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CROP BREEDING AND
APPLIED BIOTECHNOLOGY

Genetic diversity among tomato's subsamples for pre-breeding

João Paulo Alves de Castro[1], Carlos Nick[1*], Carla do Carmo Milagres[1], André Pugnal Mattedi[1], Bruno Garcia Marim[1], and Derly José Henrique da Silva[1]

ABSTRACT - *The aim of this work was to evaluate 56* Solanum lycopersicon *subsamples through agronomic descriptors, and to quantify their genetic diversity. Two essays were conducted with three replications in a randomized block design. There was significant variability among subsamples for all phenotypic descriptors. Four distinct groups were formed by the Tocher procedure, and there was a projection of distances in the plan. The efficiency of the group was denoted by the low apparent error rate of discriminant functions, 1.66%. The phenotypic traits that contributed most to the dissimilarity were: fruit length, width of the central axis, total commercial fruit number, commercial fruit weight and total fruit number. The following subsamples were considered promising for use in future breeding programs: BGH 7222, BGH 7267 and BGH 887, group 3, BGH 2143, BGH 6866 and BGH 7218, group 1 and the subsamples BGH 6889 and BGH 7213, group 2.*

Key words: *Solanum lycopersicon*, genetic resources, germplasm.

INTRODUCTION

The decrease in the intraspecific genetic diversity of cultivated species is a consequence of the continuous selection by breeders of more homogenous genotypes with more specific adaptability (Haussman et al. 2004). Consequently, modern cultivars replace the landraces without their due characterization (Goedert 2006).

The landraces present great variability for agronomic traits interest. However, in spite of their great potential as a source of variability, the lack of information about their origin, genealogy, agronomic performance and genetic background has hindered the use of these varieties in breeding programs (Carelli et al. 2006), causing a narrowing of the genetic base of the new cultivars.

The intraspecific genetic diversity of *Solanum lycopersicum* has decreased dramatically over time, characterizing the occurrence of genetic erosion. It is due to the development of cultivars with a limited number of genotypes, among other factors (Saavedra and Spoor 2002).

In Brazil, in the beginning of the twentieth century, only three varieties were used in the production of tomatoes (Rei Umberto, Pera and Perungo), with the introduction of new varieties occurring only near 1920. Another evidence of the narrowing of the genetic base is the breeding of the cultivar Santa Cruz, which, for decades, was based on the selection of individuals from the crossing between Redondo Japonês and Rei Humberto (Alvarenga 2004).

This narrowing increases the probability of pest occurrence and vulnerability, as well as diseases, and, considering the socioeconomic significance to tomato plants, a viable and necessary measure is to promote the decrease of the genetic erosion by introducing common and rare alleles locally distributed, from wild species, of local and traditional varieties.

[1] Universidade Federal de Viçosa, Departamento de Fitotecnia, 36570-000, Viçosa, MG, Brazil. *E-mail: carlos.nick@yahoo.com.br

The introduction of new alleles can be carried out because of the pre-breeding procedure and the development of works related to the characterization and evaluation of accessions preserved in collections and germplasm banks. The term subsamples (accessions) refers to the portion of the biological material or component of the genetic patrimony, properly accompanied by biological, chemical or documentary information which allows the background and taxonomic identification of the material, following the technical regulation number 2, of October 30th, 2003, of the Conselho de Gestão do Patrimônio Genético - CGEN (Council of Genetic Patrimony Management).

The main reason for the establishment and maintenance of a germplasm bank is to provide information about the preserved accessions, identifying significant characteristics for genetic breeding programs (Carvalho and Quesenberry 2009, Ramos et al. 2007, Nass and Paterniani 2000).

To evaluate the possible genetic contributions of the accessions, several statistical and biometric tools have been used for the study and discrimination of the variability existing in the banks. Among these, the multivariate techniques are noteworthy because they discriminate a great number of accessions, considering several characteristics at the same time, making them widely used for the study on diversity in several cultures.

