

Genetic diversity of pepper genotypes in the municipality of Floriano – PI

Diversidade genética de genótipos de pimenta no município de Floriano – PI

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ABSTRACT – The genetic diversity of germplasm collections must be characterized to conserve and use the genetic resources of *Capsicum* spp. efficiently. Evaluation of this germplasm allows superior genotypes to be selected for breeding programs. In this context, the objective of this study was to characterize and estimate the genetic diversity among *Capsicum* spp. genotypes in Floriano, Piauí, Brazil, using multivariate analyses. Thirteen genotypes were evaluated in a completely randomized design with three replicates and one plant per plot. Thirteen qualitative traits and 13 quantitative traits were assessed. Significant differences were detected among genotypes for all quantitative traits evaluated, indicating genetic variability among the accessions studied. According to Scott–Knott mean grouping, plant height formed nine distinct classes, whereas stem diameter had the fewest groups, with only three classes. The combined analysis of quantitative and qualitative traits was effective for determining genetic divergence among pepper genotypes. The genotypes GENZ3, GEN28, and GEN37 produced fruits with potential for fresh consumption or sauce processing. The genotypes GEN38, GEN40, GEN75, and GEN77 had traits consistent with ornamental use. These findings provide information for *Capsicum* breeding programs focused on fresh-market and ornamental uses.

RESUMO – A diversidade genética de coleções de germoplasma deve ser caracterizada para conservar e utilizar eficientemente os recursos genéticos de *Capsicum* spp. A avaliação desse germoplasma permite a seleção de genótipos superiores para programas de melhoramento. Assim, o objetivo deste estudo foi caracterizar e estimar a diversidade genética entre genótipos de *Capsicum* spp., em Floriano, Piauí, Brasil, por meio de análises multivariadas. Treze genótipos foram avaliados em delineamento inteiramente casualizado, com três repetições e uma planta por parcela. Foram avaliados 13 caracteres qualitativos e 13 caracteres quantitativos. Diferenças significativas foram detectadas entre os genótipos para todos os caracteres avaliados, indicando variabilidade genética entre os acessos estudados. De acordo com o agrupamento de Scott–Knott, a altura de plantas formou nove classes distintas, enquanto o diâmetro do caule apresentou o menor número de grupos, com apenas três classes. A análise conjunta dos caracteres quantitativos e qualitativos foi eficiente para determinar a divergência genética entre os genótipos de pimenteiros. Os genótipos GENZ3, GEN28 e GEN37 produziram frutos com potencial para consumo in natura ou processamento na forma de molhos. Os genótipos GEN38, GEN40, GEN75 e GEN77 apresentaram características compatíveis com o uso ornamental. Esses resultados fornecem informações para programas de melhoramento de *Capsicum* voltados ao mercado de frutos frescos e ao uso ornamental.

Keywords: Multivariate Analysis. *Capsicum* spp. Genetic Resources.

Palavras-chave: Análise Multivariada. *Capsicum* spp. Recursos Genéticos.

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INTRODUCTION

Peppers of the genus *Capsicum* belong to the family Solanaceae and comprise 42 cataloged species (BURGOS-VALENCIA et al., 2020). Five domesticated species are recognized: *C. annuum* L., *C. baccatum* L., *C. chinense* Jacq., *C. frutescens* L., and *C. pubescens* Ruiz & Pav. (PERRY et al., 2007).

Peppers are widely marketed as fresh fruits, paprika, sauces, and preserves and are also used in sprays, medicines, and cosmetics (FERRAZ et al., 2016). Their fruits are rich in vitamins and are also sources of antioxidants and carotenoids (UARROTA et al., 2021). According to Rêgo and Rêgo (2018), demand has increased for pepper plants used as ornamentals. This demand is associated with traits that confer aesthetic value to pepper plants, such as variegated foliage, dwarf growth habit, and variation in fruit size and color at different maturation stages (NASCIMENTO et al., 2019).

Pepper cultivation is an important agribusiness segment because it generates employment and income and supports family farming (CAMARA, 2020). Agribusiness can be strengthened by expanding agricultural production through cultivar development to meet market demand (FERRAZ et al., 2016).

