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GENETIC DIVERSITY OF BRAZILIAN PEPPER BASED ON QUALITATIVE REPRODUCTIVE TRAITS

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ABSTRACT: In Brazil, pepper cultivation gives producers more marketing opportunities in various segments, either for fresh consumption or industry. Reproductive traits are efficient methods for comparing genetic divergence in pepper, once most differences among accessions could be verified at this stage. This study aimed to evaluate the genetic divergence in the reproductive phase of pepper accessions by multivariate analysis and test the efficiency of different methods. Sixty-five genotypes from the Federal University of Uberlândia*Capsicum* spp. Germplasm Bank were evaluated 145 days after sowing, and morphological characterization was performed at reproductive phase. Graphical representation of genetic distances was obtained by UPGMA. Tocher optimization method was also used to group accessions. Genotypes were arranged in seventeen different groups by Tocher method. UPGMA dendrogram collaborated with Tocher method, indicating the wide genetic variability of genotypes. Tocher and UPGMA methods were partially in agreement, allowing grouping 44 of the 65 analyzed accessionsequally. Multicategorical traits have the advantage of easy observation and require less time and labor, being ideal for use in gene bank and collections that do not have high human and financial resources. Moreover, these traits are not affected by the environment. Genetic divergence detected in this paper encourages other researchers to perform the characterization of pepper collections as completely as possible, because it becomes possible to generate more reliable information of the variability and genetic divergence among accessions. Our research discloses the reproductive biodiversity of pepper in “Alto Paranaíba” and “TriânguloMineiro” regions and the importance of maintaining these genotypes.

KEYWORDS: *Capsicum* spp.;Active germplasm bank;Multivariate clustering analysis; Multicategorical traits; Pepper breeding programs.

DIVERSIDADE GENÉTICA DE PIMENTAS BRASILEIRAS COM BASE EM CARACTERES REPRODUTIVOS QUALITATIVOS

RESUMO: O cultivo de pimentas no Brasil permite maiores oportunidades de mercado em vários segmentos aos produtores, seja *in natura* ou para indústria. Caracteres reprodutivos são métodos eficientes para comparação da diversidade genética das pimentas, uma vez que muita das diferenças entre acessos pode ser verificada neste estágio. O estudo objetivou avaliar a diversidade genética na fase reprodutiva em acessos de pimenta pela análise multivariada e testar a eficiência destes métodos. Sessenta e cinco genótipos do banco de germoplasma de *Capisicum* spp da Universidade Federal de Uberlândia, foram avaliados. Cento e quarenta e cinco dias após semeadura, a caracterização morfológica foi realizada na fase reprodutiva. A representação gráfica dos genótipos foi obtida pelo método UPGMA. O método de otimização de Tocher foi também empregado para agrupamento dos acessos. Os genótipos foram agrupados em 17 grupos pelo método de otimização de Tocher. O dendrograma de UPGMA corroborou com os resultados do agrupamento de Tocher, indicando alta variabilidade genética entre os genótipos. Os agrupamentos formados pelo método de Tocher e UPGMA foram parcialmente de acordo, agrupando igualmente 44 dos 65 genótipos analisados. Caracteres multicategóricos possuem a vantagem de fácil observação e requerem menos tempo e trabalho, sendo ideais para uso em bancos genéticos e coleções que não possuem muitos recursos financeiros ou mão-de-obra. Além disso, estes caracteres praticamente não sofrem variação ambiental. A diversidade genética detectada neste trabalho representa estímulo para outros pesquisadores realizarem a caracterização de suas coleções de forma mais completa, permitindo a geração de informações mais precisas sobre a variabilidade e divergência genética entre seus acessos. A pesquisa revela a biodiversidade de pimentas nas regiões do Alto Paranaíba e Triângulo Mineiro e a importância da manutenção destes genótipos.

PALAVRASCHAVE: *Capsicum* spp.; Banco de germoplasma ativo; Análise de agrupamento multivariada; Caracteres multicategóricos; Melhoramento de pimentas.

INTRODUCTION

Pepper belongs to the genus *Capsicum* and family Solanaceae. It is estimated that the world's *Capsicum* production is over 30 million tons in almost four million hectares. India is the major producer and consumer (Faostat, 2016). In Brazil, pepper cultivation gives producers more marketing opportunities in various segments, either for fresh consumption or industry(Signorini et al., 2013). The importance of pepper cultivation is directly associated with its consumption, being considered one of the most important species used by family farmers (Costa et al., 2015; Signorini et al., 2013). According to ABCSEM (2016), more than 3,322 kg of pungent and not pungent hot pepper seeds were sold in Brazil in 2011, with an estimate of 2,460 ha planted area.