The intraspecific diversity is strategically important to meet the increasing world demand for food and maintain the species' capacity to cope with climate changes and other kinds of stress. Therefore, studies aiming at estimating the diversity of several plant species have been reported for several cultures (Carvalho and Quesenberry 2009, Serqueira-Silva et al. 2009, Gonçalves et al. 2008, Mazzucato et al. 2008, Nick et al. 2008, Nizio et al. 2008, Rocha et al. 2008, Carelli et al. 2006, Karasawa et al. 2005, Silva et al. 2001).

Knowledge about similarity/dissimilarity may contribute for the rational planning of genetic breeding programs, the management optimization of the preserved germplasm and for the selection of materials for the expansion of the genetic base of future cultivars (Saavedra et al. 2001).

As part of a pre-breeding work of *Solanum lycopersicun*, our objective was to evaluate 56 accessions of the UFV germplasm bank by means of agronomic descriptors and multivariate techniques aiming at genetic diversity.

MATERIAL AND METHODS

Two experiments were conducted at the Experimental Field of the Department of Plant Science of the Universidade Federal de Viçosa, located in the city of Viçosa, at lat 20° 45' 14" S and long 42° 52' 53" W and alt 648 m asl.

The first experiment was sown on February 14 and the second on June 18, 2008, both in polystyrene trays with 128 cells using commercial substrate.

The transplanting was carried out when the plants presented, in average, two pairs of definite leaves. The soil was previously plowed, harrowed and corrected according to the recommendations of the Soil Fertility Commission of the state of Minas Gerais (Comissão de Fertilidade do Solo do Estado de Minas Gerais 1999).

The spacing used in the experiments was of 1.15 m between the lines and 0.60 m among the plants. The fertirrigations with potassium chloride and ammonium sulfate were applied weekly by means of a drip irrigation system. The vertical staking with ribbon was used, and the conduction of one stem per plant. The pruning was carried out three leaves above the sixth racimo. The cultural practices, such as weeding and thinning were performed according to the recommendations of Guimarães et al. (2007).

The treatments were composed of 56 subsamples of the UFV vegetable Germplasm bank (Table 1). Twenty-seven were evaluated in the first experiment and twenty-nine in the second experiment. Four commercial cultivars common to both experiments were used as controls: Santa Clara, Fanny, Débora-Plus and Andréa. A casualized block experimental design with three replications was conducted. The experimental units were composed of five plants, and the three central plants were useful.

The following phenotypical traits were evaluated: fruit length (mm), fruit width (mm), width of the pedicel scar (mm), mesocarp thickness (mm), endocarp thickness (mm), central axis width (mm), number of locules, number of marketable fruits per plot, weight of marketable fruits per plot (g), fruit average weight (g), total number of fruits per plot and total fruit weight per plant (g), according to the recommendation guide of descriptors proposed by the Biodiversity International, IPGRI (1996), (http://www.ipgri.cgiar.org/publications/pdf/286.pdf).

Table 1. Identification, origin and common name of accessions of the tomato plant *Solanum lycopersicon* from the UFV vegetable Germplasm bank (BGH – UFV)

