



Artificial neural networks and genetic dissimilarity among saladette type dwarf tomato plant populations

Camila Soares de Oliveira^a, Gabriel Mascarenhas Maciel^{b,*}, Ana Carolina Silva Siquieroli^c, Danilo Araújo Gomes^a, Nádia Mendes Diniz^b, José Magno Queiroz Luz^a, Rickey Yoshio Yada^d

^a Institute of Agricultural Sciences, Federal University of Uberlândia, Uberlândia, Brazil

^b Institute of Agricultural Sciences, Federal University of Uberlândia, Monte Carmelo, Brazil

^c Institute de Biotechnology, Federal University of Uberlândia, Monte Carmelo, Brazil

^d Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada

ARTICLE INFO

Keywords:

Solanum lycopersicum
Dwarfism
Backcrossing
Computational intelligence
Genetic dissimilarity

ABSTRACT

Studies have shown that dwarf plants have the potential for use in obtaining hybrids. The aim of this study was to evaluate the agronomic potential and genetic dissimilarity of saladette type dwarf tomato plant populations through the use of artificial neural networks (ANNs). The following traits were analyzed: mean fruit weight, transverse and longitudinal fruit diameter, fruit shape, pulp thickness, locule number, internode length, soluble solids content, and β -carotene, lycopene, and leaf zingiberene contents. A dendrogram obtained by the unweighted pair-group method with arithmetic mean (UPGMA) and Kohonen self-organizing maps (SOM) agreed in the distinction of the BC₁F₃ populations from the dwarf donor parent. SOM was more consistent in identifying the genetic similarities among the BC₁F₃ dwarf tomato plant populations and allowed for the determination of weights of each variable in the cluster formation. The UFU SDi 13-1 BC₁F₃ population was revealed to be a promising option for obtaining saladette type dwarf tomato plant lines.

1. Introduction

Tomato is one of the main vegetable crops produced and consumed worldwide (Maham et al., 2020). The market demand for fresh tomatoes with enhanced taste and cooking versatility has expanded the cultivation of saladette/roma tomato plants (Shirahige et al., 2010). However, high production costs, along with the strong susceptibility of the crop to various types of biotic and abiotic stresses have driven the search for alternative, more feasible growth varieties for producers (Wamser et al., 2012; Almeida et al., 2015).

Plant breeding has been an important strategy for increasing crop yield in a profitable and sustainable manner (Barbosa et al., 2011). In cherry/grape tomatoes, internode reduction through breeding with a dwarf parental line (Maciel et al., 2015) has led to promising results in obtaining hybrids with compact plant architectures and high yields (Finzi et al., 2017). Dwarf tomato plant populations have previously been cultured for round/salad-type tomatoes intended for *in natura* consumption (Finzi et al., 2020), but similar dwarf plants have not yet been identified for the saladette/roma tomato segment.

Characterizing and analyzing the genetic dissimilarity of populations are essential for distinguishing divergent and promising genotypes (Maciel et al., 2018). Traditionally, multivariate techniques have been used, such as dendrograms, the Tocher grouping method, canonical variables, and principal components to characterize the germplasm of normal tomato plants (Maciel et al., 2018; Alsamir et al., 2019; Peixoto et al., 2020) and dwarf tomato varieties (Finzi et al., 2020).

Greater difficulties arise in characterizing and analyzing the germplasm of dwarf tomato plants (Finzi et al., 2017; Finzi et al., 2020), as they have considerably different morphologies than normal-sized tomatoes, which requires the refinement of methods and the use of new optimization techniques. Artificial neural networks (ANNs) have been used to obtain self-organizing maps (SOMs), which may be beneficial alternatives for the study of genetic dissimilarity in saladette type dwarf tomatoes.

These ANNs have comparative advantages in relation to the traditional methodologies, such as the enabling of a non-parametric approach that tolerates loss of data and effectively recognizes patterns and establishes clusters (Kavzoglu and Mather, 2003). SOMs are a class

* Corresponding author.

E-mail address: gabrielmaciel@ufu.br (G. Mascarenhas Maciel).

<https://doi.org/10.1016/j.fochms.2021.100056>

Received 22 June 2021; Received in revised form 1 November 2021; Accepted 25 November 2021

Available online 29 November 2021

2666-5662/© 2021 Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

of ANN that use a competitive learning mechanism through distance as an activation function to recognize similarities between input patterns and establish groupings (Cruz and Nascimento, 2018). This allows for the study of genetic dissimilarity in different germplasms such as rice (Santos et al., 2019), alfalfa (Santos et al., 2020), and cotton (Cardoso et al., 2021).

Thus, the aim of this study was to assess the agronomic potential and genetic dissimilarity of saladette/roma type dwarf tomato plant populations using computational intelligence (ANNs).

2. Material and methods

2.1. Plant material and experimental design

The experiment was conducted from October 2019 to March 2020 at the vegetable crop experimental station of the Universidade Federal de Uberlândia (UFU), Monte Carmelo Campus, MG, Brazil (18°42'43.19" S, 47°29'55.8" W; altitude 873 m) in an arch-type greenhouse (7 × 21 m) covered with a 150 µm transparent polyethylene film with ultraviolet radiation protection and anti-aphid white screen lateral curtains.

The dwarf tomato plant populations (BC₁F₃) used in this study were obtained from the tomato germplasm bank of UFU. They were derived from two self-fertilizations of a first backcross after hybridization of a pre-commercial homozygous line (UFU MC TOM 5) with a saladette/roma type fruit (recurrent parent) × a dwarf plant line (UFU MC TOM1) with cherry/grape type fruit (Maciel et al., 2015).

Nineteen populations were evaluated from this germplasm bank (1: UFU SDi 11-4, 2: UFU SDi 17-8, 3: UFU SDi 7-4, 4: UFU SDi 17-5, 5: UFU SDi 4-3, 6: UFU SDi 5-4, 7: UFU SDi 17-7, 8: UFU SDi 13-1, 9: UFU SDi 13-2, 10: UFU SDi 17-1, 11: UFU SDi 13-3, 12: UFU SDi 7-2, 13: UFU SDi 11-5, 14: UFU SDi 10-5, 15: UFU SDi 4-6, 16: UFU SDi 17-9, 17: UFU SDi 17-6, 18: UFU SDi 18-1, and 19: UFU SDi 6-1), along with the donor parent (UFU MC TOM1), the recurrent parent (UFU MC TOM5), and the commercial hybrid Pizzadoro, for a total of 22 treatments.

The genotypes were sown in polystyrene trays (200 cells) filled with a coconut fiber-based substrate (Bioplant Ltda, Nova Ponte-MG, Brazil). Seedlings were transplanted 40 days after sowing (DAS) in 5 L plastic pots containing the same substrate. Crops were treated as recommended for growing tomato plants in a protected environment (Alvarenga, 2013).

The experiment was conducted in a randomized block design (RBD) with four replications, and each experimental plot was composed of six plants distributed in double rows at a spacing of 0.3 × 0.3 m. A spacing of 0.8 m was used between the double rows.

2.2. Agronomic evaluation of fruits

At 90 days after sowing, the fruit from each plot was harvested, counted, and weighed to determine the mean fruit weight (MW). Fifteen tomatoes per plot were subsequently taken as samples, and the following traits were evaluated: transverse fruit diameter (TD), measured from the pedicel scar to the blossom end of the tomato fruit; longitudinal fruit diameter (LD), measured in the transverse direction of the cut fruit; fruit shape (FS), determined by the ratio between the TD and LD of the tomato; and pulp thickness (PT), determined by the greatest distance (thickness) of the mesocarp of the fruit. The number of locules (NL) was determined by directly counting the locules in the tomato.

2.3. Internode length evaluation

Internode length (IL) was calculated as the ratio between the height and the number of plant nodes measured at the end of the crop cycle (155 DAS).

2.4. Fruit quality evaluation

The soluble solids content (SS) was measured using a digital pocket refractometer (Atago PAL-1 3810; Atago Co. Ltd., Tokyo, Japan) in °Brix.