However, unlike other countries with higher productions, pepper cultivation in Brazil is restricted to low diversity of varieties available to farmers, mostly occurring with informal marketing. In addition, with the growth of large urban centers,of the number of small farmershas reduced, resulting in the extinction of many *Capsicum* genotypes, narrowing the genetic base (Domenico et al., 2012). Several researches on*Capsicum* have evaluated aspects related to fruit productivity (Büttow et al., 2010; Domenico et al., 2012; Moura et al., 2010; Paulus et al., 2015), but there is little database with descriptions of reproductive features in a pepper germplasm. Reproductive traits are efficient methods for comparing genetic divergence in pepper, once most differences among accessions could be verified at this stage (Bianchi et al., 2016). Qualitative traits are little influenced by the environment, allowing an efficiency genetic distinction among accessions. Furthermore, classification is simpler and faster compared to quantitative methods, and several qualitative descriptors have already been proposed for the species (IPGRI, 1995).

Efficient description of accessions in a gene bank can define the future of the genetic diversity of a species (Costa et al., 2015). In Brazil, few studies had reported the genetic diversity of pepper, compromising the possibility of interesting crosses for plant breeding. Moreover, there is no consensus regarding the best multivariate analysis method able to characterize the reproductive phase of *Capsicum* spp. accessions. Therefore, this study aimed to evaluate the genetic divergence in the reproductive phase of pepper accessions by multivariate analysis and test the efficiency of different methods.

MATERIAL AND METHODS

Sixty-five genotypes from the *Capsicum* spp. Germplasm Bank were evaluated at the Federal University ofUberlândia-UFU, Campus of Monte Carmelo, MG, Brazil (Table 1). Currently, the bank has 250 accessions that have been acquired through donation, collection and purchase in farmer's markets. All analyses were conducted at the Laboratory of Seed and Genetic Resource Analysis, UFU (LAGEN). This genetic bank includes part of the pepper biodiversity of "Alto Paranaíba" and "TriânguloMineiro" regions of Minas Gerais that is home of small-scale pepper producers.

The experiment was conducted at the Horticultural Experiment Station, (18º42'43"S, 47º29'55"W and 873 ma.s.l., humid temperate climate with hot summers and dry winters). Sowing was performed on September of 2013, in 128-cell polystyrene trays filled with commercial coconut-fiber substrate. After sowing, trays were kept in gable-roofed greenhouse covered by transparent 150-micron polyethylene film activated against ultraviolet rays with 30% shade. Seedlings were transplanted 54 days after sowing, with twenty seedlings of each accession planted in four rows, spaced one meter between lines and 0.7 meter between plants, with total experimental area of 1,316 m^2. Four replicates of each accession were planted in a randomized block design (RBD).

Table 1. Location of accessions used in the*Capsicum* spp. gene Bank of the Federal University of Uberlândia. Monte Carmelo, UFU, 2016.

Accession	Location	Species	Accession	Location	Species
UFU 02	Estrela do Sul	*C. chinense*	UFU 41	Estrela do Sul	*C. chinense*
UFU 03	Estrela do Sul	*C. baccatum*	UFU 42	Monte Carmelo	*C. chinense*
UFU 04	Monte Carmelo	*C. annuum*	UFU 43	Monte Carmelo	*C. chinense*
UFU 05	Gonçalves	*C. frutescens*	UFU 44	Monte Carmelo	*C. frutescens*
UFU 06	Celso Bueno	*C. chinense*	UFU 45	Estrela do Sul	*C. baccatum*
UFU 07	Monte Carmelo	*C. chinense*	UFU 47	Estrela do Sul	*C. baccatum*
UFU 08	Monte Carmelo	*C. baccatum*	UFU 48	Penedo	*C. baccatum*
UFU 09	Brejão	*C. baccatum*	UFU 49	Monte Carmelo	*C. baccatum*
UFU 10	Gonçalves	*C. chinense*	UFU 50	Monte Carmelo	*C. chinense*
UFU 11	Gonçalves	*C. baccatum*	UFU 51	Monte Carmelo	*C. chinense*
UFU 14	Brejão	*C. chinense*	UFU 52	Monte Carmelo	*C. chinense*
UFU 15	Brejão	*C. chinense*	UFU 53	Monte Carmelo	*C. chinense*
UFU 16	ÁguaEmendada	*C. baccatum*	UFU 54	Monte Carmelo	*C. chinense*
UFU 17	Penedo	*C. baccatum*	UFU 55	Celso Bueno	*C. chinense*
UFU 18	Penedo	*C. baccatum*	UFU 56	Chapada	*C. chinense*
UFU 19	Brejão	*C. chinense*	UFU 57	Tijuca	*C. chinense*
UFU 21	Brejão	*C. chinense*	UFU 58	ÁguaEmendada	*C. chinense*
UFU 22	Monte Carmelo	*C. chinense*	UFU 59	São Félix	*C. baccatum*
UFU 23	ÁguaEmendada	*C. chinense*	UFU 60	Matheus	*C. chinense*
UFU 24	ÁguaEmendada	*C. chinense*	UFU 61	Capão Alto	*C. baccatum*
UFU 25	Gamas	*C. baccatum*	UFU 62	Capão Alto	*C. chinense*
UFU 26	ÁguaEmendada	*C. chinense*	UFU 63	Estrela do Sul	*C. chinense*
UFU 27	Perdizes	*C. baccatum*	UFU 64	Capão Alto	*C. chinense*
UFU 30	Perdizes	*C. chinense*	UFU 65	Monte Carmelo	*C. chinense*
UFU 31	São Félix	*C. baccatum*	UFU 66	São Félix	*C. chinense*
UFU 32	Perdizes	*C. baccatum*	UFU 67	Monte Carmelo	*C. chinense*
UFU 33	Perdizes	*C. baccatum*	UFU 68	ÁguaEmendada	*C. chinense*
UFU 34	Perdizes	*C. chinense*	UFU 69	Monte Carmelo	*C. chinense*
UFU 35	ÁguaEmendada	*C. chinense*	UFU 72	Gamas	*C. chinense*
UFU 36	ÁguaEmendada	*C. chinense*	UFU 73	Gamas	*C. chinense*
UFU 37	Perdizes	*C. chinense*	UFU 74	Monte Carmelo	*C. chinense*
UFU 38	Perdizes	*C. chinense*	UFU 75	Tijuca	*C. chinense*
UFU 39	Estrela do Sul	*C. chinense*			