Treatment	Accessions	Origin	Common Name
1	BGH-2136	Ipameri, GO	Tomato
2	BGH-2143	Campinas, SP	Tomato "Epoch" (durvaf) IAC 3318
3	BGH-2144	Campinas, SP	Giant Tomato IAC 2129
4	BGH-2145	Campinas, SP	Tomato "Pearson" IAC 2207
5	BGH-2146	Campinas, SP	Tomato V.F.36 IAC 3071
6	BGH-2148	Belo Horizonte, MG	Tomato
7	BGH-4348	Purdue University, USA	Tomato PI 262162
8	BGH-887	Purdue University, USA	Tomato V.F.36
9	BGH-971	Purdue University, USA	Tomato (SRS) 5097-4
10	BGH-973	Purdue University, USA	Tomato (SRS) 5288-2
11	BGH-984	Purdue University, USA	Tomato PI 272444 (Bushy)
12	BGH-996	Purdue University, USA	Tomato PI 255839
13	BGH-1025	Purdue University, USA	Tomato VR Early Chateham
14	BGH-2123	Purdue University, USA	Tomato Campbells C-1327
15	BGH-2113	Purdue University, USA	Tomato PI 262159 CGS
16	BGH-2070	Purdue University, USA	Tomato PI 255847 CGS
17	BGH-2201	Purdue University, USA	Tomato Heinz 1370
18	BGH-2206	Purdue University, USA	Tomato Heinz 1369
19	BGH-2209	Purdue University, USA	Tomato Keyslone SM-SP
20	BGH-2215	Purdue University, USA	Tomato OSN 460-1
21	BGH-2218	Purdue University, USA	Tomato PI 237132
22	BGH-2030	Purdue University, USA	Tomato Tiny Tim
23	BGH-2040	Purdue University, USA	Tomato Cornell 55-542
24	BGH-2044	Purdue University, USA	Tomato OSC 348
25	BGH-2045	Purdue University, USA	Tomato OSC 399
26	BGH-2049	Purdue University, USA	Tomato W-12 (Rutter Sudlo)
27	BGH-2050	Parma, Italy	Tomato Lungo Napoli - VF
28	BGH-6893	Viçosa, MG	Apple Tomato
29	BGH-6866	Dourados, MT	Native Tomato
30	BGH-6867	Miguel Pereira, RJ	Tomato Santo Antônio
31	BGH-4377	Botu, SP	Botu-13
32	BGH-7263	Agroceres	Agroceres-AG 33
33	BGH-6851	Without the original location	CNPH 937
34	BGH-7221	Encapa	Encapa-Fuji
35	BGH-7213	Without the original location	Nemadoro
36	BGH-7267	Paracatu, MG	AG. Paracatu
37	BGH-7192	Paracatu, MG	AG. Paracatu
38	BGH-7269	Rome, Italy	vfn. 0026
39	BGH-7218	Rutgers, USA	Tomato 0028
40	BGH-7197	Without the original location	Santa Clara-mutation (yellow)
41	BGH-7193	Emcapa-Santo Antônio	Emcapa 0032
42	BGH-6861	Emcapa -Vitor Targa	Emcapa 0033
43	BGH-6877	Without the original location	Tomato RVC 2
44	BGH-6857	Without the original location	LA 1673
45	BGH-6863	Without the original location	LA 2009
46	BGH-6842	Without the original location	H73AAB.

Table 1. Cont.

Treatment	Accessions	Origin	Common Name
47	BGH-7222	Without the original location	Cultivar Stupicke
48	BGH-3500	Vitória, ES	Intense Red Tomato
49	BGH-4507	Maracaçumé, PA	Tomato "dedo de moça"
50	BGH-6854	West Virginia, USA	Mela-resistant Tomato
51	BGH-6841	Japan	Tomato Anchort rootstock
52	BGH-6859	Viçosa, MG	Tomatinho
53	BGH-6878	Venda Nova do Imigrante, ES	Tomato salada-capixaba
54	BGH-6889	La Paz, Bolivia	Tomato Santa Cruz
55	BGH-6858	USA	Tomato
56	BGH-6890	Without the original location	Tomato

The data correction of all the traits evaluated through the calculation of the environmental effect was performed. For the calculation, the general average was subtracted from the control average, for each trait considered. For data correction, the averages of the subsamples, for each trait and experiment, were subtracted from their environmental effects. All the traits were submitted to the univariate analysis of variance, grouped in blocks by scheme 1, as reported by Cruz and Carneiro (2003), with later comparison of the averages of the subsamples and those of the controls by means of the Dunnett test, with p <0.05.

For the application of the multivariate tests, a diagnosis of multicolinearity was previously performed. The genetic divergence between the subsamples was estimated, based on the dissimilarity presented by the Mahalanobis' generalized distance (D^2) (Mahalanobis 1936), with later applications of the Tocher optimization method, modified by Vasconcelos et al. (2007).

