experiment was in the horticulture sector of the Núcleo de Pesquisas em Hortaliças (NUPH) in the Universidade Estadual do Centro-Oeste campus CEDETEG in Guarapuava-PR. The soil in the experimental area is classified as a Brown Oxisol, and the climate is Cfb, according to the Köppen classification (Aparecido et al., 2016).

Evaluations were performed with 10 processing tomato hybrids with determinate growth, which were cultivated in an underbrush form. Information regarding the hybrids used in the experiment is shown in Table 1. The experimental design was a randomized complete block design with three replicates. The experimental unit consisted of two sowings spaced at 1.50 m, and each row contained 10 plants spaced at 0.30 m, with 4.5 m² of total useful area per plot.

The seedlings were produced in a heated greenhouse, with temperatures between 18 and 26 °C and a relative humidity of 70-80% in polystyrene trays with 128 cells filled with commercial substrate Plantimax[®]. Transplanting fertilization was performed with a dose of NPK fertilizer that was recommended for the culture. For the control of pests and diseases, insecticides and fungicides were applied weekly. However, the control of spontaneous invasive plants was carried out with two hand hoeings completed in the first 30 days after transplanting (DAT).

Three harvests of fruits were carried out from the breaker stage of maturation (light green fruit with the first appearance of pink, red or yellow covering up to 10% of its surface), the first being at 94 DAT (Paula et al., 2015). The following two harvests were completed in 10-day intervals. We evaluated the following response variables: total fruit yield (YT: t ha⁻¹), commercial fruit yield (YC: t ha⁻¹) and average fruit height (FM: g fruit⁻¹). The identification of non-commercial fruit followed the regulatory rules of the MAPA (Brasil, 1988). After performance evaluations, 20 fruits per plot were sorted on the basis of uniform size, extremely uniform red color, no peduncle, and free from mechanical or physiological damage, pests and diseases.

After separation, the fruits were taken to the Plant Physiology Laboratory at UNICENTRO. The following traits related to post-harvest quality were evaluated: mesocarp thickness (MT: mm), soluble solids (SS: °Brix), titratable acidity (IAL, 2008) (TA: mg citric acid 100 g⁻¹ pulp), Ratio (Ratio: the ratio SS/TA), lycopene content (LIC: µg g⁻¹ pulp lycopene), vitamin C (VC: mg ascorbic acid 100 g⁻¹ pulp), pH (pH), and reducing sugar content (RS: % reducing sugars) (IAL, 2008).

After testing for homogeneity and the normality of errors using Bartlett's and Lilliefors tests (P<0.05), respectively, we proceeded with an analysis of variance for the randomized block design, and the averages of the treatments were grouped by the Scott-Knott test (P<0.05). After completing an analysis of variance, the genetic divergence among the tomato hybrids was estimated using Gower distance (S_{ik}) and the Mahalanobis distance (D_{ii}^2). The S_{ik} between two individuals was estimated based on the

following equation: $S_{ik} = \frac{\sum_{i=1}^p S_{lki} \delta_{lki}}{\sum_{i=1}^p \delta_{lki}}$ where S_{lki} is the

distance between the individuals X_i and X_k for the variable i and δ_{lki} is a discriminating function that indicates the possibility of comparing these individuals to the variable i , which is expressed as $S_{ik} = \frac{1 - |x_i - x_k|}{R_i}$ where R_i is the amplitude of the response variable i . On the other hand,

D_{ii}^2 , is obtained by the following expression: $D_{ii}^2 = \delta' \psi \delta$ where D_{ii}^2 is the Mahalanobis distance between hybrids i and i' , δ is the matrix of genetic distances between hybrids i and i' , δ' is the transposed matrix of the genetic distances, ψ is the matrix of the residual variances and co-variances between the response variables used in this study.

With this set of distances, hybrids were divided into groups according to the agglomerative multivariate procedure of Tocher. This analysis adopted the criteria that stated that the average distance of an intragroup is less than any intergroup distance. The maximum average value of an intragroup distance was set as the maximum value of the Gower distance and D_{ii}^2 obtained in the set of shorter distances involving each hybrid. Additionally, a correlation analysis was performed between the matrixes of genetic distances using Mantel's test. Subsequently, the diversity among hybrids was evaluated with scatter graphs using the scores of the first two canonical variables as described by Cruz, Ferreira and Pessoni (2011). The statistical and genetic analyses were done using the program Genes (Cruz, 2013).