Before transplanting, the experimental site was prepared by harrowing and disking, both twice. Soil had the following characteristics: pH (H_2O) = 5.9; available P = 30.1 mg.dm^{-3}; K^{+} = 0.22 cmolc.dm^{-3}; Ca^{+2} = 2.8 cmolc.dm^{-3}; Mg^{+2} = 1.0 cmolc.dm^{-3}; exchangeable H + Al = 3.40 cmolc.dm^{-3}; organic matter = 4.2 dag Kg^{-1}; SMP = 3.40; Al^{+3} = 0.0 cmolc.dm^{-3}; CEC pH 7.0 = 7.42 cmolc.dm^{-3}; CEC base saturation (pH 7.0) = 54 %; Al saturation of effective CEC = 0; Cu^{+2} = 2.3 mg.dm^{-3}; Zn^{+2} = 6.6 mg.dm^{-3} and Mn^{+2} = 6.6 mg.dm^{-3}. Crop treatments were performed as recommended for pepper. One hundred forty-fivedays after sowing, morphological characterization was performed at reproductive phase, according to *Capsicum* descriptors (IPGRI, 1995). Genetic dissimilarity matrix based on these multicategorical variables was estimated by Gower's algorithm (1971), since this technique is efficient to simultaneously analyze quantitative and qualitative data, or only qualitative data (Moura et al., 2010). Dissimilarity among genotypes was expressed as:

$$S_{ijk} = \frac{\sum_{k=1}^{p} W_{ijk} . S_{ijk}}{\sum_{k=1}^{p} W_{ijk}}$$

where: *k* is the number of variables (*k* = 1, 2, …, *p*); *i* and *j* are two individuals representing accessions; W_{ijk} is the weight given to *ijk* comparison (1 for valid comparisons and 0 for invalid comparisons); S_{ijk} is the variable contribution of*k* in the similarity between*i* and *j* individuals.

Graphical representation of genetic distances was obtained by Unweighted Pair-Group Method using Arithmetic Average (UPGMA). The *NbClust* package from the R *software* was used to determine the best number of clusters, based on 24 indexes that establish the compactness and separation criteria among clusters. Tocher optimization method was also established to group accessions. Cophenetic correlation coefficient (CCC) was performed for UPGMA and Tocher methods to identify the clustering quality of both.

Mean Decrease Impurity (MDI) was measured to evaluate the importance of variables and Cramer's V measured the correlation among traits with Chi-Square test (x^2) to validate correlations, with 0.05 significance. Data were analyzed with R software, using *clusters* packages to estimate dissimilarity matrix, *random Forest* to measure MDI (Liaw and Wiener, 2002); *NbClust* for the number of clusters (Charrad et al., 2014); *stats* for UPGMA, its CCC and Pearson's Chi-Square; *biotools* for Tocher and its CCC (Silva and Dias, 2013). Graphic artwork was performed with the SigmaPlot® software (version 11.0).

RESULTS AND DISCUSSION

From the 16 evaluated traits, only seed color did not change among genotypes, being all categorized with yellow seeds. This variable also did not differ among 40 pepper accessions from Amazonas-Brazil, studied by Costa et al. (2015). The other 15 traits were capable of detecting genetic divergence among accessions. Vasconcelos et al. (2012) also obtained efficient distinction among 22 *Capsicum chinense* accessions, with ten qualitative descriptors used in our work.

Gower's algorithm was capable of detecting divergence among genotypes. This methodology was widely used in dissimilarity papers with qualitative and quantitative traits (Silva et al., 2016), including pepper (Moura et al., 2010; Costa et al., 2015). However, Knezovic et al. (2005) warned that this approach is not suitable, because the distance between two accessions will immediately be 0 or 1; but also, questionable, because variables will be unequally weighted, where in a multi-level situation, more weight will be given to variables with more levels, while on a single level incompatibilities will outweigh correspondences.