The modification of the Tocher method consists of the calculation of a new "α" for each group formed. "α" refers to the value that limits the increase in the average of the intra-group distance, which is the criterion used to decide whether a new genotype is included or not. The modification changes the simultaneous form through which the grouping is carried out, turning it into sequential (see Vasconcelos et al. 2007). The Anderson's discriminant analysis (1958) and the projection of the distances in the plan were also carried out.

The discriminant functions were achieved by

$$D_1(x) = \ln(p_1) + (x - \frac{1}{2}\mu_1)'\Sigma^{-1}\mu_1$$

$$D_2(x) = \ln(p_2) + (x - \frac{1}{2}\mu_2)'\Sigma^{-1}\mu_2$$

$$D_3(x) = \ln(p_3) + (x - \frac{1}{2}\mu_3)'\Sigma^{-1}\mu_3$$

$$D_4(x) = \ln(p_4) + (x - \frac{1}{2}\mu_4)'\Sigma^{-1}\mu_4$$

where:
π_1, π_2, π_3 and π_4: groups 1, 2, 3 and 4.
μ_1, μ_2, μ_3 and μ_4: vector of averages of 12 phenotypic traits evaluated in the groups 1, 2, 3 and 4.
Σ_1, Σ_2, Σ_3 and Σ_4: matrix of variances and covariances among the traits evaluated.
ρ_1, ρ_2, ρ_3 and ρ_4: probabilities, *a priori*, that the subsamples belong to the groups 1, 2, 3 and 4.
$\tilde{x}$: vector of variables representative of the traits involved in the analysis.

The t-th subsample, with a vector of average $\tilde{x}_i$, of the group π_j will be classified, if and only if $D_J(\tilde{x}_i)$ is the largest element of the set $\{D_1(\tilde{x}_i), D_2(\tilde{x}_i), D_3(\tilde{x}_i), D_4(\tilde{x}_i)\}$. Using the discriminant functions and the data of the groups π_1, π_2, π_3 and π_4, the rate of apparent error was estimated. It measures the efficiency of the discriminant function in classifying the subsamples correctly, in the groups previously established.

The relative significance of the traits in relation to the genetic divergence among the subsamples was studied according to Singh (1981). All the data analyses were carried out with the help of the GENES statistical software system, version Windows (Cruz 2001).

RESULTS AND DISCUSSION

As for the fruit traits, the subsample BGH 7197 achieved a fruit length superior to that of the controls. However, it must be noted that around 50% of the subsamples achieved fruit length similar to at least one control (Table 2).

Table 2. Statistics of 12 agronomic traits evaluated in 56 subsamples of *Solanum lycopersicon*, compared to four commercial controls (Santa Clara, Fanny, Débora and Andréa)

Subsamples Total (60)	FL* (mm)	FW (mm)	WPS (mm)	MT (mm)	ET (mm)	WCA (mm)	NL	NMF	WMF (g)	FAW (g)	TNF	FTW (g)
Mean	53.84	55.93	4.72	5.09	45.65	31.63	4.19	73.59	4673.84	76.92	79.77	1819.03
Maximum	112.09	105.06	12.21	9.66	96.67	76.98	13.86	159.75	12267.50	219.11	167.67	4535.33
Minimum	8.78	23.19	0.75	2.32	19.84	9.45	2.04	10.25	190.04	6.90	12.33	125.12
Range	103.31	81.87	11.46	7.33	76.83	67.53	11.82	149.50	12077.46	212.21	155.33	4410.21
Variance	227.63	251.14	6.35	2.12	242.60	217.67	7.15	1097.36	6650882.40	2499.74	1206.98	964370.85
CV(%)	28.02	28.33	53.39	28.61	34.12	46.64	63.80	45.02	55.18	65.00	43.55	53.99
Subtotal (56)												
Mean	53.75	55.34	4.63	4.92	45.46	31.50	4.29	71.97	4267.50	74.62	77.77	1675.55
Maximum	112.09	105.06	12.21	9.66	96.67	76.98	13.86	159.75	10184.29	219.11	167.67	3882.35
Minimum	24.34	23.19	0.75	2.32	19.84	9.45	2.04	10.25	190.04	6.90	12.33	63.12
Range	87.75	81.87	11.46	7.33	76.83	67.53	11.82	149.50	9994.25	212.21	155.33	3819.23
Variance	197.36	259.08	6.63	1.81	255.04	230.94	7.51	1133.92	4463269.91	2567.60	1227.44	650012.42
CV(%)	26.13	29.09	55.61	27.36	35.13	48.24	63.94	46.79	49.51	67.91	45.05	48.12
Controls (4)												
Mean	54.81	64.27	5.95	7.52	48.30	33.45	2.84	96.25	10.36	109.15	107.67	3.92
Maximum	76.32	75.74	6.86	8.03	59.90	39.31	3.50	102.67	12.27	143.75	115.50	4.54
Minimum	8.78	52.66	4.49	7.28	37.48	24.95	2.43	85.50	8.48	88.20	91.50	3.22
Range	67.54	23.08	2.37	0.75	22.42	14.36	1.07	17.17	3.79	55.55	24.00	1.32
Variance	699.44	90.01	1.10	0.12	85.50	42.24	0.23	59.27	2.75	605.32	122.28	0.31
CV(%)	48.25	14.76	17.62	4.62	19.14	19.43	16.72	8.00	16.00	22.54	10.27	14.22