In this context, knowledge of available variability is a basic requirement for plant breeding programs. This knowledge is obtained through germplasm characterization, which is an initial requirement for studies of genetic diversity.

Multivariate analysis techniques have been used to estimate genetic diversity among genotypes because they allow quantitative and qualitative traits to be integrated (BARBÉ et al., 2010). Germplasm can be characterized using morphological, agronomic, biochemical, and molecular descriptors. Morphological characterization is especially important because it allows genotypes with traits of interest to be identified and selected. This enables the practical use of genetic variability in breeding programs (FERRAZ et al., 2016).

Gower's algorithm and principal component analysis (PCA) are widely used multivariate techniques applied to genetic divergence studies for genotype clustering and data dimensionality reduction, respectively. The integrated use of these tools provides a comprehensive assessment of variability and is important for identifying and selecting superior genotypes (BENTO et al., 2007). These studies generally use clustering methods, such as optimization and hierarchical methods, depending on the desired precision, ease

of analysis, and data collection method (CRUZ; FERREIRA; PESSONI, 2011).

In this context, the objective of this work was to characterize and estimate genetic diversity among *Capsicum* spp. genotypes in Floriano, Piauí, Brazil, using multivariate analyses.

MATERIAL AND METHODS

Genetic Material

The experiment was conducted from August 2018 to July 2019 in a greenhouse covered with screen mesh at the Federal University of Piauí, Amílcar Ferreira Sobral Campus (UFPI/CAFS), Floriano, Piauí, Brazil (6°47'28.9" S, 43°02'50.3" W). Thirteen pepper accessions from the Seed Collection of the UFPI/CAFS were used (Table 1).

Table 1. Scientific name, local common name, and source of *Capsicum* spp. accessions from the Seed Collection of the Federal University of Piauí, Amílcar Ferreira Sobral Campus, Floriano, State of Piauí, Brazil.

Accession	Scientific name	Local common name	Source
GEN11	<i>Capsicum baccatum</i>	Pimenta dedo de moça	Teresina, PI
GEN26	<i>Capsicum frutescens</i>	Pimenta malagueta	Floriano, PI
GEN28	<i>Capsicum annuum</i>	Pimentão vermelho	Floriano, PI
GEN32	<i>Capsicum chinense</i>	Pimenta de cheiro	Floriano, PI
GEN35	<i>Capsicum baccatum</i>	Chapéu de bispo	Floriano, PI
GEN37	<i>Capsicum annuum</i>	Pimentão amarelo	Floriano, PI
GEN38	<i>Capsicum annuum</i>	Pimenta ornamental	Floriano, PI
GEN40	<i>Capsicum annuum</i>	Pimenta ornamental	Floriano, PI
GEN63	<i>Capsicum chinense</i>	Pimenta de cheiro	Floriano, PI
GEN75	<i>Capsicum annuum</i>	Pimenta ornamental	Floriano, PI
GEN77	<i>Capsicum annuum</i>	Pimenta ornamental	Floriano, PI
GEN89	<i>Capsicum baccatum</i>	Pimenta dedo de moça	Teresina, PI
GENZ3	<i>Capsicum annuum</i>	Pimentão vermelho	Floriano, PI

Sowing was performed in 150-mL plastic containers filled with Garden Plus® vegetable substrate without chemical additives. When the seedlings had four to six pairs of true leaves, they were transplanted into 2.8-L plastic pots filled with sand, manure, and commercial substrate at a 1:1:1 ratio. A completely randomized experimental design was used, with three replicates and one plant per plot. Crop management practices were performed according to the technical recommendations for pepper production (FILGUEIRA, 2008).

Morphological Characterization

Accessions were characterized based on 13 qualitative descriptors and 13 quantitative descriptors proposed by the International Plant Genetic Resources Institute (IPGRI, 1995). The qualitative descriptors used were stem color, nodal anthocyanin, growth habit, leaf density, leaf color, leaf shape, flower position, anther color, corolla color, corolla spot color, intermediate fruit color, mature fruit color, and fruit shape.