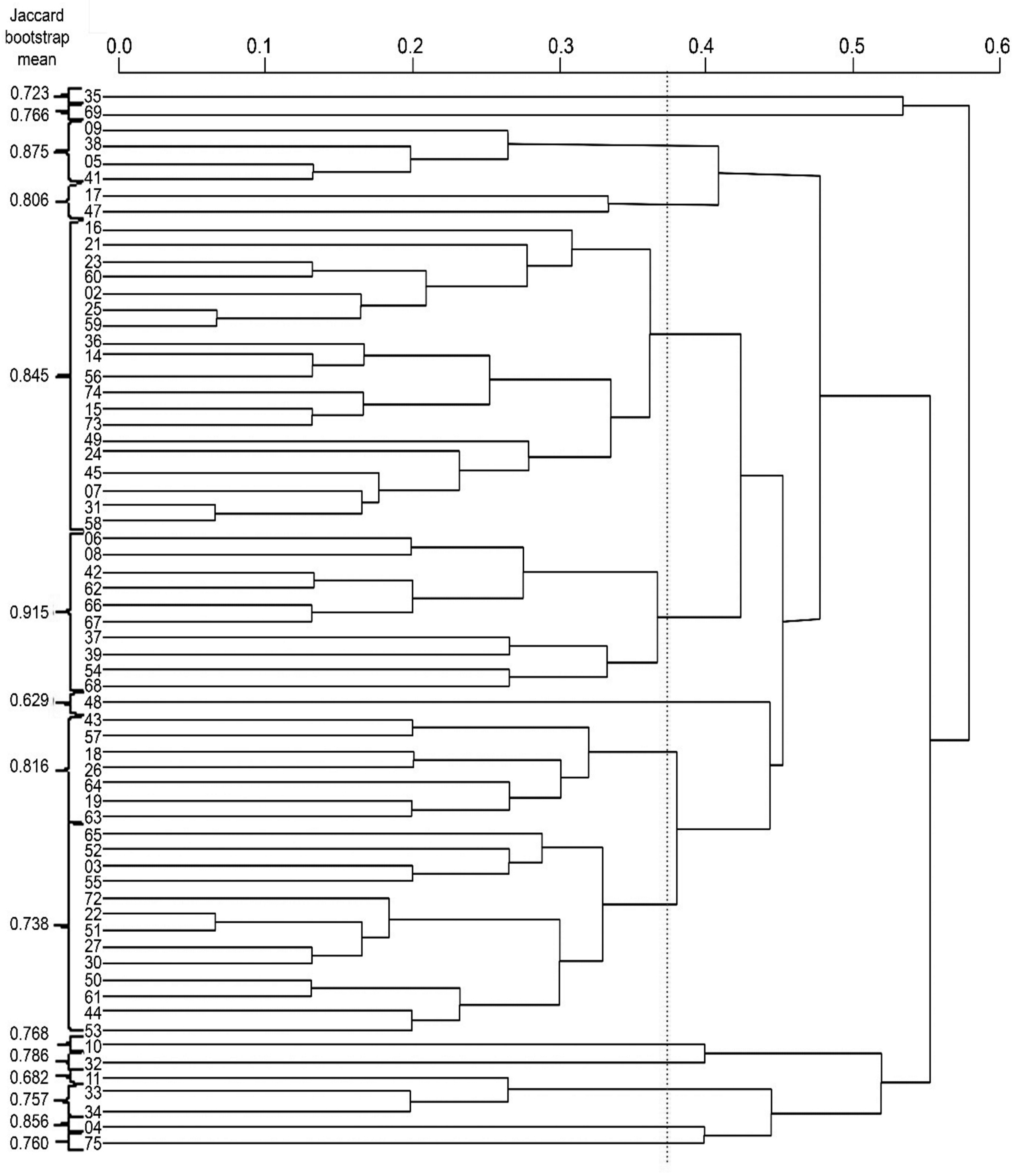
Genotypes were arranged in 17 different groups by the Tocher optimization method (Table 2), showing that these descriptors were efficient to detect genetic divergence in *Capsicum* accessions, justified by the large variability at reproductive stage for that genus. Six clusters had only one genotype. Other five clusters had two genotypes. These clusters could be used to search genotypes with different traits to improve genetic diversity among crosses. On the other hand, if the aim of crossingsis to keep high fruit quality (for example, dark red fruit and small seeds), Group 1 and 2 detected large number of genotypes that would be recommended for that case.

Table 2. Clustering of 65 *Capsicum* accessions by the Tocher optimization procedure obtained from reproductive traits. Monte Carmelo, UFU, 2016.