Extraction and quantification of β-carotene (BCC) and lycopene (LC) were conducted according to the methodology adapted from Rodriguez-Amaya (2001). The tomato pulp was ground and 1 g of the material obtained was placed in a glass vial containing 3 mL of 100% acetone (Dinâmica Ltda, Indaiatuba-SP, Brazil). The samples were kept in the dark at a temperature of 8 °C for 48 h. The supernatant was then evaluated by spectrophotometry (Tecnal Ltda, Piracicaba-SP, Brazil), and the absorbance values were obtained for BCC and LC at wavelengths of 450 nm and 470 nm, respectively. Pigments were quantified according to the protocols described by Rodriguez-Amaya (2001) and Rodriguez-Amaya and Kimura (2004).

2.5. Extraction and quantification of zingiberene

The leaf zingiberene content (ZGB) was determined at 80 DAS using a sample composed of eight leaf disks (equivalent to 4.2 cm²) from each plant in the plot. The disks were collected from leaflets from the upper third of the plants and placed in test tubes. The allelochemical zingiberene was extracted and quantified following the methodology described by Freitas et al. (2000).

2.6. Statistical analysis

Analysis of variance was performed using the F-test ($\alpha = 0.05$). The mean values were compared using the Scott-Knott test ($\alpha = 0.05$) and Dunnett's test ($\alpha = 0.05$), with the dwarf plant donor line (UFU MC TOM1) considered the control for the purpose of determining the gains obtained by backcrossing. The following genetic parameters were also analyzed: genotypic coefficient of variation (h^2), genetic coefficient of variation (CV_g), and the ratio between the genetic and environmental coefficient of variation (CV_g/CV_e).

2.7. Multivariate analysis and self-organizing map by artificial neural networks

The genetic dissimilarity among the populations was studied using the conventional method by obtaining the Mahalanobis generalized distance matrix. Genetic diversity was represented by the dendrogram obtained by the unweighted pair-group method with arithmetic mean (UPGMA) hierarchical method, validated by the cophenetic correlation coefficient (CCC). In addition, an analysis was performed using computational intelligence (ANN).

The SOM was obtained by applying a non-supervised traditional approach according to the characteristics evaluated and the requirements of the study. Network training to obtain the SOM was performed in 5000 epochs (equal to the total number of comparisons made), with four neurons in each dimension and a pattern of radius neighbor = 1.

The model was validated using different configurations for the number of neurons. Combinations were tested by varying the number of rows (2–5) and columns (2–5). To select the best architecture, 5000 training sessions were conducted for each combination. Thus, it was observed that the combination that best represented the genetic dissimilarity of the dwarf tomato germplasm of the saladette type was that of four rows and four columns (16 neurons) with a neighboring radius pattern of 1, hexagonal neighbor topology, feedforward network architecture with an input layer (means) and an output neuron, and a Euclidean distance-type activation function.

For the determination of the SOM classes, there was competition between the output neurons, with the Euclidean distance as a discriminant function for each input vector. The neuron with the highest

discriminant function value was deemed the winning neuron. Thus, each genotype was allocated to its most representative neuron. Subsequently, the winning neuron determined the spatial location of the neighboring neurons. By adjusting the synaptic weights of each variable, the excited neurons increased the values of their discriminant function in relation to the input pattern, which allowed the network to build a topological map, in which the closer neurons respond, in the manner of similar input patterns.

All analyses were performed using GENES software, integrated with the R and MATLAB software (Cruz, 2016).

3. Results

3.1. Univariate analysis

3.1.1. Agronomic characterization

The genotypes under study differed in agronomic traits, fruit quality, and leaf zingiberene content (F test, $\alpha = 0.05$) (Table 1).

The BC₁F₃ dwarf populations produced larger tomatoes than those of the UFU TOM 1 donor parent (Scott-Knott and Dunnett, $\alpha = 0.05$). The UFU-SDi 13-1, UFU-SDi 17-1, and UFU-SDi 18-1 populations were noteworthy for the production of tomatoes with MWs greater than 30 g. The UFU-13-1 and UFU-17-1 populations were superior to the other populations, with LDs equal to 5.49 cm and TDs of 3.43 and 3.75 cm, respectively.

The recurrent parent had a mean of 3.38 locules per tomato, while the donor parent had a mean of two units per tomato. The tomatoes of the populations showed intermediate NLs compared to the parents, ranging from 2.28 to 2.85 units. However, the UFU SDi 11-4, UFU SDi 17-8, and UFU SDi 17-9 populations did not differ statistically from the donor parent by the Dunnett test ($\alpha = 0.05$), and revealed the lowest number of locules among the populations.

The PT of tomatoes from the dwarf plant populations was 155% greater than that of the tomatoes from the donor parent. In general, 42.1% of the populations had a PT greater than 0.55 cm.

An elongated FS was predominant among the BC₁F₃ populations, parents, and the commercial control. Despite statistical differences, all genotypes had an FS index greater than 1.

The normal phenotype plants had internodes greater than 6.5 cm, whereas the ILs of the BC₁F₃ dwarf plant populations ranged from 1.66 to 2.44 cm. An IL shorter than 2 cm was found in 47.4% of the population. The UFU SDi 7-4, UFU SDi 4-3, and UFU SDi 13-3 populations did not differ statistically from the donor parent with an IL of 1.31 cm (Dunnett $\alpha = 0.05$).

In the present study, the UFU TOM1 donor parent had a greater ZGB (0.22 nm) than the other genotypes in both tests (Scott Knott and Dunnett, $\alpha = 0.05$). Lower contents of this allelochemical were observed in cv. Pizzadoro (0.03 nm), the recurrent parent, and the UFU SDi 17-5, UFU SDi 4-3, UFU SDi 13-3, UFU SDi 11-5, UFU SDi 17-6, and UFU SDi 6-1 populations. Intermediate contents of this allelochemical were observed in the UFU SDi 7-4, UFU SDi 5-4, UFU SDi 13-1, UFU SDi 7-2, UFU SDi 10-5, and UFU SDi 17-9 populations.

The expression increases in the BC₁F₃ populations compared to the donor parent in relation to the agronomic traits attest to the effectiveness of the first backcross (Fig. 1).

3.1.2. Fruit quality characterization

The fruit quality parameters for the BC₁F₃ dwarf populations, parents, and the commercial cultivar differed for all traits evaluated by the Scott-Knott test ($\alpha = 0.05$) (Table 2).

The greatest SS (7.10 °Brix) was observed in the fruit produced by the UFU TOM 1 donor parent. The UFU SDi 4-3 and UFU SDi 17-9 populations, together with cv. Pizzadoro predominated, expressing SSS greater than 5.70 °Brix. The UFU SDi 7-4, UFU SDi 13-2, UFU SDi 17-1, and UFU SDi 13-3 populations expressed SSS less than 5.0 °Brix.

The fruit from the UFU TOM 1 donor parent had a high SS, but also a

considerable BCC (2.39 mg/100 g). A BCC similar to that of the donor parent was observed in 76.2% of the BC₁F₃ dwarf populations. In addition, 68.4% of the BC₁F₃ populations produced fruit with LC greater than 2.71 mg/100 g and equaled the UFU TOM1 donor parent in both tests (Dunnett and Scott-Knott $\alpha = 0.05$). The UFU SDi 6-1, UFU SDi 11-5, UFU SDi 13-1, UFU SDi 17-8, UFU SDi 17-7, UFU SDi 17-6, and UFU SDi 18-1 populations had notably high content of both carotenoids.

Except for the LC and BCC, all variables exhibited h^2 values greater than 0.70, and CV_g/CV_e ratios greater than 1 (Tables 1 and 2).

3.2. Multivariate analysis

3.2.1. Hierarchical cluster analysis (UPGMA)

The dendrogram obtained by the UPGMA (Fig. 2) had a CCC of 0.88 and a distortion of 16.67.

The cutoff point of the dendrogram was established by abrupt level changes in the dendrogram at 8% dissimilarity, by which five groups were retrieved. The UFU TOM 1 donor parent, UFU MC TOM 5 recurrent parent, and cv. Pizzadoro formed three distinct groups. The dwarf populations were divided into two groups, one of which was formed by 84.2% of the BC₁F₃ populations and the other by the genotypes UFU SDi 17-1, UFU SDi 18-1, and UFU SDi 13-1.

3.2.2. Kohonen self-organizing maps (ANNS/SOM)

Using the SOM method, of the 16 neurons established with the four rows and four columns for the command, the 22 genotypes were classified into 12 classes (Fig. 3).