The quantitative descriptors evaluated and their respective measurement methods were plant height (PH),

canopy diameter (CD), stem length (SL), leaf length (LL), and leaf width (LW) were expressed in centimeters. Stem diameter (SD), fruit length (FL), fruit width (FWD), pedicel length (PL), and fruit wall thickness (FWT) were measured with a digital caliper and expressed in millimeters. Fruit weight (FWG) was determined with a precision scale (g). Days to flowering (DFL) and days to fruiting (DFR) were counted as the number of days after transplanting.

Statistical analysis

The mode was used to analyze qualitative descriptors. For quantitative descriptors, plot means were subjected to analysis of variance (ANOVA). Means were grouped using the Scott-Knott test at the 5% significance level. The genetic dissimilarity matrix was estimated using Gower's algorithm (1971), considering both qualitative and quantitative descriptors. Hierarchical clustering was then performed from this matrix to generate a dendrogram. The number of groups was defined based on the internal biological coherence of each cluster, considering the discriminant morphological

characteristics of the accessions.

In addition, principal component analysis (PCA) (PEARSON, 1901) was used to graphically represent variability based on quantitative descriptors. All statistical analyses were performed using R software version 4.4.2 (R CORE TEAM, 2025). The cluster package was used to calculate Gower's dissimilarity matrix, which is suitable for mixed data. Hierarchical clustering was performed using the hclust function, and principal component analysis was performed using the prcomp function in the base stats package.

RESULTS AND DISCUSSION

Significant differences ($p < 0.01$) were detected for all quantitative descriptors evaluated (Table 2), indicating genetic variability among the pepper accessions. This information allows accessions with desirable traits to be selected. According to Ferreira et al. (2025), knowledge of genetic diversity is essential for selecting genotypes with alleles of interest that can be used as parents in breeding programs.

Table 2. Mean squares, coefficients of variation (CV), and F-test values from the analysis of variance of 13 descriptors evaluated in 13 pepper accessions from the Seed Collection of the Federal University of Piauí, Amílcar Ferreira Sobral Campus (UFPI/CAFS), Floriano, State of Piauí, Brazil.

SV	DF	Mean square				
		PH	SL	CD	SD	LL
Accessions	12	4551.4	923.70	815.43	1165.07	556.43
Error	26	28.4	10.71	23.17	0.81	1.99
CV (%)		8.35	11.98	11.66	11.76	12.03
F		160.26***	86.24***	35.19***	1438.35***	279.61***

SV	DF	Mean square			
		LW	DFL	DFR	PL
Accessions	12	2299.28	1311.70	783.15	487.67
Error	26	0.32	41.03	45.74	12.92
CV (%)		9.70	11.41	6.49	10.78
F		7185.25***	31.97***	17.12***	37.74***

SV	DF	Mean square			
		FWG	FL	FWD	FWT
Accessions	12	2382.95	3377.20	1088.29	711.64
Error	26	15.31	27.20	1.76	0.09
CV (%)		20.85	10.99	5.21	13.42
F		155.64***	124.16***	618.34***	7907.11***

***Significant at the 1% probability level according to the F test. SV = source of variation; DF = degrees of freedom; CV = experimental coefficient of variation; PH = plant height (cm); SL = stem length (cm); CD = canopy diameter (cm); SD = stem diameter (mm); LL = leaf length (cm); LW = leaf width (cm); DFL = days to flowering; DFR = days to fruiting; PL = pedicel length (mm); FWG = fruit weight (g); FL = fruit length (mm); FWD = fruit width (mm); FWT = fruit wall thickness (mm).

Based on Scott-Knott mean grouping, plant height formed nine distinct classes (Table 3), with means ranging from 8.83 to 132.16 cm. Tall pepper plants (≥ 100 cm) with small canopies (≤ 30 cm) often require staking to support growth and maintain plant architecture. According to Bento et al. (2007), plant height in peppers is an important factor for defining appropriate field management practices. Spreading or prostrate plants can hinder crop management, especially labor operations and spray applications. Therefore, prior knowledge of plant height is necessary to optimize crop management and ensure efficient harvest (MELO et al., 2014).

Fruit width and fruit length also varied, forming eight and seven classes, respectively. This result demonstrates variability in pepper fruit morphology. Fruit length and width are important attributes for the food industry, jelly production, and fresh or dehydrated consumption (COSTA et al., 2020).