Group 1	UFU-22 UFU-51 UFU-27 UFU-30 UFU-72 UFU-56 UFU-57 UFU-58 UFU-62 UFU-31 UFU-14 UFU-44 UFU-68 UFU-50 UFU-61 UFU-63 UFU-19 UFU-26 UFU-65
Group 2	UFU-25 UFU-59 UFU-02 UFU-60 UFU-23 UFU-45 UFU-21 UFU-49 UFU-24
Group 3	UFU-05 UFU-41 UFU-38 UFU-09 UFU-18 UFU-07
Group 4	UFU-15 UFU-73 UFU-74 UFU-36 UFU-03 UFU-55
Group 5	UFU-42 UFU-67 UFU-66 UFU-08 UFU-06 UFU-39
Group 6	UFU-33 UFU-34 UFU-11
Group 7	UFU-10 UFU-53
Group 8	UFU-48 UFU-52
Group 9	UFU-16 UFU-54
Group 10	UFU-17 UFU-47
Group 11	UFU-43 UFU-64
Group 12	UFU-04
Group 13	UFU-32
Group 14	UFU-35
Group 15	UFU-37
Group 16	UFU-69
Group 17	UFU-75

UPGMA dendrogram collaborated with the Tocher method, indicating the wide genetic variability of genotypes (Figure 1). Thirteen of the 24 indexes from *NbClust* package indicated ideal formation of 15 clusters for the data, which helped for the cut of 37.3% of similarity on the graphic, generating 14 different groups. UPGMA also isolated UFU-35, UFU-69, UFU-32, UFU-04 and UFU-75. UFU-48 and UFU-10 genotypes once they were paired with other genotypes at Tocher's optimization. UFU-37, isolated at Tocher's, was grouped with UFU-39, UFU-54 and UFU-68, showing to be genotypes with close phenotyping in relation to UFU-37. Larger clusters had 20 and 13 genotypes, respectively, showing that UPGMA created larger groups than Tocher.

Figure 1. Cluster dendrogram from the Unweighted Pair-Group Method using the Arithmetic Average (UPGMA) method of 65 *Capsicum* accessions using Gower's algorithm matrix. Monte Carmelo, UFU, 2016

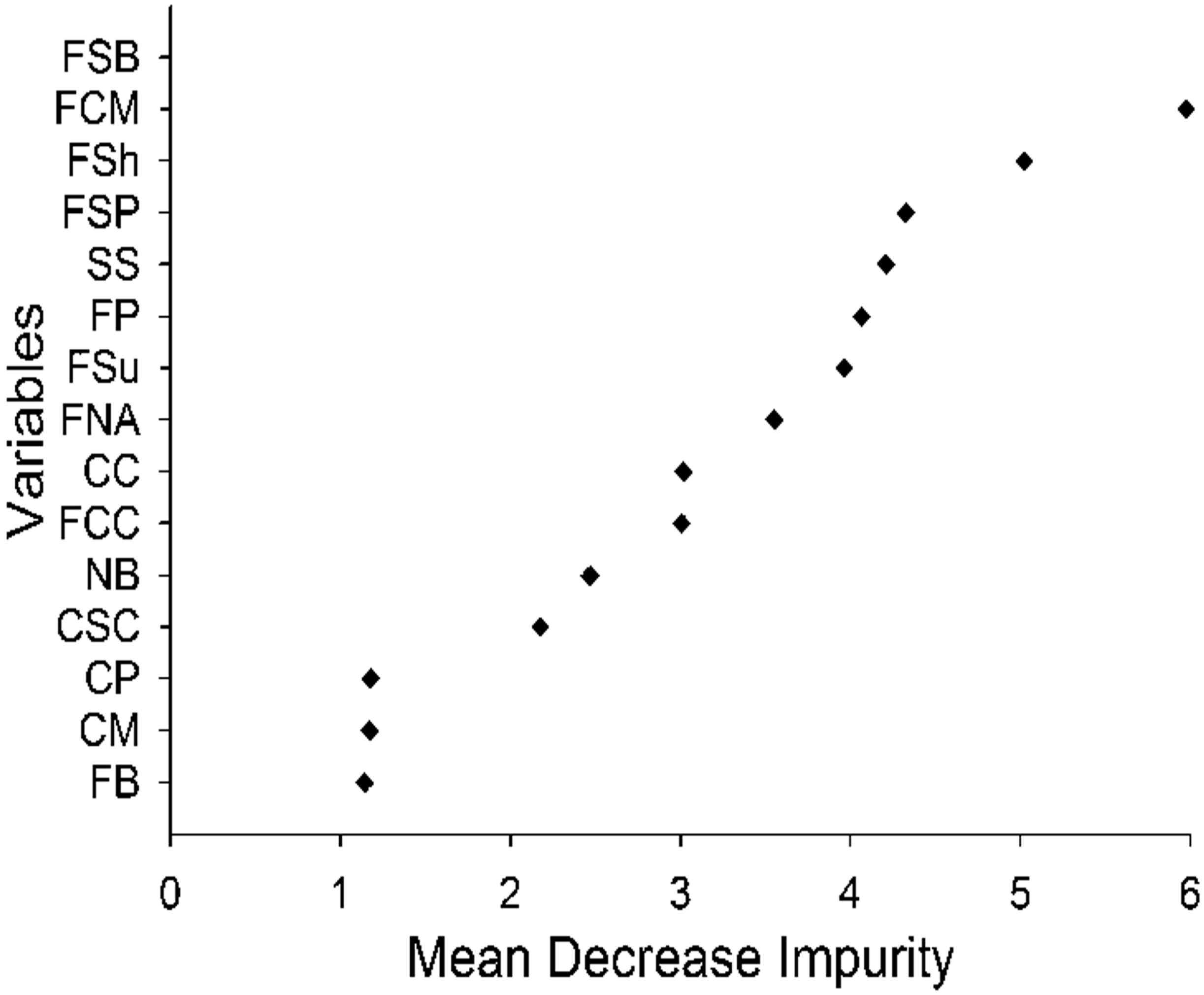


Tocher and UPGMA grouping methods were partially in agreement, allowing grouping 44 of the 65 analyzed accessionsequally. The same results were obtained by Bento et al. (2007), which grouped 19 of the 28 analyzed chili pepperaccessions equally. Tocher and UPGMA methods were also partially coincident in the separation of 137 pepper genotypes from SouthwesternGoiás (Alvares et al., 2012).