Classes 1 and 3 consisted of three genotypes and classified the largest number of accessions. Classes 2, 7, 10, and 13 held only one genotype each, showing the genetic dissimilarity of these accessions in relation to the remainder. Classes 4, 6, 8, 9, 11, and 12 each contained two genotypes. No genotype was allocated in Class 5, revealing the low similarity between the genotypes clustered in Classes 1 and 10, and those in Classes 2 and 10. The remaining classes (14, 15, and 16) contained no genotypes.

The UFU SDi 13-3, UFU SDi 11-5, and UFU SDi 13-1 populations and the UFU TOM 1 donor parent formed isolated groups of low similarity with the other populations by the SOM method (Table 3).

The groups that gathered the largest number of populations in representation of SOM were constituted by the following BC₁F₃ populations: UFU SDi 7-2, UFU SDi 10-5, and UFU SDi-4-6 (Group I); and UFU SDi 11-4, UFU SDi 17-5, and UFU SDi 13-2 (Group III). Among the 12 clusters that were formed in the SOM method, only that constituting the donor parent corroborated the representation of the dendrogram created by the UPGMA method.

Greater genetic dissimilarity was found in the UFU SDi 13-1 population than in the others, since this genotype was allocated to an isolated group corresponding to Class 10 in the SOM (Fig. 3), and to the group with the lowest number of dwarf populations in the dendrogram obtained by the UPGMA method (Fig. 2).

The effect of each variable on each group formed in the SOM was shown in the representation of the neuron topology of the network generated by means of the weights and the association of each input variable with the output neuron (Fig. 4).

The determining traits in distinguishing the UFU TOM 1 donor parent were FS, SS, BCC, and ZGB. The LC was an important trait in identifying the clusters corresponding to Classes 11 and 12, which held the UFU SDi 6-1, UFU SDi 7-4, UFU SDi 17-8, and UFU SDi 17-7 populations. MW, TD, and LD, similar to PT, NL, and LC, were relevant for distinguishing the group formed by the UFU SDi 13-1 population.

4. Discussion

It has been reported that tomato plant characteristics should be prioritized to obtain future cultivars, especially with regard to the various biotic (Ferrero et al., 2020; Zanin et al., 2021) and abiotic

Table 1
Agronomic traits evaluated in 19 BC₁F₃ tomato plant populations, the recurrent parent, donor parent, and commercial control. Monte Carmelo, MG, Brazil, 2020.

Genotypes	MW			LD			TD			FS			PT			NL			IL			ZGB		
UFU SDi 11-4	17.38	i	*	4.59	e	*	2.75	e	*	1.67	b	*	0.46	e	*	2.28	d	ns	2.36	b	*	0.10	c	*
UFU SDi 17-8	21.62	g	*	4.86	e	*	2.98	e	*	1.63	b	*	0.51	e	*	2.34	d	ns	2.16	c	*	0.08	c	*
UFU SDi 7-4	25.50	f	*	4.78	e	*	3.08	d	*	1.56	c	*	0.55	d	*	2.45	c	*	1.66	d	ns	0.17	b	*
UFU SDi 17-5	20.39	h	*	4.85	e	*	3.00	e	*	1.62	c	*	0.49	e	*	2.45	c	*	2.07	c	*	0.06	d	*
UFU SDi 4-3	23.35	g	*	4.84	e	*	3.05	d	*	1.59	c	*	0.54	d	*	2.44	c	*	1.73	d	ns	0.06	d	*
UFU SDi 5-4	26.31	f	*	5.18	d	*	3.15	d	*	1.65	b	*	0.57	d	*	2.47	c	*	1.94	d	*	0.16	b	*
UFU SDi 17-7	18.54	h	*	4.88	e	*	2.96	e	*	1.65	b	*	0.52	d	*	2.57	c	*	2.03	c	*	0.09	c	*
UFU SDi 13-1	41.89	c	*	5.49	c	*	3.75	b	*	1.46	d	*	0.76	b	*	2.65	b	*	2.02	c	*	0.13	b	*
UFU SDi 13-2	19.33	h	*	4.81	e	*	2.79	e	*	1.73	b	ns	0.46	e	*	2.53	c	*	1.96	d	*	0.11	c	*
UFU SDi 17-1	30.22	e	*	5.49	c	*	3.43	c	*	1.60	c	*	0.60	c	*	2.47	c	*	1.96	d	*	0.10	c	*
UFU SDi 13-3	22.73	g	*	4.79	e	*	3.00	e	*	1.60	c	*	0.45	e	*	2.74	b	*	1.71	d	ns	0.05	d	*
UFU SDi 7-2	25.20	f	*	4.66	e	*	3.08	d	*	1.52	d	*	0.51	e	*	2.85	b	*	1.91	d	*	0.16	b	*
UFU SDi 11-5	16.46	i	*	4.53	e	*	2.86	e	*	1.59	c	*	0.46	e	*	2.45	c	*	2.08	c	*	0.05	d	*
UFU SDi 10-5	22.71	g	*	4.05	f	*	2.82	e	*	1.44	d	*	0.44	e	*	2.58	c	*	1.89	d	*	0.14	b	*
UFU SDi 4-6	26.37	f	*	4.81	e	*	3.10	d	*	1.56	c	*	0.50	e	*	2.82	b	*	1.82	d	*	0.10	c	*
UFU SDi 17-9	19.36	h	*	5.14	d	*	2.90	e	*	1.78	a	ns	0.49	e	*	2.30	d	ns	2.44	b	*	0.12	b	*
UFU SDi 17-6	22.03	g	*	5.00	e	*	3.02	d	*	1.66	b	*	0.48	e	*	2.47	c	*	2.40	b	*	0.04	d	*
UFU SDi 18-1	33.86	d	*	5.75	c	*	3.22	d	*	1.79	a	ns	0.62	c	*	2.73	b	*	2.18	c	*	0.08	c	*
UFU SDi 6-1	25.68	f	*	4.66	e	*	3.08	d	*	1.51	d	*	0.56	d	*	2.48	c	*	2.31	b	*	0.07	d	*
UFU MC TOM5	74.34	a	*	7.53	a	*	4.48	a	*	1.69	b	*	0.94	a	*	3.38	a	*	6.93	a	*	0.05	d	*
Pizzadoro	55.43	b	*	6.33	b	*	4.30	a	*	1.50	d	*	0.95	a	*	2.78	b	*	6.79	a	*	0.03	d	*
UFU TOM 1	5.00	j		3.44	g		1.85	f		1.87	a		0.21	f		2.00	e		1.31	e		0.22	a	
Mean	26.95			5.01			3.12			1.62			0.55			2.55			9.35			0.10		
%CV	4.38			4.86			5.57			4.57			6.92			6.15			2.44			28.23		
h ²	99.32			97.67			97.31			88.13			98.63			91.58			97.66			91.87		
CV _g	53.35			15.76			16.76			6.24			29.41			10.14			59.51			47.98		
CV _g /CV _e	12.36			3.24			3.00			1.36			4.24			1.64			6.36			1.68		

MW: mean fruit weight (g); LD: longitudinal diameter (cm); TD: transverse diameter (cm); FS: fruit shape; PT: pulp thickness (cm); NL: number of locules (locules per fruit); IL: internode length (cm); ZGB: zingiberene content (270 nm). ¹Mean values followed by different letters in the column differ from each other by the Scott-Knott test at 0.05. *Mean values in the column differ from the UFU MC TOM 1 dwarf donor line control by the Dunnett test at a level of 0.05. h²: genotypic coefficients of determination; CV_g: genetic coefficients of variation; CV_g/CV_e: ratio between genetic and environmental coefficients of variation.