RESULTS AND DISCUSSION

Significant effects were observed (P<0.05) with the hybrids in the assessment of all traits in the trial, which indicated the presence of genetic variability among the evaluated hybrids and confirmed a favorable selection of the best hybrids for the study of breeding (Table 2). Although tomato has a narrow

Table 1: Phenotypic and genetic characteristics of the processing tomato hybrids.

Hybrid	Company	Genetic Base	Growth Type	Fruit Type	Cycle	Resistances ²
Supera	Agristar	HS	Determinate	Saladete	110	Fol: 1, 2; Mj, Mi; Pst, Va and Vd
Granadero	Agristar	HS	Indeterminate	Saladete	105	Fol: 0,1, ToMV, TsWV, TyLCV, Va and Vd
AP-529	Seminis	HS	Determinate	Piriformis	120	Va e Vd; Fol, Mi/Ma/Mj, Aal and Ss
AP-533	Seminis	HS	Determinate	Piriformis	125	Va/Vd, Fol, Mi/Ma/Mj, Aal and Ss
Kátia	Blue Seeds	HS	Determinate	Italian	80	Va.; Fol: 1, 2
Vênus	Blue Seeds	HS	Determinate	Italian	80	Va, Fol. 1, 2 and 3, Va
Fascínio	Feltrin	HS	Determinate	Saladete	90	ToMV, Fol: 1, 2; Va, Vd, Ma, Mi, Mj
Laura	Feltrin	HS	Determinate	Saladete	90	Va, Vd, Fol: 1 and 2, Mi, Mj.
Tinto	Nunhems	HS	Determinate	Saladete	95	TYLCV, TSWY
Red Spring	Nunhems	HS	Determinate	Saladete	115	Va, Vd, Fol:0,1, Pst Ma, Mj, Mi.

¹HS: Single Hybrid; ²Fol: *Fusarium oxysporum* f. sp. *lycopersici* race 1 and 2; Mj: *Meloidogyne javanica*; Mi: *Meloidogyne incognita*; Ma: *Meloidogyne arenaria*; Pst: *Pseudomonas syringae* pv. *tomato*; Va: *Verticillium albo-atrum*; Vb: *Verticillium dahliae*; TOMV: *Tomato Mosaic Tobamo Virus*; TSWV: *Tomato Spotted Wilt Tosporovirus*; TYLCV: *Tomato Yellow Leaf Curl Begomo Virus*; Aal: *Alternaria alternata* f.sp. *lycopersici*; Ss: *Stemphylium solani*.

genetic base and commercial cultivars have few phenotypic variations, the literature corroborates the results observed in this experiment, indicating that there is sufficient genetic variability among genotypes for the selection of the most promising hybrids (Gonçalves et al., 2008; Andrade et al., 2014).

Luz et al. (2016) evaluated several yield and postharvest quality traits in 53 processing tomato hybrids and found significant ($P < 0.05$) genetic variability among genotypes for all measured traits. These authors recommended the selection of some hybrids for release as commercial cultivars and other hybrids for use as base populations to obtain new elite inbred lines with disease resistance.

Figueiredo et al. (2015; 2016a) worked to improve processing tomatoes and evaluated ten elite lines, their crossings and two processing tomato hybrids for yield and postharvest fruit traits. These authors observed high genetic variability among the inbred lines, experimental hybrids and commercial hybrids and concluded that the best hybrids can be selected for release with the commercial hybrids. The best

inbred lines can be selected for further breeding programs aimed at recurrent intrapopulation selection.

The estimates of the broad heritability coefficient concerns the proportion of phenotypic variability in the source genetic variation. In this sense, the higher the heritability associated with a trait, the lower the environmental influence of such traits, and traits having high heritability levels were similar between the observed phenotype and the genotype (Hallauer; Carena; Miranda Filho, 2012). We observed that the estimates of the heritability coefficient had a wide range for all traits studied. This result indicates that much of the phenotypic variability between hybrids is genetic, favoring the selection of the most promising genotypes, which contributes positively to maximizing genetic gain with the selection process. Other studies show a range of heritability estimates for various agronomic traits and fruit postharvest quality in tomato, facilitating the selection of the best individuals in tomato breeding programs (Bhattarai et al., 2015; Shapurenko et al., 2015).