Cophenetic correlation coefficient (CCC) can be used to compare clustering results of the same data set, using different distance measures or clustering algorithms. In general, CCC is a measure of how accurately a cluster method preserves the pairwise distances among individuals (Kumar & Toshniwal, 2016). Both clustering methods showed similar CCC (0.72 for Tocher and 0.65 for UPGMA) significant at 1% probability. Furthermore, Jaccard bootstrap method showed that clusters formed by UPGMA were consistent. Both clustering methods should be used in combination, because one statistical approach complements the other.

Traits with less impact on Mean Decrease Impurity (MDI), and respectively with less impact to detect genetic divergence among accessions were endof flowering appendage, calyx margin and calyx pigmentation (Figure 2). Endof flowering appendagewas absent for all formed clusters. Calyx pigmentation was present only in two clusters, for Tocher and UPGMA method. Calyx margin had small variation among clusters, being intermediate or dentate (Tables 3 and 4).

Figure 2. Mean Decrease Impurity of 15 reproductive traits used to evaluate divergence genetic of Brazilian pepper. Monte Carmelo, UFU, 2016.



FNA: Number of flowers per axil; FP: Flower position; CC: Corolla color; CSC: Corolla spot color; CP: Calyx Pigmentation; CM: Calyx margin; FCM: Fruit color at mature stage; FSh: Fruit shape; FSP: Fruit shape at pedicel attachment; NB: Neck at fruit base; FSB: Fruit shape at end of flowering; FB: End of flowering appendage; FCC: Fruit cross-sectional corrugation; FSu: Fruit surface; SS: Seed size.

Table 3.Reproductive traits of clusters formed by the Tocher method from 65 *Capsicum* spp. accessions. Values obtained by the mode of representatives of each cluster. Monte Carmelo, UFU, 2016.

	FNA	FP	CC	CSC	CP	CM	FCM	FSh	FSP	NB	FSB	FB	FCC	FSu	SS	Species
1	2	Intermediate	White	White	Absent	Intermediate	Dark red	Triangular	Acute	Absent	Sunken	Absent	Slightly corrugated	Semi-wrinkled	Small	*C. baccatum, C. chinense,C.frutescens*
2	2	Intermediate	Yellow-green	White	Absent	Intermediate	Dark red	Almost round	Truncate	Absent	Blunt	Absent	Slightly corrugated	Smooth	Small	*C. baccatum, C. chinense*
3	3	Erect	Yellow-green	White	Absent	Intermediate	Dark red	elongate	Acute obtuse truncate	Absent	Pointed	Absent	Slightly corrugated	Semi-wrinkled	Intermediate	*C. baccatum, C. chinense, C. frutescens*
4	2	Pendant	White	White	Absent	Intermediate	Dark red	Triangular	Truncate	Absent	Blunt	Absent	Slightlycorrugated	Smooth	Large	*C. baccatum, C. chinense*
5	2	Intermediate	White	White	Absent	Intermediate	Dark red	Campanulate	Truncate	Absent	Other	Absent	Intermediate	wrinkled	Intermediate	*C. baccatum, C. chinense*
6	1	Erect	White	Green-yellow	Absent	dentate	Dark red	Triangular	Obtuse	Absent	Pointed sunken	Absent	Slightly corrugated	Semi-wrinkled	Small	*C. baccatum, C. chinense*
7	2	Erect Pendant	White	White	Absent	Dentate Intermediate	Dark red	Triangular	Obtuse	Present	Sunken	Absent	Intermediate	Semi-wrinkled	Intermediate	*C. chinense*
8	2	Pendant	White Yellow-green	White	Absent Present	Intermediate	Dark red	Campanulate	Acute	Present	Pointed sunken	Absent	Slightlycorrugated	Semi-wrinkled	Small intermediate	*C. baccatum, C. chinense*
9	1 /3	Intermediate	White Yellow-green	White	Absent	Intermediate	Dark red Purple	Campanulate	Truncate	Absent	Sunken	Absent	Slightlycorrugated	Smooth	Small intermediate	*C. baccatum, C. chinense*
10	3	Erect Intermediate	White Yellow-green	White	Absent	Intermediate	Lemon-yellow	Triangular	Truncate obtuse	Absent present	Blunt	Absent	Slightly corrugated	Semi-wrinkled	Intermediate	*C. baccatum*
11	2 / 3	Erect Pendant	White Yellow-green	White	Absent	Intermediate	Lemon-yellow	Triangular	Acute	Absent	Pointed sunken	Absent	Slightly corrugated	Smooth	Small	*C. chinense*
12	3	Intermediate	White	Other	Absent	Dentate	Dark red	Elongate	Obtuse	Absent	Pointed	Absent	Slightly corrugated	Smooth	Large	*C annum*
13	1	Erect	White	White	Absent	Intermediate	Lemon-yellow	Elongate	Obtuse	Absent	Sunken	Absent	Slightly corrugated	Semi-wrinkled	Small	*C. baccatum*
14	2	Erect	Yellow-green	Other	Absent	Intermediate	Dark red	Campanulate	Obtuse	Absent	Pointed	Absent	Slightly corrugated	Wrinkled	Intermediate	*C. chinense*
15	3	Intermediate	Yellow-green	White	Absent	Intermediate	Dark red	Campanulate	Lobate	Absent	Sunken pointed	Absent	Corrugated	Wrinkled	Intermediate	*C. chinense*
16	2	Erect	Yellow-green	Green-yellow	Absent	Dentate	Purple	Triangular	Truncate	Absent	Other	Absent	Slightly corrugated	Semi-wrinkled	Large	*C. chinense*
17	2	Intermediate	White	Red	Present	Dentate	Dark red	Round	Obtuse	Absent	Pointed	Absent	Corrugated	Semi-wrinkled	Intermediate	*C. chinense*