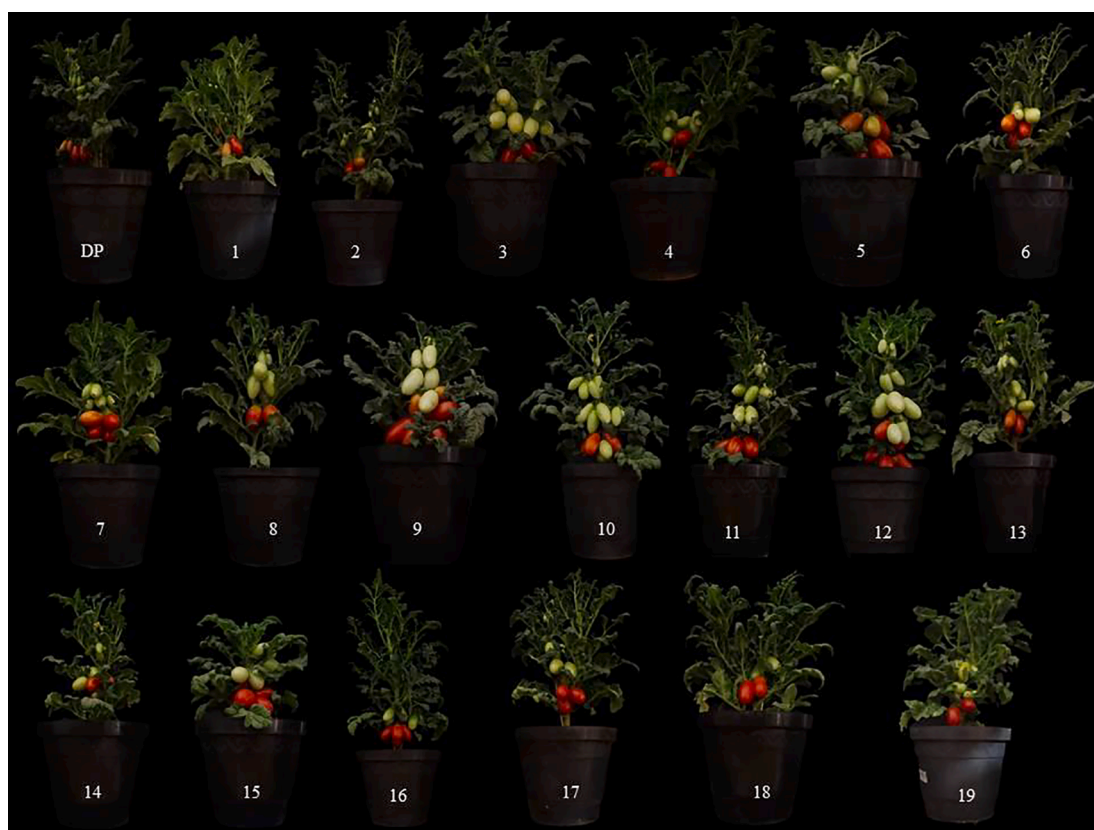


Fig. 1. Comparison among dwarf phenotype tomato plants: DP = donor parent; 1 = UFU SDi 11-4; 2 = UFU SDi 17-8; 3 = UFU SDi 7-4; 4 = UFU SDi 17-5; 5 = UFU SDi 4-3; 6 = UFU SDi 5-4; 7 = UFU SDi 17-7; 8 = UFU SDi 13-1; 9 = UFU SDi 13-2; 10 = UFU SDi 17-1; 11 = UFU SDi 13-3; 12 = UFU SDi 7-2; 13 = UFU SDi 11-5; 14 = UFU SDi 10-5; 15 = UFU SDi 4-6; 16 = UFU SDi 17-9; 17 = UFU SDi 17-6; 18 = UFU SDi 18-1; 19 = UFU SDi 6-1.

stressors (Oliveira et al., 2021; Wen et al., 2021), as well as the nutritional quality of the fruit (Londoño-Giraldo et al., 2020; Gomes et al., 2021; Oliveira et al., 2022) for a healthy diet (Asensio et al., 2019). A major obstacles to this is the narrow genetic base of the tomato germplasm (Hassan et al., 2021).

Several studies have sought to increase genetic variability and gene introgression by using interspecific crosses of wild species (Peixoto et al., 2020; Zanin et al., 2021). However, the biggest challenge has been in recovering the agronomic potential and nutritional quality of the fruits after each crossing with wild species (Peixoto et al., 2020; Dariva et al., 2021).

In order to conduct the introgression of genes of interest for different types of biotic stress and fruit nutritional quality, and promote higher productivity, research with dwarf tomato plants has been intensified (Maciel et al., 2015; Finzi et al., 2017; Finzi et al., 2020; Cavasin et al., 2021; Gomes et al., 2021; Oliveira et al., 2022). The use of dwarf plants has provided multiple advantages, and obtaining saladette/roma dwarf tomato populations is a promising technology for the future development of higher yielding hybrids, similar to that observed with cherry/grape tomatoes (Finzi et al., 2017).

The potential of dwarf plants is clear for the provision of gene introgression aimed at several agronomic, morphological, and nutritional advantages and a broad spectrum of pest resistance (Tables 1 and 2). Plants with shorter internodes have been used in breeding programs for various crops, and improvements have been reported in yield and plant architecture when a dwarf parent is used (Finzi et al., 2017; Wu et al., 2018; Cho et al., 2021). The dwarf tomato plant populations obtained in this study exhibited short internodes and could be viable alternatives for increasing the yield of future hybrid tomato plants, and thereby obtain plants with more compact architecture that will facilitate management and harvest activities (Frasca et al., 2014; Sun et al., 2019).

The superiority in the size of the tomatoes of the BC_1F_3 dwarf populations compared to those produced by the donor parent confirms the success of the breeding method used in this study. The increase in tomato fruit size is associated with increases in MW, TD, LD, PT, and NL (Marques et al., 2019; Tijksens et al., 2020). Similar results were observed by Finzi et al. (2020), who evaluated the same agronomic variables and reported the superiority of the BC_1F_2 dwarf populations of round type tomatoes in relation to the dwarf donor parent belonging to the cherry/grape segment.

Elongated fruit were predominant among the BC_1F_3 dwarf populations, parents, and commercial control, since all genotypes had a FS index greater than 1. The increase in fruit size and the FS index ($LD/TD > 1.5$) corroborate the standard exhibited by the saladette/roma type tomato fruit (Andrade et al., 2014).

Fruit firmness is generally related to a smaller NL and greater PT (Rodrigues et al., 2010; Amaral Júnior et al., 2017). Thus, the UFU SDi 13-1 population proved to be promising for obtaining firmer fruit.

Resistance to arthropod pests by antixenosis and antibiosis mechanisms has been correlated with high ZGB levels in tomato plant leaflets (Rezende et al., 2020; Zanin et al., 2021). The BC_1F_3 populations had ZGBs that were intermediate to that of the parents. According to Oliveira et al. (2020a), this response is indicative of incomplete dominance of gene activity for this trait. The superiority of ZGB in 68.4% of BC_1F_3 populations of dwarf tomato in relation to the commercial cultivar Pizzadoro reveals the potential of this germplasm for the resistance to a broad spectrum of pests. There is great interest in the introgression of genes related to the presence of this allelochemical in cultivated tomatoes (Rezende et al., 2020). The plants of the populations obtained in this study can be considered excellent alternatives to increase productivity (Finzi et al., 2017) and resistance to pests (Zanin et al., 2021), and minimize the period of the crop genetic improvement program.

Table 2

Fruit quality traits evaluated in 19 BC₁F₃ tomato populations and the recurrent parent, donor parent, and commercial control. Monte Carmelo, MG, Brazil, 2020.

Genotypes	SS	LC	BCC
UFU SDi 11-4	5.01c *	2.77 a	1.61b
UFU SDi 17-8	5.18c *	3.55 a	2.24 a
UFU SDi 7-4	4.50 d *	3.52 a	1.72b
UFU SDi 17-5	5.26c *	2.34b	1.41b *
UFU SDi 4-3	6.28b *	2.91 a	1.61b
UFU SDi 5-4	5.05c *	2.75 a	1.75b
UFU SDi 17-7	5.10c *	3.07 a	2.25 a
UFU SDi 13-1	5.40c *	3.34 a	2.32 a
UFU SDi 13-2	4.82 d *	1.89b	1.99 a
UFU SDi 17-1	4.64 d *	2.87 a	1.61b
UFU SDi 13-3	4.32 d *	2.27b	1.20b *
UFU SDi 7-2	5.25c *	1.88b	1.49b *
UFU SDi 11-5	5.18c *	2.88 a	1.88 a
UFU SDi 10-5	5.32c *	2.79 a	1.59b
UFU SDi 4-6	5.45c *	2.41b	1.37b *
UFU SDi 17-9	5.85b *	2.60b	1.84 a
UFU SDi 17-6	5.10c *	3.09 a	1.98 a
UFU SDi 18-1	5.55c *	3.12 a	2.05 a
UFU SDi 6-1	4.93c *	3.38 a	1.91 a
UFU MC TOM5	5.21c *	2.43b	1.65b
Pizzadoro	5.73b *	2.63b	1.49b *
UFU TOM1	7.10 a	2.71 a	2.39 a
Mean	5.28	2.77	1.78
%CV	6.86	22.57	28.53
h ²	90.73	54.06	51.87
CV _g	10.74	12.54	13.15
CV _g /CV _e	1.56	0.54	0.51

SS: soluble solids content (°Brix); LC: lycopene content (mg/100 g); BCC: β-carotene content (mg/100 g). ¹Mean values followed by different letters in the column differ from each other by the Scott-Knott test at 0.05. *Mean values in the column differ from the UFU MC TOM 1 dwarf donor line control by the Dunnett test at a level of 0.05. h²: genotypic coefficients of determination; CV_g: genetic coefficients of variation; CV_g/CV_e: ratio between genetic and environmental coefficients of variation.