Table 2: Summary of the analysis of variance for the average estimates, heritability and mean square assessment of ten commercial processing tomato hybrids.

SV	DF	Mean Square					
		YT	YC	MF	MT	SS	AT
		(t ha ⁻¹) ²	(t ha ⁻¹) ²	(g fruit ⁻¹) ²	(mm) ²	(° Brix) ²	(g acid 100 g ⁻¹) ²
Blocks	2	200.84	186.99	172.93	0.17	0.008	0.0007
Hybrids	9	1403.50*	826.11*	1038.85*	1.73*	0.96*	0.0040*
Error	18	115.93	92.24	151.87	0.28	0.015	0.0001
Average	-	54.60	42.16	68.53	5.37	4.51	0.38
H (%)	-	91.73	88.83	85.38	83.89	95.86	97.69
CV _{exp} (%)	-	19.71	22.78	17.98	9.84	2.73	2.71

FV	GL	Mean Square				
		Ratio	LIC	VC	pH	AR
		(SS/AT) ²	(µg g ⁻¹) ²	(mg acid ascorbic) ²	pH ²	(sugars) ²
Blocks	2	0.12	0.85	0.73	0.0006	0.0020
Hybrids	9	2.65*	646.80*	11.44*	0.0120*	0.1030*
Error	18	0.23	0.21	0.091	0.00004	0.0033
Average	-	11.69	37.24	8.16	4.48	1.74
H (%)	-	91.17	99.96	99.19	99.68	96.78
CV (%)	-	4.13	1.23	3.70	0.13	3.30

*Significant by F test at 5% ($P < 0.05$) error. H (%): broad heritability (%). YT: Total fruit yield (t ha⁻¹) YC: commercial yield (t ha⁻¹), MF: mean fruit weight (g fruit⁻¹). MT: mesocarp thickness (mm), SS: Total content of soluble solids (° Brix), AT: titratable acidity (g citric acid 100 g⁻¹ fresh fruit), Ratio: relation AA / AT, LIC: lycopene (µg g⁻¹ fresh fruit lycopene), VC: vitamin C (mg ascorbic acid 100 g pulp⁻¹), pH (potential hydrogenionic), AR reducing sugars (%).

Tomato breeding programs aimed at exploring hybrids perform many crossings between lineages with the intention of forming hybrids that have concomitant high yield, high soluble solids content (SS), proper titratable acidity (TA), high lycopene content (LIC), and a high content of reducing sugars (RS), as well as resistance to the major crop diseases. Hence, the need to involve multiple traits into the same individual hinders plant breeding and requires a preliminary assessment of these characters in genotypes, which eventually form the base population for the extraction of elite inbred lines (Boiteux et al., 2012; Paula et al., 2015).

The overall averages for variables YT, YC, MF and SS were 54.60 and 42.16 t ha⁻¹, 5.37 mm, and 4.51 ° Brix, respectively (Table 2). The averages grouping test Scott-Knott (P<0.05) showed the formation of two groups of averages for the MT and YC variables and three different groups for YT and SS (Table 3). The hybrid Granadero stood out as the highest average genotype for the variables YT, YC, FT and SS by being isolated from the other hybrids in the experiment (Table 3). In the current literature, there are widely variable results regarding processing tomato fruit yield, indicating the existence of differential behaviors of the genotypes in a wide range of Brazilian soil and climate conditions (Aragão et al., 2004; Figueiredo et al., 2016a; Santos et al., 2011; Schwarz et al., 2013).

The overall average for MF was 68.53 g fruit⁻¹, and the hybrids were summarized in two groups according to the Scott-Knott test (P<0.05); the hybrids Vênus, Fascínio, Tinto and Granadero were ranked in descending order and were the largest MF hybrids in the experiment

(Table 3), corroborating the results obtained by Figueiredo et al. (2016a). The TA and LIC variables showed overall averages of 0.38 mg citric acid 100 g⁻¹ of pulp and 37.24 µg lycopene g⁻¹ pulp, respectively, and the Scott-Knott test (P<0.05) allowed the formation of 5 and 7 groups for the variables TA and LIC, respectively (Table 3). The hybrid Laura stood out from the other hybrids in the experiment by being grouped apart from the other hybrids (Table 3).