Table 4.Reproductive traits of the clusters formed by UPGMA method from 65 accessions of *Capsicum* spp. Values obtained by the mode of the representatives of each cluster. Monte Carmelo, UFU, 2016.

	FNA	FP	CC	CSC	CP	CM	FCM	FSh	FSP	NB	FSB	FB	FCC	FSu	SS	Species
1	2	Erect	Yellow-green	Other	Absent	Intermediate	Dark red	Campanulate	Obtuse	Absent	Pointed	Absent	Slightlycorrugated	Wrinkled	Intermediate	C. *chinense*
2	2	Erect	Yellow-green	Green-yellow	Absent	Dentate	Purple	Triangular	Truncate	Absent	Other	Absent	Slightly corrugated	Semiwrinkled	Large	C. *chinense*
3	3	Erect	Yellow-green	White	Absent	Intermediate	Dark red	Elongate	Obtuse	Absent	Pointed	Absent	SlightlyCorrugated	Semiwrinkled	Intermediate	*C. baccatum, C. chinense,C.frutescens*
4	3	Erect Intermediate	White Yellow-green	White	Absent	Intermediate	Lemon-yellow	Triangular	Truncate Obtuse	Absent present	Blunt	Absent	Slightly corrugated	Semiwrinkled	Intermediate	*C. baccatum*
5	2	Intermediate	Yellow-green	White	Absent	Intermediate	Dark red	Round	Truncate	Absent	Blunt	Absent	Slightly corrugated	Smooth	Small	*C. baccatum, C. chinense*
6	2	Intermediate	White	White	Absent	Intermediate	Dark red	Campanulate	Truncate	Absent	Other	Absent	Corrugated	Wrinkled	Intermediate	*C. baccatum, C. chinense*
7	2	Pendant	Yellow-green	White	Present	Intermediate	Lemon-yellow	Campanulate	Acute	Present	Sunken	Absent	Slightlycorrugated	Semiwrinkled	Intermediate	*C. baccatum*
8	2	Erect	White	White	Absent	Intermediate	Lemon-yellow	Triangular	Acute	Absent	Sunken	Absent	Slightlycorrugated	Semiwrinkled	Small	*C. baccatum, C. chinense*
9	2	Erect	White	White	Absent	Dentate	Dark red	Triangular	Obtuse	Present	Sunken	Absent	Intermediate	Semiwrinkled	Small	*C. baccatum, C. chinense,C.frutescens*
10	2	Intermediate	White	White	Absent	Intermediate	Dark red	Triangular	Acute	Present	Sunken	Absent	Slightlycorrugated	Semiwrinkled	Intermediate	C. *chinense*
11	1	Erect	White	White	Absent	Intermediate	Lemon-yellow	Elongate	Obtuse	Absent	Sunken	Absent	Slightly corrugated	Semiwrinkled	Small	*C. baccatum*
12	1	Erect	White	Green-yellow	Absent	Dentate	Dark red	Triangular	Truncate	Absent	Sunken	Absent	Slightly corrugated	Semiwrinkled	Intermediate	*C. baccatum*
13	1	Erect	White	Green-yellow	Absent	Dentate	Dark red	Elongate	Obtuse	Absent	Suken pointed	Absent	Slightly corrugated	Semiwrinkled Smooth	Small	*C. baccatum, C. chinense*
14	3	Intermediate	White	Other	Absent	Dentate	Dark red	Elongate	Obtuse	Absent	Pointed	Absent	Slightly corrugated	Smooth	Large	*C annum*
15	2	Intermediate	White	Red	Present	Dentate	Dark red	Round	Obtuse	Absent	Pointed	Absent	Corrugated	Semiwrinkled	Intermediate	C. *chinense*

Cramer's V correlation among the 105 inter-coefficients presented 22 significant correlations by Chi-Square test at 5% significance (Table 5). Traits with more correlations were Fruit shape (seven); Fruit shape at pedicel attachment (five); Fruit surface, Flower position, Corolla spot color, Calyx margin, Fruit shape at the endof flowering, Fruit cross-sectional corrugation (four). Fruit color at mature stage and endof flowering appendage had no correlation with any other trait.