The saladette/roma tomato is prominent among the traditional fresh tomato segments, as it has an SS that ranges from 4 to 5 °Brix, leading to a better taste and sweeter flavor of the tomato fruit (Ikeda et al., 2013; Schwarz et al., 2013). In the present study, the SS of the fruit produced by the BC₁F₃ dwarf populations was similar to that of the recurrent parent and the Pizzadoro commercial cultivar that belongs to the saladette/roma segment. In addition, the mean values expressed for this trait corroborate the SS found in saladette/roma tomato hybrids,

showing that the populations are promising for this segment (Andrade et al., 2014).

An increase in LC and BCC in tomato fruit is one of the aims of crop breeding programs (Hazra et al., 2018; Londoño-Giraldo et al., 2020; 2021). Therefore, the characterization of germplasm regarding the levels of these carotenoids can provide relevant information to achieve this aim. In this study, LC and BCC were expressive and consistent, corroborating the values obtained by Bhandari et al. (2021) and Asensio et al. (2019), respectively.

The change in eating habits toward an adequate caloric intake and efficient nutritional scheme has stimulated research into the development of biofunctional foods for improved health and reduction of disease risk (Stajčić et al., 2015; Asensio et al., 2019; Athinodorou et al., 2021). The populations BC₁F₃: UFU SDi 6-1, UFU SDi 11-5, UFU SDi 13-1, UFU SDi 17-8, UFU SDi 17-7, UFU SDi 17-6, and UFU SDi 18-1 evaluated in this study are promising for aggregating these traits in a

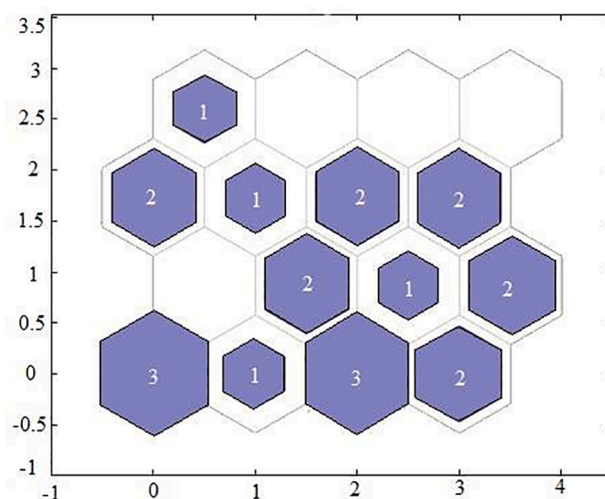


Fig. 3. Kohonen self-organizing map for twelve classification classes, formed by the artificial neural network. Class 1: row 1 column 1; Class 2: row 1 column 2; Class 3: row 1 column 3; Class 4: row 1 column 4; Class 5: row 2 column 1; Class 6: row 2 column 2; Class 7: row 2 column 3; Class 8: row 2 column 4; Class 9: row 3 column 1; Class 10: row 3 column 2; Class 11: row 3 column 3; Class 12: row 3 column 4; Class 13: row 4 column 1; Class 14: row 4 column 2; Class 15: row 4 column 3; Class 16: row 4 column 4.

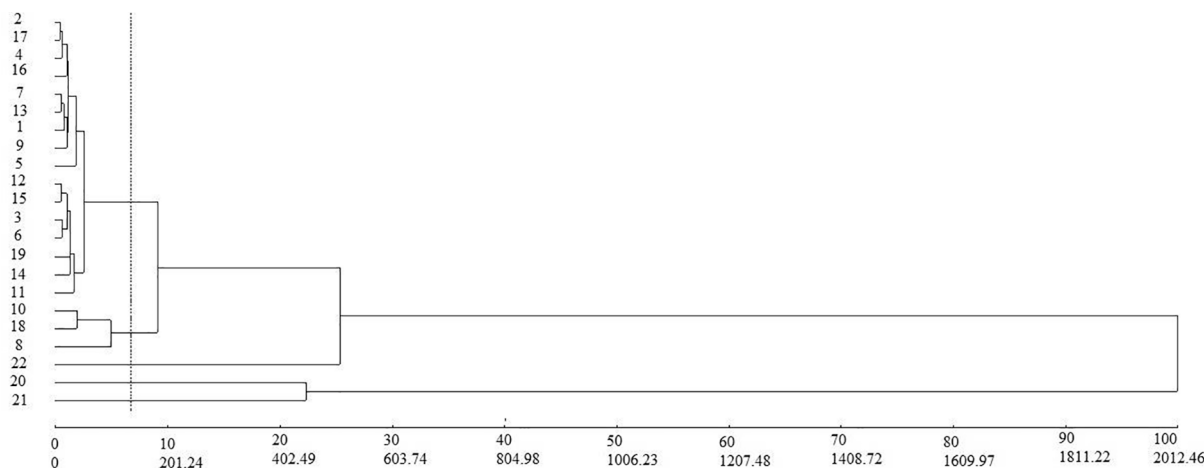


Fig. 2. Dendrogram of genetic divergence obtained by the unweighted pair-group method with arithmetic mean “UPGMA” based on Mahalanobis generalized distance: 1 = UFU SDi 11-4; 2 = UFU SDi 17-8; 3 = UFU SDi 7-4; 4 = UFU SDi 17-5; 5 = UFU SDi 4-3; 6 = UFU SDi 5-4; 7 = UFU SDi 17-7; 8 = UFU SDi 13-1; 9 = UFU SDi 13-2; 10 = UFU SDi 17-1; 11 = UFU SDi 13-3; 12 = UFU SDi 7-2; 13 = UFU SDi 11-5; 14 = UFU SDi 10-5; 15 = UFU SDi 4-6; 16 = UFU SDi 17-9; 17 = UFU SDi 17-6; 18 = UFU SDi 18-1; 19 = UFU SDi 6-1; 20 = UFU MC TOM 5; 21 = Pizzadoro; 22 = UFU TOM 1.

Table 3

Grouping obtained by classification of the observations of the clusters (4×4 of radius 1) of genotypes in the classes formed through the artificial neural network by SOM.

Groups	Classes	Genotypes
I	1	UFU SDi 7-2; UFU SDi 10-5; UFU SDi-4-6
II	2	UFU SDi 13-3
III	3	UFU SDi 11-4; UFU SDi 17-5; UFU SDi 13-2
IV	4	UFU SDi 17-9; UFU SDi 4-3
VII	6	UFU SDi 17-6; UFU SDi 18-1
VI	7	UFU SDi 11-5
V	8	UFU SDi 5-4; UFU SDi 17-1
VIII	9	UFU MC TOM 5; cv. Pizzadoro
IX	10	UFU SDi 13-1
X	11	UFU SDi 6-1; UFU SDi 7-4
XI	12	UFU SDi 17-8; UFU SDi 17-7
XII	13	UFU TOM 1

saladette/roma type dwarf tomato plant breeding program to obtain a functional food rich in antioxidants, given its superiority over the recurring parent and the commercial cultivar Pizzadoro. Saladette/Italian tomato cultivars have gained popularity in the tabletop consumption market because of their high SS, pleasant aroma, PT, and texture (Shirahige et al., 2010; Andrade et al., 2014).