Pedicel lengths of accessions GEN38, GEN40, GEN75, and GEN77 were 24.06, 16.57, 13.89, and 17.43 mm, respectively. This trait is relevant for ornamental use because fruits with longer pedicels are more visible against the foliage (MELO et al., 2014).

Stem diameter had the fewest classes, with three distinct classes. The highest Scott-Knott class included GEN11, GEN26, GEN32, GEN37, GEN63, and GEN89. Numerically, GEN37 and GEN11 had the largest means, at 10.63 and 9.51 mm, respectively. This trait is important for genotype selection because larger stem diameter provides greater resistance to plant lodging. According to Bianchi et al. (2016), plants with thin stems tend to lodge and lose fruit, which causes losses to farmers and decreases commercial value.

Table 3. Means of 13 *Capsicum* spp. accessions based on quantitative descriptors evaluated in Floriano, State of Piauí, Brazil.

Accessions	PH	SL	CD	SD	LL	LW	FWT
GEN11	132.16a	50.43a	83.66a	9.51a	11.83b	7.15c	1.93d
GEN26	79.00e	13.15f	41.90c	9.22a	17.56a	8.39b	0.53e
GEN28	46.80g	29.16d	37.46c	6.64b	11.77b	5.86d	4.22b
GEN32	76.33e	45.66b	41.66c	9.39a	15.25a	9.86a	1.78d
GEN35	114.36b	49.83a	53.33b	7.51b	13.43b	7.32c	2.68c
GEN37	62.20f	18.56e	45.66c	10.63a	15.92a	7.93c	5.97a
GEN38	15.83i	4.16g	25.73d	5.34c	7.89c	2.63e	1.89d
GEN40	8.83i	4.33g	19.36d	4.04c	5.84d	1.94f	1.45d
GEN63	88.43d	37.23c	40.36c	9.48a	15.34a	7.54c	1.88d
GEN75	25.33h	10.33f	29.66d	5.36c	4.05d	1.31f	0.84e
GEN77	23.50h	11.76f	23.03d	7.00b	7.26c	2.68e	1.05e
GEN89	98.83c	42.16b	50.53b	8.10a	10.82b	6.60d	1.89d
GENZ3	57.90f	38.40c	44.33c	7.30b	15.39a	7.07c	3.95b
Accessions	DFL	DFR	PL	FWG	FL	FWD	
GEN11	70.00a	118.00a	46.43b	10.78c	84.11c	22.60d	
GEN26	72.66a	109.00b	29.43d	0.50d	22.73h	5.37h	
GEN28	55.66b	109.00b	53.08a	54.20b	116.08a	42.40c	
GEN32	78.33a	120.00a	33.07d	6.74d	41.96e	23.54d	
GEN35	66.00a	116.66a	39.19c	14.57c	33.80f	41.62c	
GEN37	73.33a	119.00a	42.30c	89.72a	47.94e	69.98a	
GEN38	42.33c	91.00c	24.06e	3.11d	29.63f	16.68e	
GEN40	19.66d	71.00d	16.57f	1.48d	26.83f	9.97g	
GEN63	70.33a	108.66b	29.47d	4.07d	29.77f	22.84d	
GEN75	22.00d	75.66d	13.89f	0.20d	8.20h	5.73h	
GEN77	29.66d	97.00c	17.43f	0.81d	12.65h	10.84g	
GEN89	56.33b	104.33b	41.91c	5.92d	65.80d	14.69f	
GENZ3	73.66a	114.66a	46.48b	51.77b	97.29b	44.55b	

Means followed by the same letter within each column belong to the same class according to the Scott–Knott criterion ($p < 0.05$). PH = plant height (cm); SL = stem length (cm); CD = canopy diameter (cm); SD = stem diameter (mm); LL = leaf length (cm); LW = leaf width (cm); FWT = fruit wall thickness (mm); DFL = days to flowering; DFR = days to fruiting; PL = pedicel length (mm); FWG = fruit weight (g); FL = fruit length (mm); FWD = fruit width (mm).

In the combined analysis of traits, four groups were formed (Figure 1), indicating genetic diversity. According to Cansian Junior et al. (2021), genotype identification through morphological characterization is essential for understanding diversity among genotypes. This knowledge is important for estimating genetic diversity among available genotypes and promoting their more efficient use in breeding programs, thereby improving knowledge and use of the accessions (BIANCHI et al., 2016).