* FL. Fruit length, FW. Fruit width, WPS. Width of the pedicel scar, MT. Mesocarp thickness, ET. Endocarp thickness, WCA. Width of the central axis, NL. Number of locules, NMF. Number of marketable fruits per plot, WMF. Weight of marketable fruits per plot, FAW. Fruit average weight, TNF. Total number of fruits per plot and, FTW. Fruit total weight per plant.

A similar behavior was observed for fruit width and average diameter, since the values of the subsamples BGH 7222 and BGH 887 were higher than those of the controls. In approximately 82% of the subsamples, diameters equal to at least one of the controls were observed.

For the width of the pedicel scar and central axis width, 37.5% and 16.07%, of the subsamples did not differ from the controls (Table 2).

The phenotypical traits mesocarp thickness, endocarp thickness and width of the fruit central axis are related to firmness, which, according to Rezende et al. (2000), is one of the most important attributes associated to the fruit quality, both for *in natura* consumption and industrial use. It is also determinant for the storage period. Andrade Júnior et al. (2001) reported that the achievement of firmer tomatoes would allow the decrease in their perishability, thus increasing the time to market them.

In the subsamples BGH 6857, BGH 6866, BGH 1025, BGH 6863, BGH 6842, BGH 6858, BGH 973, BGH 6867, BGH 2044, BGH 6841 and BGH 6859, average values of mesocarp thickness dissimilar to those of the controls (Table 2) were observed. The average value of the subsamples BGH 6854 for this trait was higher than the averages of the controls Santa Clara and Andréa. It is noteworthy that the cultivar Santa Clara is considered a standard cultivar, responsible for more than 90% of the planted area of tomato of the group Santa Cruz in Brazil (Andrade Júnior et al. 2001). We also point out that, among the controls used, the cultivar Santa Clara is the only one that is a pure line, which strengthens the significance of the subsamples BGH 6854 as a source of alleles favorable to the mesocarp thickness.

The endocarp thickness is another trait that defines the fruit firmness. In the subsamples BGH 7222, BGH 7267, BGH 887 and BGH 2143, thicker endocarps were observed, compared to all of those of the controls. It is noteworthy that 84% of the subsamples evaluated achieved average values equal to at least one of the controls (Table 2).

In the subsamples BGH 2209, BGH 2030, BGH 2136, BGH 6890, BGH 7192, BGH 984, BGH 6854 and BGH 1025, values for the central axis width statistically equal to the control values were observed, while BGH 7222, BGH 7267, BGH 887, BGH 2143, BGH 7263, BGH 2113 and BGH 2146 were higher (Table 2). For this trait, higher values are desired because they are associated to firmness.