However, there are few studies on LC and BCC for the fruits of this segment. The populations that presented greater contents of these compounds than the Pizzadoro cultivar expressed an average of 2.09 and 3.20 mg/100 g for BCC and LC, respectively. Seabra Junior et al. (2022) evaluated six commercial Italian tomato cultivars and reported BCC and LC below 1.33 mg/100 g and 2.73 mg/100 g, respectively. This demonstrates that saladette-type dwarf tomato plants have the potential to increase crop productivity (Finzi et al., 2017) and improve the fruit quality of future hybrids and cultivars.

Univariate analyses were important for the comparison of the individual performance of each genotype evaluated in this study. The high magnitude of the genetic parameters (h^2 and CV_g/CV_e ratio) for most of the traits evaluated reaffirms the genetic variability among the genotypes (Laviola et al., 2014).

The genetic dissimilarity among the genotypes evaluated was well represented by the UPGMA clustering method, which showed an adequate relationship between the representation and the Mahalanobis

distance (D^2) matrix (Cruz et al., 2012). Through this method, genetic dissimilarity was found between the BC_1F_3 populations, parents, and the commercial cultivar by the formation of five groups. This methodology is traditionally used to represent genetic dissimilarity among tomato plant populations in various segments (Maciel et al., 2018; Finzi et al., 2020; Peixoto et al., 2020).

SOMs are obtained by computational intelligence tools through neural networks, and they are promising technologies in the study of genetic dissimilarity among populations (Santos et al., 2019). Such maps allow the visualization of similar patterns and classification of data based on the distances between them (Oliveira et al., 2020b). The hexagonal topology used in this study allowed for a better arrangement of the neurons and a minimization of possible errors in the classification process (Kohonen, 2014). The organization of the topological structure reflects the similarity among the genotypes under study, allowing for classification by approximation (Santos et al., 2019; Gomes et al., 2021).

The SOM had a greater discriminating power among the genotypes compared to the UPGMA method. While the UPGMA clustering method allocated the BC_1F_3 dwarf populations into two groups, the SOM, distributed them among ten groups. The better capacity of the SOM in discriminating the genotypes in relation to the UPGMA method was also reported by Cardoso et al. (2021), who compared the two methods in the evaluation of genetic dissimilarity of colored cotton genotypes. Gomes et al. (2021) classified salad-type dwarf tomato populations and also observed a greater number of groups by the SOM method than the UPGMA method, and determined that this methodology was more efficient for studying the genetic dissimilarity in dwarf tomato germplasm.

The differences found in the clustering performed by the two methodologies used in this study can be explained by the fact that the dendrogram obtained by D^2 takes the means and variances of the traits under study into consideration in the clustering process (Cruz et al., 2012). However, in the Kohonen method, clustering is not affected by experimental errors, and this method has a strong ability to simulate neural networks, which amplify the input data and estimate new values with different synaptic weights for each neuron, and organize the groups by order of proximity based on Euclidean distance (Oliveira et al., 2020b).

One of the advantages of using the Kohonen network in relation to other multivariate techniques is the ability to determine the weights of the variables in the formation of the groups and visualize the related

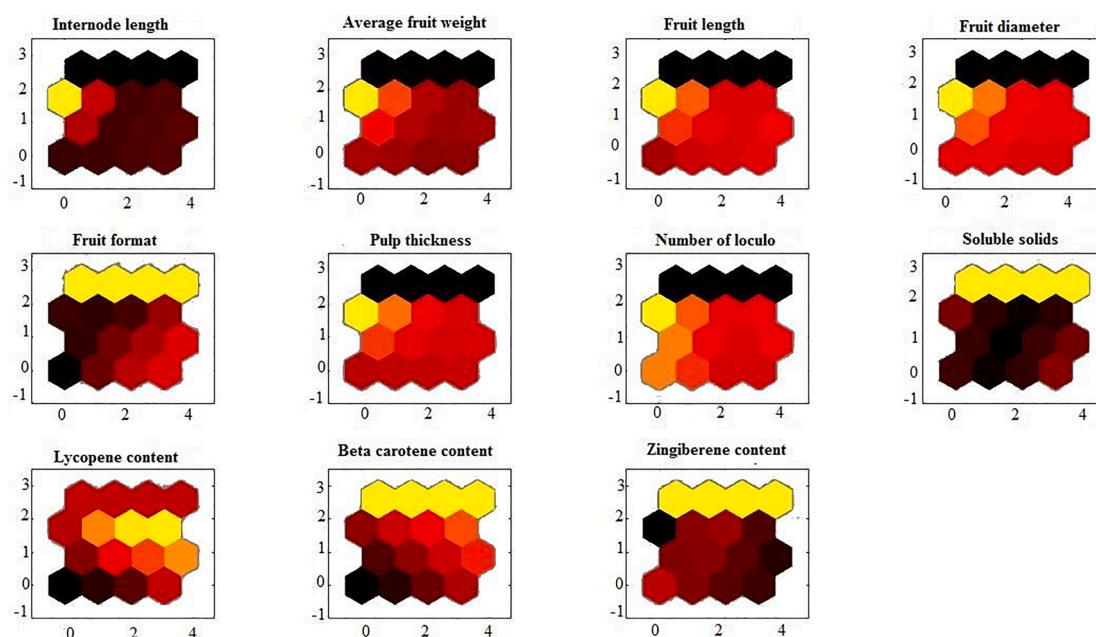


Fig. 4. Traits and weights in the activation of each SOM neuron. Lighter colors represent greater effect of a variable on the group determined by the neuron.

correlations (Cardoso et al., 2021; Gomes et al., 2021). The similarity in the patterns of colors observed for the MW, LD, and TD, and PT traits emphasizes their correlations, showing that these traits are closely related to fruit size (Tijskens et al., 2020).

The traits that distinguished the donor parent (UFU TOM 1) were FS, SS, BCC, and ZGB. In means comparison testing, this genotype showed superior results for these traits. The association between the univariate analyses and SOM showed that UFU TOM 1 is a promising line for improving fruit quality and pest resistance in tomato plant breeding programs.

Distinction of the group formed by the UFU SDi 13-1 population was important for confirming the superiority of this population over the rest for traits related to fruit size and quality.

5. Conclusions

The SOM was more consistent in distinguishing genetic similarity among the BC₁F₃ populations of saladette/roma type dwarf tomato plants, resulting in a larger number of clusters.

The UFU SDi 13-1 BC₁F₃ dwarf population revealed agronomic potential and superior fruit quality, and is a promising population for the saladette/roma type dwarf tomato plant breeding program.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

The authors thank the Federal University of Uberlândia (UFU), the Minas Gerais State Research Foundation (FAPEMIG), the National Council for Scientific and Technological Development (CNPq), and the Coordination for the Improvement of Higher Education Personnel (CAPES) for funding this research.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.fochms.2021.100056>.