Group I included genotypes GEN38, GEN40, GEN75, and GEN77, all belonging to *C. annuum* and having ornamental traits. GEN40 has white petals with purple spots, which gives this accession ornamental value. According to Silva et al. (2015), pigments that contrast with the petals indicate high aesthetic value. Accession GEN75 also has traits associated with ornamental use, such as anthocyanin in the stem and corolla and purple anthers. According to Silva et al. (2015), anthocyanin in the stem and flowers increases visual

conspicuousness and commercialization potential. At maturity, GEN38 fruits are bright yellow. Bianchi et al. (2020) reported that *Capsicum* fruits can have several colors, with intermediate stages ranging from orange to green and purple, whereas red is the most frequent color at maturity. Genotypes with these traits are suitable for ornamental purposes. GEN40 had the lowest means for plant height (8.8 cm) and canopy diameter (19.3 cm). Accessions GEN38, GEN75, and GEN77 had mean plant heights of 15.8, 25.3, and 23.5 cm, respectively. These values characterize these genotypes as small and compact, which are desirable traits for pot cultivation (RIVAS et al., 2023). These values did not differ statistically between GEN38 and GEN40 or between GEN75 and GEN77 according to the Scott–Knott criterion.

Group II consisted of accessions GEN28, GEN37, and GENZ3, which belong to *C. annuum*. This group differed from the others because it contained accessions with higher means for fruit length, fruit width, and fruit wall thickness.

GEN28 had the highest mean for fruit length (116.08 mm). According to Silva et al. (2021), fruit size is important for defining fruit use; larger fruits can be consumed fresh or dehydrated, whereas smaller fruits are often used in products such as sauces. Accessions GEN37 and GEN23 had the highest means for fruit width, at 69.98 and 44.55 mm,

respectively. GEN37 had the highest mean for fruit wall thickness (5.97 mm). At maturity, GEN28 and GEN23 have red fruits, whereas accession GEN37 has yellow fruits. Andrade Júnior et al. (2018) emphasized that larger fruits and red coloration are important for paprika production.

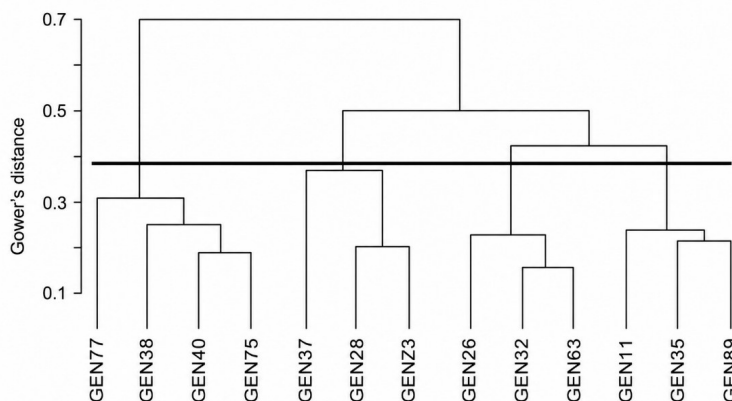


Figure 1. Dendrogram of genetic dissimilarity among 13 pepper accessions of the genus *Capsicum*, obtained using Gower's distance in the combined analysis of quantitative and qualitative descriptors.

Group III comprised accessions GEN26, GEN32, and GEN63, which had an erect growth habit. GEN32 and GEN63 had green stems with purple stripes and green leaves, whereas GEN26 had light-green leaves. GEN32 and GEN63 had canopy diameters of 41.66 and 40.36 cm, respectively, and fruit widths of 23.54 and 22.84 mm, respectively. GEN26 belongs to *C. frutescens*, whereas GEN32 and GEN63 belong to *C. chinense*. These accessions are part of the same gene pool, the *C. annuum* complex. Within each complex, greater relatedness and gene exchange occur, which facilitates interspecific crosses (PIMENTA et al., 2020).