The overall ratio average was 11.69, and the hybrids used in the experiment were grouped into three groups; the hybrids Kátia, Supera, Granadero, AP-533 and Tinto were the hybrids with the highest averages of the experiment. For VC content, the formation of six groups of genotypes with identical means was observed with the hybrids Granadero, Laura and Red Spring, which belong to the genotype group with the highest averages (Table 3). In the industrialization of tomato pulp, it was necessary to reduce the pH to prevent the proliferation of microorganisms, and an appropriate pH value should be less than 4.5 (Figueiredo et al., 2015; Soares; Rangel, 2012). In this experiment, the hybrid with a lower pH value was Laura, and this hybrid was isolated from other hybrids and had a pH of 4.37 (Table 3). Regarding the AR content, the Fascínio hybrid had the highest average of the experiment (2.15%) and was not grouped with any of the other hybrids tested (Table 3).

If we excluded the reciprocal effects and performed biparental crossings with the ten processing tomato hybrids, we would have 45 double tomato hybrids. Therefore, the evaluation of these entire hybrids in experiments delayed the obtainment of higher segregating

Table 3: Groupings of the average agronomic and postharvest quality characteristics of processing tomato hybrids.

Hybrid	YT	YC	MF	MT	SS	AT	Ratio	LIC	VC	pH	AR
Granadero	108.9a	84.13a	77.97a	7.21a	5.41a	0.43b	12.5a	38.7d	10.6a	4.45c	1.87b
Venus	66.70b	51.07b	104.6 a	5.39b	4.41c	0.41c	10.7b	16.11h	9.3b	4.44c	1.83b
Tinto	61.46b	41.88bb	84.10a	4.18b	4.33c	0.35e	12.2a	34.3f	8.6c	4.53e	1.61d
AP-533	55.53b	48.61b	54.61b	5.40b	4.25c	0.34e	12.3a	38.9d	5.5f	4.55f	1.64d
Kátia	50.80b	37.35b	56.67b	5.0 b	4.66b	0.36d	12.7a	26.6g	5.3f	4.58g	1.75c
R. Spring	44.53c	35.21b	53.71b	5.52b	4.5 b	0.38d	11.6b	41.8b	10.1a	4.43b	1.71c
Fascínio	43.13c	30.93b	86.67a	5.58b	4.25c	0.38d	11.2b	26.2g	6.7e	4.46d	2.15a
AP-529	41.10c	32.33b	54.61b	5.01b	4.33c	0.40d	11.1b	37.4e	7.5d	4.53e	1.50d
Supera	39.50c	32.01b	62.17b	5.07b	4.33c	0.34e	12.6a	41.78c	7.5d	4.47d	1.56d
Laura	34.36c	28.07b	47.90b	5.34b	4.66b	0.46a	9.9c	72.1a	10.4a	4.37aA	1.77c

Averages followed by the same letter in columns belong to the same group by Scott Knott test (P<0.05). YT: Total fruit yield (t ha⁻¹), YC: marketable yield (t ha⁻¹), FM: average weight of fruit (g⁻¹), MT: mesocarp thickness (mm), SS: total content of soluble solids (° Brix), TA: titratable acidity (g citric acid 100 g⁻¹ fresh fruit), Ratio: relation SS/ TA, LIC: lycopene (µg g⁻¹ fresh fruit lycopene), VC: vitamin C (mg ascorbic acid 100 g pulp⁻¹), pH (potential hydrogenionic), RS: Reducing sugar (%).

populations. Multivariate predictive techniques can only recognize the most promising crossings, which are only crossings among the most distant genotypes from a genetic point of view (Oliveira; Scapim; Casalli, 1998). Thus, combining genetically different individuals is expected to subsequently create segregating populations with high genetic variability and high averages, making the selection of transgressive genotypes important for breeding possible.