References

- Almeida, V. S., Silva, D. J. H., Gomes, C. N., Antonio, A. C., Moura, A. D., & Lima, A. L. R. (2015). Sistema Viçosa para o cultivo de tomateiro. *Horticultura Brasileira*, 33, 74–79. <https://doi.org/10.1590/S0102-053620150000100012>
- Alsamir, M., Ahmad, N., Arief, V., Mahmood, T., & Trethowan, R. (2019). Phenotypic diversity and marker-trait association studies under heat stress in tomato (*Solanum lycopersicum* L.). *Aust. J. Crop Sci.*, 13, 578–587. <https://doi.org/10.21475/ajcs.19.13.04.p1581>
- Alvarenga, M. A. R. (2013). *Tomate: produção em campo, em casa-de-vegetação e em hidroponia* (2th ed.). Lavras: Editora UFLA.
- Amaral Júnior, A. T., Graça, A. J., Vivas, M., Viana, A. P., & Rodrigues, R. (2017). Prospecting of tomato hybrids for table and industry via mixed modeling and multivariate analysis. *Horticultura Brasileira*, 35, 20–25. <https://doi.org/10.1590/s0102-053620170104>
- Andrade, M. C., Silva, A. A., Conrado, T. V., Maluf, W. R., Andrade, T. M., & Oliveira, C. D. (2014). Capacidade combinatória de linhagens de tomateiro em híbridos do tipo italiano. *Bragantia*, 73, 237–245. <https://doi.org/10.1590/1678-4499.0039>
- Asensio, E., Sanvicente, I., Mallor, C., & Menal-puey, S. (2019). Spanish traditional tomato. Effects of genotype, location and agronomic conditions on the nutritional quality and evaluation of consumer preferences. *Food Chem.*, 270, 452–458. <https://doi.org/10.1016/j.foodchem.2018.07.131>
- Athinodorou, F., Foukas, P., Tsaniklidis, G., Kotsiras, A., Chrysargyris, A., Delis, C., ... Nikoloudakis, N. (2021). Morphological diversity, genetic characterization and phytochemical evaluation of cyprotot tomato germplasm. *Plants*, 10, 1–24. <https://doi.org/10.3390/plants10081698>
- Barbosa, C. D., Viana, A. P., Quintal, S. S. R., & Pereira, M. G. (2011). Artificial neural network analysis of genetic diversity in *Carica papaya* L. *Crop Breeding Appl. Biotechnol.*, 11, 224–231. <https://doi.org/10.1590/S1984-70332011000300004>
- Bhandari, H. R., Srivastava, K., Tripathi, M. K., Chaudhary, B., & Biswas, S. (2021). Genotype-environment interaction for quality traits in tomato hybrids. *Agric. Res.*, 1–8. <https://doi.org/10.1007/s40003-021-00579-3>
- Cardoso, D. B. O., Medeiros, L. A., Carvalho, G. O., Pimentel, I. M., Rojas, G. X., Souza, L. A., ... Sousa, L. B. (2021). Use of computational intelligence in the genetic divergence of colored cotton plants. *Biosci. J.*, 37, 1–9. <https://doi.org/10.14393/BJv37n0a202153634>
- Cavasin, P. Y., Fumes, L. A. A., Fonseca, A. R., & Silva, D. J. H. (2021). Evaluation of families derived from backcrosses of processed tomato with dwarfism gene. *Crop Breed. Appl. Biotechnol.*, 21, 1–5. <https://doi.org/10.1590/1984-70332021v21n1n13>
- Cho, Y., Lee, S., Park, J., Kwon, S., Park, G., Kim, H., & Park, Y. (2021). Identification of a candidate gene controlling semi-dwarfism in watermelon, *Citrullus lanatus*, using a combination of genetic linkage mapping and QTL-seq. *Hortic. Environ. Biotechnol.*, 1–13. <https://doi.org/10.1007/s13580-020-00330-x>
- Cruz, C. D. (2016). Genes Software – extended and integrated with the R, Matlab and Selegen. *Acta Scientiarum. Agronomy*, 38, 547–552. <https://doi.org/10.4025/actasciagr.v38i4.32629>
- Cruz, C. D., & Nascimento, M. (2018). *Inteligência computacional aplicada ao melhoramento genético* (1th ed.). Viçosa: Editora UFV.
- Cruz, C. D., Regazzi, A. J., & Carneiro, P. C. S. (2012). *Modelos biométricos aplicados ao melhoramento genético* (4th ed.). Viçosa: Editora UFV.
- Dariva, F. D., Pessoa, H. P., Copati, M. G. F., de Almeida, G. Q., de Castro Filho, M. N., Picoli, E. A. T., & Nick, C. (2021). Yield and fruit quality attributes of selected tomato introgression lines subjected to long-term deficit irrigation. *Sci. Hortic.*, 289, 1–11. <https://doi.org/10.1016/j.scienta.2021.110426>
- Ferrero, V., Baeten, L., Blanco-Sánchez, L., Planelló, R., Díaz-Pendón, J. A., Rodríguez-Echeverría, S., ... de la Peña, E. (2020). Complex patterns in tolerance and resistance to pests and diseases underpin the domestication of tomato. *New Phytol.*, 226, 254–266. <https://doi.org/10.1111/nph.16353>
- Finzi, R. R., Maciel, G. M., Perez, H. G., Silva, M. F., Peixoto, J. V. M., & Gomes, D. A. (2020). Agronomic potential of BC₁F₂ dwarf round tomato populations. *Ciência e Agrotecnologia*, 44, Article e028819. <https://doi.org/10.1590/1413-7054202044028819>
- Finzi, R. R., Maciel, G. M., Silva, E. C., Luz, J. M. Q., & Borba, M. E. A. (2017). Agronomic performance of mini-tomato hybrids from dwarf lines. *Ciência e Agrotecnologia*, 4, 15–21. <https://doi.org/10.1590/1413-70542017411021416>
- Frasca, A. C., Ozores-Hampton, M., Scott, J., & Mcavoy, E. (2014). Effect of plant population and breeding lines on fresh-market, compact growth habit tomatoes growth, flowering pattern, yield, and postharvest quality. *HortScience*, 49, 1529–1536. <https://doi.org/10.21273/HORTSCI.49.12.1529>
- Freitas, J. A., Maluf, W. R., Cardoso, M. G., & Benites, F. R. G. (2000). Métodos para quantificação do zingibereno em tomateiro, visando à seleção indireta de plantas resistentes aos artrópodes-praga. *Acta Scientiarum. Agronomy*, 22, 943–949. <https://doi.org/10.4025/actasciagr.v22i0.2823>
- Gomes, D. A., Maciel, G. M., Siquieroli, A. C. S., Oliveira, C. S., Finzi, R. R., & Marques, D. J. (2021). Selection of BC₁F₃ populations of Santa Cruz type dwarf tomato plant by computational intelligence techniques. *Bragantia*, 80, 1–12. <https://doi.org/10.1590/1678-4499.20210046>
- Hassan, Z., Ul-Allah, S., Khan, A. A., Shahzad, U., Khurshid, M., Bakhsh, A., ... Manzoor, Z. (2021). Phenotypic characterization of exotic tomato germplasm: An excellent breeding resource. *PLoS One*, 16, 1–12. <https://doi.org/10.1371/journal.pone.0253557>
- Hazra, P., Longjam, M., & Chattopadhyay, A. (2018). Stacking of mutant genes in the development of “purple tomato” rich in both lycopene and anthocyanin contents. *Sci. Hortic.*, 239, 253–258. <https://doi.org/10.1016/j.scienta.2018.05.039>
- Ikeda, H., Hiraga, M., Shirasawa, K., Nishiyama, M., Kanahama, K., & Kanayama, Y. (2013). Analysis of a tomato introgression line, IL8-3, with increased Brix content. *Sci. Hortic.*, 153, 103–108. <https://doi.org/10.1016/j.scienta.2013.02.006>
- Kavzoglu, T., Mather, P.M. (2003). The use of back propagating artificial neural networks in land cover classification. *Int. J. Remote Sens.* 24, 4907–4938. [10.1080/0143116031000114851](https://doi.org/10.1080/0143116031000114851)
- Kohonen, T. (2014). MATLAB implementations and applications of the self-organizing map. Unigrafia Oy, Helsinki, Finland.
- Laviola, B. G., Silva, S. D. A., Juhász, A. C. P., Rocha, R. B., Oliveira, R. J. B., Albrecht, J. C., ... Rosado, T. B. (2014). Desempenho agrônomico e ganho genético pela seleção de pinhão-mansão em três regiões do Brasil. *Pesquisa Agropecuária Brasileira*, 49, 356–363. <https://doi.org/10.1590/S0100-204X2014000500005>
- Londoño-Giraldo, L. M., Baena-Pedroza, A. M., Martínez-Seidel, F., Corpas-Iguarán, E., & Taborda-Ocampo, G. (2021). Gene wild: Integration of antioxidative, physicochemical, volatilmic and sensorial profiles ratify rustic relatives of cherry tomato as ideal mating partners. *Sci. Hortic.*, 277, 1–10. <https://doi.org/10.1016/j.scienta.2020.109814>
- Londoño-Giraldo, L. M., Gonzalez, J., Baena, A. M., Tapasco, O., Corpas, E. J., & Taborda, G. (2020). Selection of promissory crops of wild cherry-type tomatoes using physicochemical parameters and antioxidant contents. *Bragantia*, 79, 169–179. <https://doi.org/10.1590/1678-4499.20190276>
- Maciel, G. M., Finzi, R. R., Carvalho, F. J., Marquez, G. R., & Clemente, A. A. (2018). Agronomic performance and genetic dissimilarity among cherry tomato genotypes. *Horticultura Brasileira*, 36, 167–172. <https://doi.org/10.1590/s0102-053620180203>
- Maciel, G. M., Silva, E. C., & Fernandes, M. A. R. (2015). Ocorrência de nanismo em planta de tomateiro do tipo grape. *Revista Caatinga*, 28, 259–264. <https://doi.org/10.1590/1983-21252015v28n429rc>
- Maham, S. G., Rahimi, A., Subramanian, S., & Smith, D. L. (2020). The environmental impacts of organic greenhouse tomato production based on the nitrogen-fixing plant (*Azolla*). *J. Cleaner Prod.*, 245, Article 118679. <https://doi.org/10.1016/j.jclepro.2019.118679>