There are few works in literature that analyze fruit traits separately, mainly those related to the divergence in germplasm collections. However, this work demonstrates the variability among the subsamples (Tables 2 and 3) which are potentially useful to the tomato plant breeding programs.

Approximately 65% of the subsamples present four locules or less and are compatible with the values achieved by the controls (Table 2). Most subsamples evaluated are classified as belonging to the group Santa Cruz, with prevalence of bi or trilocular fruits. The other subsamples present plurilocular fruits, in other words, fruits with more than four locules.

As for the trait related to production, the subsamples BGH 6889 and BGH 7213 achieved a higher number of marketable fruits, in comparison to the controls. Approximately 72% of them obtained values equal to at least one control considered (Table 2).

For the weight of marketable fruits, the highlight is deserved by the subsamples BGH 6866 and BGH 7218, with values equal to those of the controls (Table 2). The subsamples BGH 7222, BGH 7267 and BGH 887 were superior to the controls in fruit average weight. Concerning fruit number and fruit total weight, the subsample BGH 6889 achieved a number higher to that of the controls; and the subsamples BGH 6866 and BGH7218 obtained a total weight equal to that of the controls (Table 2).

The subsamples which were promising to be used in future breeding programs are: BGH 7222, BGH 7267 and BGH 887, and belong to the group 3; BGH 2143, BGH 6866, and BGH 7218, of group 1; and the subsamples BGH 6889 and BGH 7213, of group 2. Considering that these subsamples present good agronomic traits and belong to different groups, heterotic gains can be expected in hybridization programs (Tables 1 and 2).

The genetic divergence among the subsamples was assessed by biometric methods. The most dissimilar subsamples were the BGH's 7197 and 6889, with a distance of 541.25; and the most similar, the BGH's 7269 and 3500, with a distance of 2.44. Since the distance matrix is very extensive, only the highest and lowest distances between subsamples are presented.

By the Tocher optimization method, four different groups were formed among the subsamples considered. In group 1, approximately 90% of the subsamples and the four controls were allocated, demonstrating a great

similarity among the subsamples in relation to the phenotypical traits evaluated (Table 3).

With the projection of the distances in the plan (Figure 1), it was possible to discriminate the subsamples into 5 groups. There is a coincidence in the grouping of the groups 1, 3 and 4 between the multivariate methods applied. Nevertheless, when the distances are projected in the plan, a higher proximity of the subsample BGH 2201, subsamples BGH 7213 and BGH 6889, as well as a tendency of the BGH 2050 to separate from these subsamples can be observed. These modifications are caused by the distortions when points of a multidimensional space are transposed for a bidimensional space.

The efficiency of the grouping can be confirmed by the low rate of apparent error of the discriminant functions, 1.66%. The modification in the classification occurred in the allocation of the subsample BGH 7221, which originally belonged to group 1, in group 2 (Table 3).

The phenotypical traits which contributed most for dissimilarity were: fruit length, central axis width, number of marketable fruits, weight of marketable fruits and the total number of fruits. The average fruit weight provided the least relative contribution for genetic diversity. The trait fruit length is considered by Rocha et al. (2008) as one of the characteristics which contributed most for genetic divergence (Table 4).

Therefore, it is possible to conclude that there is a significant variability among the subsamples for all the phenotypical descriptors and that the biometric techniques used are efficient to discriminate the subsamples of the collection studied. The subsamples
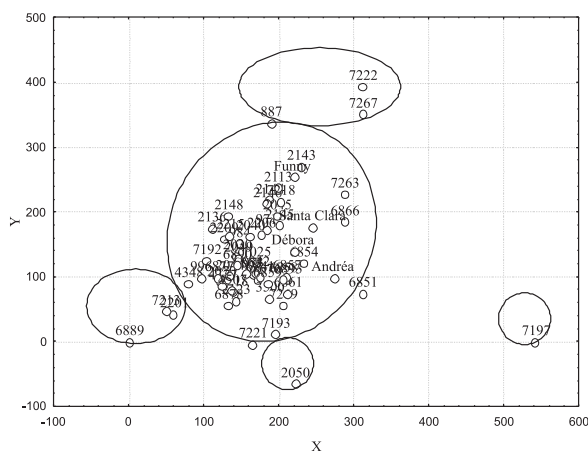

