GENETIC DIVERSITY OF BRAZILIAN PEPPER BASED ON QUALITATIVE REPRODUCTIVE TRAITS

Gabriel Mascarenhas Maciel¹, Fábio Janoni Carvalho², Camila Soares de Oliveira², Lucas Medeiros Pereira³, Aline José da Silveira³, Igor Forigo Beloti³

¹Professor, Instituto de Ciências Agrárias, Universidade Federal de Uberlândia campus Monte Carmelo (UFU), km 1, LMG-746, Monte Carmelo/MG-CEP: 38500-000
²Doutorandos em Agronomia, Programa de Pós graduação em Agronomia, Instituto de Ciências Agrárias, Universidade Federal de Uberlândia (UFU), BR-050, km 78, Uberlândia/MG-CEP: 38410-337
³Graduandos em Agronomia, Instituto de ciências Agrárias, Universidade Federal de Uberlândia campus Monte Carmelo (UFU), km 1, LMG-746, Monte Carmelo/MG-CEP: 38500-000

*Autor para correspondência: Igor ForigoBeloti, agroifb@gmail.com

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 accessions equally. 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.
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.

PALAVRAS-CHAVE: 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, the number of small farmers has 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 (Bütow 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 of Uberlândia-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 “Triângulo Mineiro” regions of Minas Gerais that is home of small-scale pepper producers.

The experiment was conducted at the Horticultural Experiment Station, (18°42’43”S, 47°29’55”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 m². Four replicates of each accession were planted in a randomized block design (RBD).
Before transplanting, the experimental site was prepared by harrowing and diskng, both twice. Soil had the following characteristics: pH (H₂O) = 5.9; available P = 30.1 mg.dm⁻³; K⁺ = 0.22 cmolc.dm⁻³; Ca²⁺ = 2.8 cmolc.dm⁻³; Mg²⁺ = 1.0 cmolc.dm⁻³; exchangeable H + Al = 3.40 cmolc.dm⁻³; organic matter = 4.2 dag Kg⁻¹; SMP = 3.40; Al³⁺ = 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; Cu²⁺ = 2.3 mg.dm⁻³; Zn²⁺ = 6.6 mg.dm⁻³ and Mn²⁺ = 6.6 mg.dm⁻³. Crop treatments were performed as recommended for pepper. One hundred forty-five days after sowing, morphological characterization was performed at reproductive phase, according to Capsicum descriptors (IPGRI, 1995). Genetic dissimilarity matrix based on these multategorical variables was estimated by Gower’s algorithm (1971), since this technique is efficient to simultaneously analyze quantative and qualitative data, or only qualitative data (Moura et al., 2010). Dissimilarity among genotypes was expressed as:

\[ S_{ijk} = \frac{\sum_{k=1}^{p} W_{ijk} \cdot W_{ijk}}{\sum_{k=1}^{p} W_{ijk}} \]

where: \( k \) is the number of variables \((k = 1, 2, \ldots, p)\); \( i \) 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 ($\chi^2$) 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.

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

| Group  | Accessions                           |
|--------|--------------------------------------|
| 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 accessions equally. The same results were obtained by Bento et al. (2007), which grouped 19 of the 28 analyzed chili pepper accessions equally. Tocher and UPGMA methods were also partially coincident in the separation of 137 pepper genotypes from Southwestern Goiás (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 end of flowering appendage, calyx margin and calyx pigmentation (Figure 2). End of flowering appendage was 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  | FC/M  | 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 | 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 | Slightly corrugated | 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 | Absent | Present | Intermediate | Dark red | Campanulate | Acute | Present | Pointed sunken | Absent | Slightly corrugated | 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 | Slightly corrugated | Smooth | Small Intermediate | C. baccatum, C. chinense |
| 10| 3   | Erect     | Intermediate | White | Yellow-green | White | Absent | Intermediate | Lemon-yellow | Triangular | Truncate | Obtuse | Present | Absent | 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 | Slightly corrugated | 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 | Bongate | Obtuse | Absent | Pointed | Absent | Slightly corrugated | 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 | Smooth | Semiwrinkled | Intermediate | C. baccatum, C. chinense |
| 7 | 2   | Pendant | Yellow-green | White | Present | Intermediate | Lemon-yellow | Campanulate | Acute | Present | Sunken | Absent | Slightly corrugated | Semiwrinkled | Intermediate | C. baccatum                          |
| 8 | 2   | Erect | White | White | Absent | Intermediate | Lemon-yellow | Triangular | Acute | Absent | Sunken | Absent | Slightly corrugated | 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 | Slightly corrugated | Semiwrinkled | Intermediate | C. chinense                          |
| 11| 1   | Erect | White | White | Absent | Intermediate | Lemon-yellow | Bongate | 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 | Bongate | Obtuse | Absent | Sunken | Pointed | Absent | Slightly corrugated | Semiwrinkled | Small | C. baccatum, C. chinense        |
| 14| 3   | Intermediate | White | Other | Absent | Dentate | Dark red | Bongate | 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 end of flowering, Fruit cross-sectional corrugation (four). Fruit color at mature stage and end of flowering appendage had no correlation with any other trait.