Group IV consisted of GEN11, GEN35, and GEN89, which belong to *C. baccatum*. These accessions had white corollas with spots and yellow anthers. GEN11 and GEN89

fruits were green at the intermediate stage, whereas GEN35 fruits were orange. Accessions in this group had the highest means for plant height: 132.16 cm for GEN11, 114.36 cm for GEN35, and 98.83 cm for GEN89, indicating greater suitability for cultivation in open areas, such as vegetable gardens and ornamental gardens, and potential use in landscaping.

The relative positions of the accessions and quantitative traits, considering the first two components, which explained 82.3% of the variation, showed that GEN38, GEN40, GEN75, and GEN77 clustered together because they had lower means for plant height, canopy diameter, leaf length, fruit length, and days to fruiting (Figure 2).

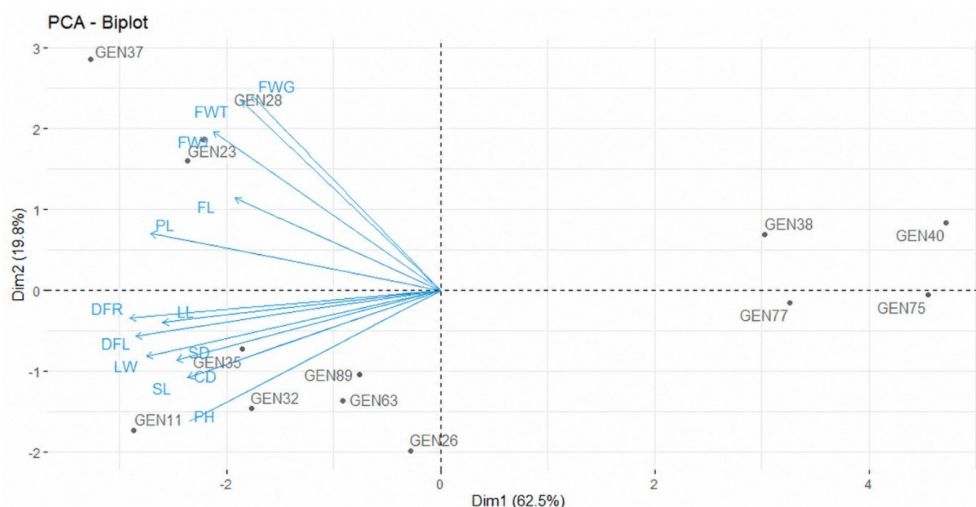


Figure 2. PCA biplot of 13 *Capsicum* spp. accessions generated by principal component analysis based on 13 quantitative descriptors: plant height (PH); canopy diameter (CD); stem length (SL); stem diameter (SD); leaf length (LL); leaf width (LW); fruit length (FL); fruit width (FWD); fruit weight (FWG); pedicel length (PL); fruit wall thickness (FWT); days to flowering (DFL); and days to fruiting (DFR), evaluated in Floriano, State of Piauí, Brazil.

Low means for fruit length and fruit width were recorded for accessions GEN38, GEN40, GEN75, and GEN77. According to Pessoa et al. (2018), small fruit size and compact plant habit are considered ornamental traits because they contribute to suitable plant conformation for potted pepper production.

GEN38, GEN40, GEN75, and GEN77 were distinguished by earliness in days to flowering, which ranged from 22 to 42 days, and days to fruiting, which ranged from 71 to 97 days. According to Pessoa, Rêgo, and Rêgo (2021), traits such as earliness are of great interest to producers because they allow rapid commercialization. The authors emphasized the importance of using alleles related to this trait in breeding programs because early maturity is important for developing superior genotypes. In the present study, the accessions evaluated had this trait, which indicates that they are promising genetic resources for obtaining earlier cultivars. Based on the pepper ideotype, accessions GEN38, GEN40, GEN75, and GEN77, which had small and compact plants, small fruits, and early flowering and fruiting, are recommended for ornamental use.

CONCLUSIONS

Genetic variability was detected among the pepper accessions analyzed. Multivariate techniques were effective for morphological characterization and estimation of genetic divergence among the genotypes studied. Accessions GEN28, GEN37, and GENZ3 can be recommended for the fresh market and sauce processing. Accessions GEN38, GEN40, GEN75, and GEN77 have ornamental potential. The genetic variability detected confirms the potential of the collection evaluated as a useful resource for *Capsicum* breeding programs focused on both fresh-market and ornamental production.

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