Figure 1. Projection of the dissimilarity expressed by the Mahalanobis' generalized distance, among 56 subsamples and four cultivars of *Solanum lycopersicon*, in the bidimensional space. The correlation among the original and estimated distances was 0.93, and the distortion was 29.63%

Table 4. Relative importance of twelve agronomic traits for the study of genetic diversity among 56 tomato subsamples

Phenotypical traits	Relative Contribuition (%)
Fruit length	20.5518
Fruit width	3.5524
Width of the pedicel scar	4.3994
Mesocarp thickness	2.8894
Endocarp thickness	8.8261
Width of the central axis	12.889
Number of locules	6.2312
Number of good fruits	10.2112
Weight of good fruits	11.2986
Fruit average weight	1.1533
Total number of fruits	11.4353
Total weight of fruits	6.5622

Table 3. Groups established by the modified Tocher optimization method*, based on 12 phenotypical traits, evaluated in 56 subsamples and four commercial cultivars of *Solanum lycopersicon*, expressed by the Mahalanobis' generalized distance

Groups	Subsamples (Accessions)**
1	7269(1)***, 3500(1), 6861(1), 6893(1), 6859(1), 6858(1), 6841(1), 6857(1), 6842(1), 6863(1), 6867(1), 4507(1), 2218(1), 2044(1), 973(1), 6877(1), 1025(1), 4377(1), 2070(1), 2123(1), 6890(1), 2030(1), 7192(1), 984(1), 6878(1), 2215(1), 2040(1), 2049(1), 2206(1), 2209(1), Débora(1), 6854(1), 971(1), Andréa(1), Santa Clara(1), 6866(1), 7218(1), 996(1), 7193(1), 2045(1), 2144(1), 2145(1), 2148(1), 2146(1), 6851(1), 2113(1), 2136(1), 2143(1), Funny(1), 7263(1), 4348(1), 7221(2), 2201(1)
2	7213(2), 6889(2), 2050(2)
3	7267(3), 7222(3), 887(3)
4	7197(4)

*Method modified by Vasconcelos et al. (2007)
**The abbreviation BGH – UFV vegetable Germplasm bank precedes the number that identifies each subsamples
*** The numbers in parentheses correspond to the group in which the subsamples were classified using the Anderson (1958)' discriminant function as criterion
Number of wrong classifications: 1; total number of classifications: 60.
Rate of apparent error (%): 1.67

BGH 7222 BGH 7267, BGH 887, BGH 2143, BGH 6866, BGH 7218, BGH 6889 and BGH 7213 can be used in tomato plant genetic breeding as parents in future hybridizations, and as lineages, since they present a better agronomic performance.

Diversidade genética entre subamostras de tomateiro para pré-melhoramento

RESUMO - *O objetivo do trabalho foi avaliar 56 subamostras de* Solanum lycopersicon *por meio de descritores agronômicos e quantificar a diversidade genética. Dois experimentos foram conduzidos em blocos casualizados com três repetições. Substancial variabilidade foi verificada entre as subamostras para todos os descritores fenotípicos. Quatro grupos foram formados pelo método de otimização de Tocher e projeção das distâncias no plano. A eficiência do agrupamento foi denotada pela baixa taxa de erro aparente das funções discriminantes, 1,66%. As características fenotípicas que mais contribuíram para a dissimilaridade foram: comprimento do fruto, largura do eixo central, peso de frutos comercializáveis, número de frutos comercializáveis e número total de frutos. As subamostras promissoras para utilização em programas futuros de melhoramento foram: BGH 7222, BGH 7267 e BGH 887, pertencentes ao grupo 3; BGH 2143, BGH 6866, e BGH 7218, pertencentes ao grupo 1 e as subamostras BGH 6889 e BGH 7213 pertencentes ao grupo 2.*

Palavras chave: *Solanum lycopersicon*, recursos genéticos, germoplasma.

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