A positive and highly significant correlation with the Mantel test was observed, indicating that the distances of Gower and D_{ii}^2 agreed. The average Gower distance was 3.72 and ranged from 1.59 among the closest hybrids AP-529 and Supera to 6.22 between the Laura and Granadero hybrids. The D_{ii}^2 estimated average was 10,146.40 and ranged from 298.07 between the AP-529 and Red Spring hybrids to 50,467.33 between the Kátia and Laura hybrids (Table 4).

Considering D_{ii}^2 , the Tocher method allowed the formation of two mutually exclusive groups; the first group contained the hybrids AP529, AP533, Supera, Vênus, Fascínio, Tinto, Red Spring, Kátia and Granadero, and the second group contained Laura, which was separated from the other hybrids. On the other hand, using Gower's genetic distances, the agglomerative method of Tocher showed the formation of three mutually exclusive clusters; group I contained AP529, AP533, Supera, Vênus, Fascínio, Tinto, Red Spring and Kátia hybrids, group II included Granadero, and group III only contained Laura. It is worth noting that for both measures of genetic divergence, the

hybrid Laura was grouped apart from the other hybrids by the Tocher agglomerative method, which is an indicative of the high genetic diversity that this hybrid presents compared to the other genotypes evaluated. This hybrid is a key parent in the direction of future crossings.

The interpretation of genetic diversity from the pool and the dispersion in the coordinate systems agreed because the first two canonical variables (VC) concentrated 98.32% of the total variance (VC1: 82.61% and VC2: 15.71%), justifying further studies of genetic diversity via the projection of individuals in a Cartesian plane (Table 5). The cophenetic correlation coefficients (r) obtained for the genetic distances of D_{ii}^2 and Gower were 0.854** and 0.911**, respectively, suggesting an excellent fit between the graphical representation of the distances of the hybrids in the Cartesian plane with its array of original distances.

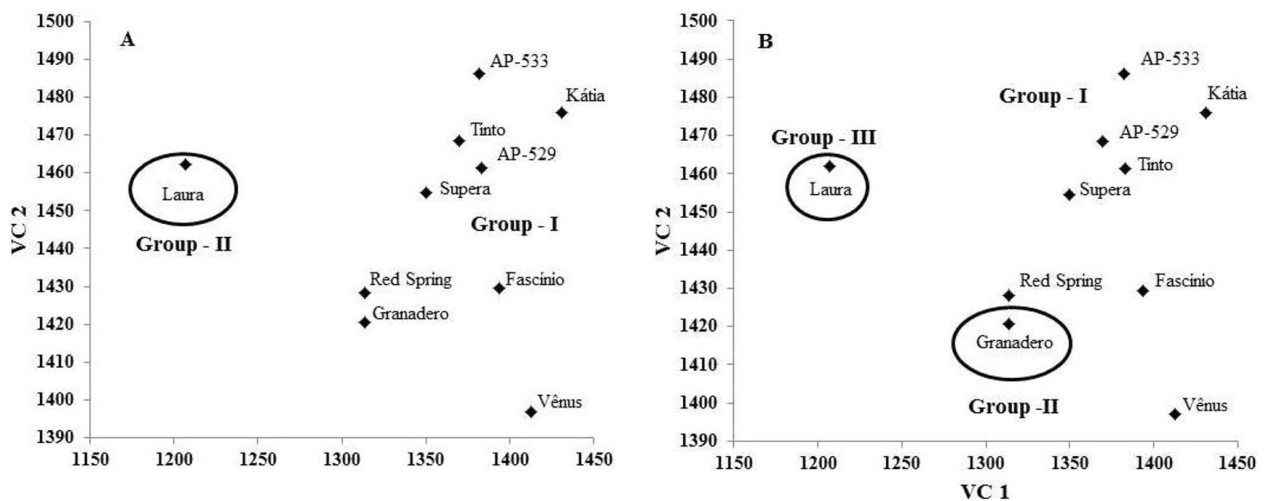
Analyzing the Tocher pool of information with D_{ii}^2 and the dispersion of the hybrids in the Cartesian plane based on the first two canonical variables, it was observed that if a breeder chose to perform 15% of the most promising crossings, the best hybrid combinations would be Kátia x Laura, Vênus x Laura, Fascínio x Laura, AP-533 x Laura, Tinto x Laura, AP-529 x Laura, and Supera x Laura (Figure 1A). On the other hand, when considering the Tocher pool of information with the Gower distance, the best hybrid combinations would be Granadero x Laura, Laura x AP529, Laura x AP533, Laura x Kátia, Laura x Venus, Granadero x AP533, Granadero x Kátia, and Granadero x AP533 (Figure 1B).