Table 5. Cramer's V correlation of 15 reproductivequalitative traits used to detect genetic diversity of pepper. Monte Carmelo, UFU, 2016.

Trait	FNA	FP	CC	CSC	CP	CM	FCM	FSh	FSP	NB	FSB	FB	FCC	Fsu	SS
FNA	-	0.263	0.238	***0.471***	0.183	***0.459***	0.252	0.326	0.262	0.171	0.268	0.205	0.142	0.130	0.161
FP		-	0.189	***0.313***	0.166	***0.328***	0.267	***0.353***	0.224	0.153	0.198	0.197	0.212	***0.276***	0.222
CC			-	0.147	0.192	0.173	0.217	***0.395***	0.230	0.158	0.367	0.023	0.115	0.104	0.035
CSC				-	***0.494***	***0.850***	0.193	0.259	0.219	0.229	0.266	0.088	0.149	0.263	0.193
CP					-	0.118	0.202	***0.448***	0.038	0.002	0.121	0.056	0.146	0.115	0.088
CM						-	0.270	0.225	***0.430***	0.083	0.265	0.076	0.139	0.151	0.247
FCM							-	0.276	0.267	0.205	0.284	0.135	0.256	0.226	0.285
FSh								-	***0.442***	0.331	***0.485***	0.330	***0.473***	***0.517***	0.245
FSP									-	***0.487***	***0.426***	0.088	***0.354***	0.299	0.214
NB										-	***0.417***	0.045	0.194	*0.274*	0.075
FSB											-	0.231	***0.387***	0.297	0.282
FB												-	0.224	0.145	0.126
FCC													-	***0.603***	0.178
Fsu														-	***0.281***
SS															-

Values in bold represent significant correlation by Chi-Square test. FNA: Number of flowers per axil; FP: Flower position; CC: Corolla color; CSC: Corolla spot color; CP: Calyx Pigmentation; CM: Calyx margin; FCM: Fruit color at mature stage; FSh: Fruit shape; FSP: Fruit shape at pedicel attachment; NB: Neck at base of fruit; FSB: Fruit shape at the end of flowering; FB: End of flowering appendage; FCC: Fruit cross-sectional corrugation; FSu: Fruit surface; SS: Seed size.

On the other hand, fruit shape at the endof flowering and fruit color at mature stage had great contribution to distinguish genotypes, presenting higher MDI values. Large diversity between clusters can be observed for fruit color at mature stage varying between lemon-yellow, dark red, and purple. All fruit shape classes at the endof flowering were observed in clusters (pointed, blunt, sunken, sunken and pointed and others), demonstrating high variation of this genetic trait among accessions. Fruit shape was also detected as one of the most effective descriptors for *Capsicum* accessions by Costa et al. (2015).

MDI exhibit desirable properties for assessing the relevance of a variable: it is equal to zero only if the variable is irrelevant and depends only on relevant variables (Liaw and Wiener, 2002). MDI also showed that all 15 traits contributed to analyze genetic divergence and should be used in further similar studies. If the number of traits under analysisshould be reduced, Calyx margin and Calyx Pigmentation should be discarded due to their lower reduction on mean impurity and also because Calyx margin was correlated with FP, FNA, CSC and Fsh; and Calyx Pigmentation with CSC. Fruit blossom end appendage also showed lower score on MDI; however, this trait was not correlated with any other variable.

Capsicum spp. Germplasm Bank from UFU has high variability and qualitative reproductive traits were capable of distinguishing genotypes in several clusters. These results are in accordance with other published papers that accessed genetic divergence in peppers of the genus *Capsicum* (Baba et al., 2015; Maciel et al., 2016; Sudré et al., 2010). The same accessions were used to detect divergence based on the physiochemical characteristics of fruits (Maciel et al., 2016). Unlike this study, genotypes were clustered in only four groups, evidencing that reproductive traits were more variant in the germplasm. Our study also allowed isolating more genotypes. For plant breeders, isolated genotypes represent a possibility of new crossings that could explore maximum heterosis.

Multicategorical traits have the advantage of easy observation and require less time and labor, being ideal for use in gene bank and collections with short human and financial resources. Moreover, these traits are not affected by the environment. Genetic divergence detected in this paper encourages other researchers to perform the characterization of pepper collections as completely as possible, because it becomes possible to generate more reliable information of the variability and genetic divergence among accessions. Our research discloses the reproductive biodiversity of peppers in 'Alto Paranaíba' and 'TriânguloMineiro' regions and the importance of maintening these genotypes. For users of other pepper collections, there is possibility of using this genetic bank, ensuring new materials for plant breeders.

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