Table 5. Cramer’s V correlation of 15 reproductive qualitative 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| 0.151| 0.247| -    | -    | -    |
| CM                     | -    | 0.270| 0.225| **0.430** | 0.083| 0.265| 0.076| 0.139| 0.151| 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 end of 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 end of 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 analysis should 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 physicochemical 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 Paranaiba’ and ‘Triângulo Mineiro’ regions and the importance of maintaining these genotypes. For users of other pepper collections, there is possibility of using this genetic bank, ensuring new materials for plant breeders.

REFERENCES

ABCSEM Associação Brasileira do Comércio de Mudas e Sementes. 2016, June 14. Pesquisa de mercado de sementes de hortaliças. Available at: http://www.abcsem.com.br/dadosdosegmento.php.

Alvares, R.C.; Reis, E.F.; Pinto, J.F.N. Genetic divergence in pepper genotypes from southwest Goiás. Ciência e Agrotecnologia, 2012, 36, 498-506. http://dx.doi.org/10.1590/S1413-70542012000500002

Baba, V.Y.; Rocha, K.R.; Gomes, G.P.; Ruas, C.F.; Ruas, P.M.; Rodrigues, R.; Gonçalves, L.S.A. Genetic diversity of Capsicum chinense accessions based on fruit morphological characterization and AFLP markers. Genetic Resources and Crop Evolution, 2015, 63, 1371-138. http://doi.org/10.1007/s10722-015-0325-4

Bento, C.S.; Sudré, C.P.; Rodrigues, R.; Riva, E.M.; Pereira, M.G. Descritores qualitativos e multicategóricos na estimativa da variabilidade fenotípica entre acessos de pimenta. Scientia Agraria, 2007, 8, 149-156.http://dx.doi.org/10.5380/rsa.v8i2.8379

Büttow, M.V.; Barbierre, R.L.; Neitzke, R.S.; Heiden, G. Diversidade genética entre acessos de pimentas e pimentões da Embrapa Clima Temperado. Ciência Rural, 2010, 40, 1264-1269. http://dx.doi.org/10.1590/S0103-84782010000600004

Bianchi, P.A.; Dutra, I.P.; Moulin, I.M.M.; Santos, J.A.; Santos Júnior, A.C. Morphological characterization and analysis of genetic variability among pepper accessions. Ciência Rural, 2016, 46,1151-1157. http://doi.org/10.1590/0103-8478cr20150825

Charrad, M.; Ghazzali, N.; Boiteau, V; Nikfans, A. NbClust: An R Package for Determining the Relevant Number of Clusters in a Data Set. Journal of Statistical Software, 2014, 61, 1-36. http://doi.org/10.18637/jss.v061.i06.