- Marques, M. J., Vizú, J. F., Silva Filho, D. F., & Ticona-Benavente, C. A. (2019). Tomato progenies selection in Rondônia, Brazil. *Horticultura Brasileira*, 37, 106–111. <https://doi.org/10.1590/S0102-053620190117>
- Oliveira, C. S., Maciel, G. M., Fraga Júnior, E. F., Peixoto, J. V. M., Assunção, V. B., & Marques, D. J. (2021). Selection of tomato genotypes for drought tolerance and agronomic potential through different selection indexes. *Horticultura Brasileira*, 39, 102–111. <https://doi.org/10.1590/s0102-0536-20210115>
- Oliveira, C. S., Maciel, G. M., Siquieroli, A. C. S., Gomes, D. A., Martins, M. P. C., & Finzi, R. R. (2022). Selection of F₂RC₁ saladette-type dwarf tomato plant populations for fruit quality and whitefly resistance. *Rev. Bras. Eng. Agríc. Ambiental*, 26, 28–35. <https://doi.org/10.1590/1807-1929/agriambi.v26n1p28-35>
- Oliveira, J. R. F., Resende, J. T. V., Filho, R. B. L., Roberto, S. R., Silva, P. R., Rech, C., & Nardi, C. (2020a). Tomato breeding for sustainable crop systems: high levels of zingiberene providing resistance to multiple arthropods. *Horticulturae*, 6, 34. <https://doi.org/10.3390/horticulturae6020034>
- Oliveira, M. S., Santos, I. G., & Cruz, C. D. (2020b). Self-organizing maps: A powerful tool for capturing genetic diversity patterns of populations. *Euphytica*, 216, 49. <https://doi.org/10.1007/s10681-020-2569-0>
- Peixoto, J. V. M., Ribeiro, A. L. A., Maciel, G. M., Oliveira, C. S., Finzi, R. R., & Moraes, E. R. (2020). Productivity, acylsugar concentrations and resistance to the two-spotted spider mite in genotypes of salad tomatoes. *Revista Brasileira de Engenharia Agrícola e Ambiental*, 24, 596–602. <https://doi.org/10.1590/1807-1929/agriambi.v24n9p596-602>
- Rezende, J. F., Aoun, C. A., Oliveira, A. M. S., Nomura, J. V., Conrado, T. V., Gouveia, B. T., & Maluf, W. R. (2020). The reaction of tomato genotypes to whitefly-transmitted ToYVSV influenced by allelochemicals and the genes Mi, Ty-1, Ty-2, and Ty-3/Ty-4. *Sci. Hortic.*, 270, Article 109428. <https://doi.org/10.1016/j.scienta.2020.109428>
- Rodrigues, G. B., Marim, B. G., Silva, D. J. H. D., Mattedi, A. P., & Almeida, V. D. S. (2010). Análise de trilha de componentes de produção primários e secundários em tomateiro do grupo Salada. *Pesquisa Agropecuária Brasileira*, 45, 155–162. <https://doi.org/10.1590/S0100-204X2010000200006>
- Rodriguez-Amaya, D. B. (2001). *A Guide to Carotenoid Analysis in Foods*. Washington: International Life Sciences Institute Press.
- Rodriguez-Amaya, D. B., & Kimura, M. (2004). *Handbook for Carotenoid Analysis*. Washington: HarvestPlus.
- Santos, I. G., Carneiro, V. Q., Silva Junior, A. C., Cruz, C. D., & Soares, P. C. (2019). Self-organizing maps in the study of genetic diversity among irrigated rice genotypes. *Acta Scientiarum. Agronomy*, 41, Article e39803. <https://doi.org/10.4025/actasciagron.v41i1.39803>
- Santos, I. G., Rocha, J. D., Vigna, B. B., Cruz, C. D., Ferreira, R. P., Basigalup, D. H., & Marchini, R. M. S. (2020). Exploring the diversity of alfalfa within Brazil for tropical production. *Euphytica*, 216(72), 1–15. <https://doi.org/10.1007/s10681-020-02606-w>
- Schwarz, K., Resende, J. T. V., Preczenhak, A. P., Paula, J. T., Faria, M. V., & Dias, D. M. (2013). Desempenho agrônomo e qualidade físico-química de híbridos de tomateiro em cultivo rasteiro. *Horticultura Brasileira*, 31, 410–418. <https://doi.org/10.1590/S0102-05362013000300011>
- Seabra Junior, S., Casagrande, J. G., Toledo, C. A. L., Ponce, F. S., Ferreira, F. S., Zanuzo, M. R., ... Lima, G. P. P. (2022). Selection of thermotolerant Italian tomato cultivars with high fruit yield and nutritional quality for the consumer taste grown under protected cultivation. *Sci. Hortic.*, 291, Article 110559. <https://doi.org/10.1016/j.scienta.2021.110559>
- Shirahige, F. H., Melo, A. M. T., Purquerio, L. F. V., Carvalho, C. R. L., & Melo, P. C. T. (2010). Produtividade e qualidade de tomates Santa Cruz e Italiano em função do raleio de frutos. *Horticultura Brasileira*, 28, 292–298. <https://doi.org/10.1590/S0102-05362010000300009>
- Stajčić, S., Četković, G., Čanadanović-Brunet, J., Djilas, S., Mandić, A., & Četojević-Simin, D. (2015). Tomato waste: carotenoid content, antioxidant and cell growth activities. *Food Chem.*, 172, 225–232. <https://doi.org/10.1016/j.foodchem.2014.09.069>
- Sun, X. R., Liu, L., Zhi, X. N., Bai, J. R., Cui, Y. N., Shu, J. S., & Li, J. M. (2019). Genetic analysis of tomato internode length via mixed major gene plus polygene inheritance model. *Scientia Horticulturae*, 46, 759–764. <https://doi.org/10.1016/j.scienta.2018.11.044>
- Tijskens, L. L., Mourik, S. V., Dieleman, J. A., & Schouten, R. E. (2020). Size development of tomatoes growing in trusses: Linking time of fruit set to diameter. *J. Sci. Food Agric.*, 100, 4020–4028. <https://doi.org/10.1002/jsfa.10447>
- Wamser, A. F., Mueller, S., Suzuki, A., Becker, W. F., & Santos, J. P. (2012). Yield of tomato hybrids subjected to a super density cropping. *Horticultura Brasileira*, 30, 168–174. <https://doi.org/10.1590/S0102-05362012000100028>
- Wen, J., Jiang, F., Liu, M., Zhou, Sun, M., Shi, X., Zhu, Z., & Wu, Z. (2021). Identification and expression analysis of Cathepsin B-like protease 2 genes in tomato at abiotic stresses especially at High temperature. *Sci. Hortic.*, 277, 1–11. <https://doi.org/10.1016/j.scienta.2020.109799>
- Wu, Z., Tang, D., Liu, K., Miao, C., Zhuo, X., Li, Y., ... Cheng, Z. (2018). Characterization of a new semidominant dwarf allele of SLR1 and its potential application in hybrid rice breeding. *J. Exp. Bot.*, 69, 4703–4713. <https://doi.org/10.1093/jxb/ery243>
- Zanin, D. S., Resende, J. T. V., Zeist, A. R., Lima Filho, R. B., Gabriel, A., Diniz, F. C. P., ... Morales, R. G. F. (2021). Selection of F₂BC₁ tomato genotypes for processing containing high levels of zingiberene and resistant to tomato pinworms. *Phytoparasitica*, 49, 265–274. <https://doi.org/10.1007/s12600-020-00852-1>