Table 4: Gower (below diagonal) and Mahalanobis (D_{ii}^2) (above the diagonal) distances and the estimated distances between single industrial tomato hybrids based on average phenotypic values of the 11 quantitative traits important for industrial processing.

	Supera	Granadero	AP 529	AP 533	Kátia	Laura	Fascínio	Tinto	Red Spring	Venus
Supera	0	2,937.73	797.80	2,134.63	7,462.69	20,831.63	2,962.91	1,308.85	2,090.77	7450.56
Granadero	5.70	0	5,585.86	9,182.46	16,977.24	13,405.94	8,869.59	6,661.13	306.44	10,661.11
AP 529	1.59	6.34	0	542.68	3,946.98	26,531.73	2,328.70	298.07	4,831.26	7,047.15
AP 533	1.86	5.91	2.26	0	2,647.78	31,365.58	3,538.57	694.40	8,116.37	8,982.33
Kátia	2.36	5.95	2.57	1.64	0	5,0467.33	3,696.19	2,668.58	16,338.94	6,668.58
Laura	4.65	6.22	4.03	5.58	5.25	0	35,895.85	31,233.20	12,705.83	46,668.96
Fascínio	2.95	5.89	2.67	3.43	3.41	4.95	0	1,417.00	6,715.14	1,600.00
Tinto	2.07	5.45	2.40	2.04	2.73	5.71	3.31	0	6,011.48	5,074.64
Red Spring	2.25	4.70	2.04	2.90	3.00	2.76	2.89	3.06	0	10,927.39
Venus	4.23	4.66	3.71	4.24	4.46	4.42	2.88	3.36	2.95	0

Table 5: Eigenvalues (λ_i) corresponding to the range of percentages explained by the canonical variables (VC_i), and the relative importance of 11 quantitative agronomic and fruit quality traits evaluated in ten processing tomato hybrids.

VC_i	Eigen vectors		Relative importance of traits										
	λ_i	% cum	PT	PC	MM	EM	SS	AT	Ratio	LIC	VC	pH	AR
VC1	4190.74	82.61	1.78	-1.52	0.24	-1.91	-13.34	12.36	19.40	-1.55	-1.57	1.53	-0.01
VC2	797.19	98.32	1.47	-0.93	-0.29	-1.32	-4.23	3.88	5.63	0.73	-1.64	1.85	-0.36
VC3	42.65	99.16	0.12	-1.21	0.70	-0.33	0.60	1.45	-0.42	0.05	-0.30	0.55	1.39
VC4	28.74	99.73	0.39	0.52	-0.48	-0.03	3.04	-2.23	-3.61	0.01	0.49	0.44	-0.09
VC5	8.25	99.89	-0.08	-0.44	0.03	-0.49	-1.62	2.12	2.02	-0.05	0.35	0.24	-0.39
VC6	2.59	99.94	2.23	-2.01	0.65	-0.22	-3.55	3.30	5.64	0.04	-0.01	0.01	0.13
VC7	2.32	99.99	-0.65	0.91	-0.27	-0.14	-3.04	3.63	5.62	-0.06	-0.29	-0.20	-0.33
VC8	0.54	100.00	-0.74	1.18	0.43	0.25	-0.17	-0.03	-0.29	0.02	-0.02	0.05	-0.05
VC9	0.19	100.00	-2.00	2.17	-0.32	-0.09	-2.08	1.88	3.13	-0.02	0.35	0.18	0.40
VC10	0.00	100.00	-1.84	1.36	0.60	0.26	-0.10	0.23	0.49	0.01	0.17	0.14	0.08
VC11	0.00	100.00	0.43	-0.87	0.07	0.92	-2.13	1.87	3.01	0.00	0.17	0.13	0.04

**Figure 1:** Graphic dispersion of tomato hybrids in relation to the first two canonical variables, and the agglomerative cluster Tocher with the generalized Mahalanobis (A) and Gower (B) distances.