Costa, L.V.; Bentes, J.L.S.; Lopes, M.T.G.; Alves, S.E.M.; Viana Júnior, J.M. Caracterização de acessos de pimentas do Amazonas. Horticultura Brasileira, 2015, 33, 290-298. http://doi.org/10.1590/S0102-05362015000300003

Domenico, C.I.; Coutinho, J.P.; Godoy, H.T.; Melo, A.M.T. Caracterização agro-nômica e pungência de pimenta de cheiro. Horticultura Brasileira, 2012, 30, 466-472. http://doi.org/10.1590/S0102-05362012000300018

FAOSTAT - Food and Agriculture Organization of the United Nations. 2016, June 26. Available at: http://faostat.fao.org

Gower, J.C. A general coefficient of similarity and some of its properties. Biometrics, 1971, 27, 857-874. http://dx.doi.org/10.2307/2528823

IPGRI - INTERNATIONAL PLANT GENETIC RESOURCE INSTITUTE. Descriptor for Capsicum (Capsicum spp.). International Plant Genetic Resource Institute: Rome, Italy, 1995. 51 p.

Knezovic, Z.; Gunjaea, Z.; Satoviae, F.; Kolak, I. Comparison of Different Methods for Classification of Gene Bank Accessions. Agriculturae Conspectus Scientificus, 2005, 70, p. 87-91.

Kumar, S; Toshniwal, D. Analysis of hourly road accident counts using hierarchical clustering and cophenetic correlation coefficient (CPCC). Journal of Big Data, 2016, 3, 1-11. http://doi.org/10.1186/s40537-016-0046-3

Liaw, A; Wiener, M. Classification and Regression by random Forest. R News, 2002, 2/3, 18-22.
Maciel, G.M.; Oliveira, C.S.; Siquieroli, A.C.S.; Melo, E.I.; Oliveira, A.H.G. Genetic dissimilarity among the physiochemical characteristics of fruit from pepper accessions. *Bioscience Journal, 2016*, 32, 978-985. http://doi.org/10.14393/BJ-v32n4a2016-33893

Moura, M.C.C.L.; Gonçalves, L.S.A.; Sudré, C.P.; Rodrigues, R.; Amaral Júnior, A.A.; Pereira, T.N.S. Algoritmo de Gower na estimativa da diversidade genética em germoplasma de pimenta. *Horticultura Brasileira, 2010*, 28, 155-161.http://dx.doi.org/10.1590/S0102-05362010000200003

Paulus, D.; Valmorbida, R.; Santin, A.; Toffoli, E.; Paulus, E. Crescimento, produção e qualidade de frutos de pimenta (*Capsicum annuum*) em diferentes espaçamentos. *Horticultura Brasileira, 2015*, 33, 91-100. http://doi.org/10.1590/S0102-053620150000100001

Signorini, T.; Renesto, E.; Machado, M.F.P.S.; Bespalhok, D.N.; Monteiro, E.R. Diversidade genética de espécies de *Capsicum* com base em dados de isozimas. *Horticultura Brasileira, 2013*, 31, 534-539. http://dx.doi.org/10.1590/S0102-05362013000400005

Silva, F.C.S.; Sediyama, T.; Silva, A.F.; Bezerra, A.R.G.; Rosa, D.P.; Ferreira, LV. Identification of new descriptors for differentiation of soybean genotypes by Gower algorithm. *African Journal of Agricultural, 2016*, 11, 961-966, 2016. http://doi.org/10.5897/AJAR2015.10158

Silva, A.R.; Dias, C.T.S. Acopheneticcorrelationcoefficient for Tocher’s method. *Pesquisa Agropecuária Brasileira, 2013*, 48, 589-596. http://dx.doi.org/10.1590/S0100-204X2013000600003

Sudré, C.P.; Gonçalves, L.S.A.; Rodrigues, R.; Riva, E.M.; Amaral Júnior, A.T.; Rivasouza, E.M.; Bento, C.S. Genetic variability in domesticated *Capsicum* spp. as assessed by morphological and agronomic data in mixed statistical analysis. *Genetics and Molecular Research, 2010*, 9, 283-294. http://dx.doi.org/10.4238/vol9-1gmr698

Vasconcelos, C.S.; Barbieri, R.L.; Neitzke, R.S.; Priori, D.; Fischer, S.Z.; Mistura, C.C. Determinação da dissimilaridade genética entre acessos de *Capsicum chinense* com base em características de flores. *Revista Ceres, 2012*, 59, 493-498. http://doi.org/10.1590/S0034-737X2012000400009