Some results helped to justify the viability of the use of the prediction techniques to determine the most promising crossings in the breeding program. Figueiredo et al. (2016b) estimated the genetic distance among 10 inbred lines of processing tomato via the use of agronomic and postharvest quality traits and correlated such distances with the genetic and phenotypic parameter estimates obtained through diallel crosses with these strains and concluded that genetic distance can assist in targeting potential

crossings in a tomato breeding program, helping to reduce costs and time in achieving new hybrids. Oliveira, Scapim and Casalli (1998) correlated the estimated genetic distance values among elite inbred lines *versus* average and heterosis sweet pepper hybrids and concluded that the better hybrids originated from crossings between the lines that were most genetically distant and that multivariate techniques could be used to predict which hybrids would be most promising.

It is worth mentioning that if a breeder used only the Tocher pool of information with D_{ii}^2 , a crossing between hybrids Laura and Granadero would not be realized since the hybrids are positioned near each other on the scatter plot. However, this combination appears to be promising because Granadero has traits related to fruit yield while Laura has more qualitative characteristics (Table 3). Thus, after inbreeding and the application of adequate methodologies for creating segregating populations, new elite inbred lines can be selected in order to combine conciliating abilities and for resistance to disease because these hybrids carry good disease resistance (Table 1). An important note to consider is the necessity of the use of assisted selection with molecular markers for the main diseases in processing tomato. Molecular markers are one important tool that can accelerate the breeding program and the obtainment of new elite inbred lines and hybrids that are resistant to the main diseases in a short time period.

Of the most promising combinations of simple hybrids mentioned above, only Laura x Fascínio belongs to the same company that owns Feltrin[®], while the others are owned by different companies. This possible outcome proves the origin of these hybrids, which were possibly formed from the combination of lineages drawn from uncommon base populations and thus shared few alleles among themselves.

In general, hybrids belonging to the same company positioned themselves next to each other (Figure 1). This was highlighted with the AP-529 and AP-533 hybrids, which belong to the Seminis[®] Company and were positioned very close in the dispersion graphic (Figure 1). On the other hand, hybrids Fascínio and Laura of the Feltrin[®] Company and the Kátia and Vênus hybrids belonging to the Blue Seeds[®] company are positioned in distant regions of the graph, which demonstrates that the two hybrids showed a considerable genetic distance, even though they belong to the same company (Table 1).

One explanation for this similarity is that tomato companies conduct a constant exchange of germplasm with the different regions of the world. In Brazil, in the industrial tomato industry, the main form of breeding used by companies is the introduction of hybrids obtained from breeding programs outside Brazilian soil and climate conditions (Figueiredo et al., 2016a). Hybrids are inserted into a network of experiments and evaluated for countless characters, and the best hybrids end up being registered and commercialized in the national seed market (Santos et al., 2011). Thus, tomato hybrids marketed by multinational corporations may have been obtained from different breeding programs and therefore have distinct genetic bases, which explains the genetic divergence in the hybrids from the same company.

For the study of genetic diversity via quantitative agronomic markers to be effective, it is necessary that the variables considered in the study are not invariant and represent the genetic diversity present in the biological system in question (Cruz; Ferreira; Pessoni, 2011). The importance of the variables in the study of genetic diversity can be assessed before the determination of the magnitude of the weighted coefficients from the canonical variables, thus excluding those characters that have higher magnitudes from future studies (Cruz; Ferreira; Pessoni, 2011). In analyzing the last two canonical variables (Table 5), variables PC, Ratio and AT were the ones that contributed the least towards the study of genetic diversity and must be disregarded in future studies, corroborating with Figueiredo et al. (2016b).

CONCLUSIONS

Thus, it can be concluded that there is sufficient genetic variability among tomato hybrids enabling the selection of the best parents. The hybrid Laura stood out for its postharvest characteristics and was the most divergent genotype compared to the others evaluated. The best base population for the extraction of lineages can be derived from crossings of the hybrids Kátia x Laura, Vênus x Laura, Fascínio x Laura, AP-533 x Laura, Tinto x Laura, AP-529 x Laura, Supera x Laura, Granadero x Laura, Granadero x AP533, Granadero x Ap529 and Granadero x Kátia.

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