Universidade Federal Rural do Semi-Árido
Pró-Reitoria de Pesquisa e Pós-Graduação
https://periodicos.ufersa.edu.br/index.php/caatinga

ISSN 0100-316X (impresso)
ISSN 1983-2125 (online)
http://dx.doi.org/10.1590/1983-21252022v35n402rc

GENETIC DIVERSITY AMONG BITTER MELON GENOTYPES ASSESSED THROUGH MORPHO-AGRONOMIC VARIABLES[1]

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ABSTRACT - Bitter melon (*Momordica charantia* L.) is a plant species recommended by the Brazilian Health Regulatory Agency (Anvisa) as hypoglycemiant. The characterization of plants is an essential step in any breeding program. The objective of the present work was to organize and characterize a bitter melon germplasm collection, based on morpho-agronomic characters, to assess its genetic diversity and identify genotypes of agronomic interest. Eighty-eight genotypes were characterized for 38 descriptors. Redundant descriptors were identified through Principal Component Analysis (PCA); after their exclusions, a new PCA was carried out to verify the dispersion among the genotypes. Groups in the PCA were defined using the k-means clustering method. The groups were studied for phenotype pattern using radar chart. Populational diversity was estimated through Shannon and Pielou indexes. Intra group diversity was estimated through analysis of similarity (anosim). The relative importance of variables for diversity was also estimated. Seventeen variables were redundant. The genotypes were grouped into 5 groups. Groups G1 and G5 were antagonist regarding fruit and seed productions and fruit, leaf, and seed sizes. A trend of decrease in fruit, leaf, and seed sizes was found in groups from G1 to G5. The diversity was high. Intra group diversity was high among small fruit genotypes, and low for medium-sized fruit genotypes. The variable number of male flowers (NMFL) was identified as that presented the greatest contribution to estimation of diversity. The genotypes UFRRJ MSC072, 042, 028, and 087 stood out with the highest number of fruits produced.

Keywords: *Momordica charantia* L.. Principal Component Analysis. K-means clustering analysis. Diversity indexes. Grouping patterns.

DIVERSIDADE GENÉTICA ENTRE GENÓTIPOS DE MELÃO-DE-SÃO-CAETANO ACESSADA POR VARIÁVEIS MORFOAGRONÔMICAS

RESUMO - O melão-de-são-caetano (*Momordica charantia* L.) é uma espécie recomendada pela ANVISA como hipoglicemiante. A caracterização de plantas é uma etapa crucial em qualquer programa de melhoramento. O presente trabalho objetivou organizar e caracterizar uma coleção de germoplasmas de melão-de-são-caetano com base em caracteres morfoagronômicos, conhecer sua diversidade genética e identificar genótipos de interesse agronômico. Para tal, um total de 88 genótipos foram caracterizadas em relação a 38 descritores. Descritores redundantes foram identificados via análise dos componentes principais (PCA). Após a sua exclusão, procedeu-se uma nova análise PCA para verificação da dispersão entre os genótipos. A partir da estatística *k-means*, foram definidos grupos no plano PCA. Os grupos foram estudados quanto ao seu fenótipo padrão, utilizando-se gráficos radar. A diversidade populacional foi estimada via Shannon e Pielou. A diversidade intra-grupo foi estimada via anosim. Estimou-se também a importância relativa das variáveis sobre a diversidade. Ao todo, 17 variáveis foram redundantes. Os genótipos agruparam-se em cinco grupos. Os grupos G1 e G5 foram antagônicos quanto à produção de frutos e sementes e com relação aos tamanhos de frutos, folhas e sementes. Identificou-se uma tendência de redução no tamanho de frutos, folhas e sementes ocorrendo do grupo G1 ao G5. A diversidade foi alta. Porém, a diversidade intra-grupo foi alta entre genótipos com frutos pequenos, e baixa para genótpos com frutos intermediários. A variável número de flores masculinas foi identificada como de maior contribuição na estimação da diversidade. Os genótipos UFRRJ MSC072, 042, 028 e 087 destacaram-se para o número de frutos produzidos.

Palavras-chave: *Momordica charantia* L.. Análise de componentes principais. Análise de agrupamento K-means. Índices de diversidade. Padrões de agrupamento.

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[1]Received for publication in 03/18/2022; accepted in 07/12/2022.
Paper approved from V Symposium of the Northeast Plant Genetic Resources Network 2021.
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INTRODUCTION

Bitter melon (*Momordica charantia* L.) is a monoecious diploid species, with 2n = 2x = 22 chromosomes (ALAM; HAQUE; GOSH, 2018), that belongs to the Cucurbitaceae family. The origin of bitter melon is still unknown or controversial; possibly it is from Australia and the African continent (CABI, 2022). In Brazil, bitter melon is found in practically all regions of the country; it is a fickle, liana plant with a twining habit (LUTZ, 2022) known as a medicinal species. Bitter melon is included in the official list of medicinal plant species of interest by the Brazilian Health System (BRASIL, 2009) and is recommended for dermatitis and scabies treatments (BRASIL, 2010).

According to Lenzi, Orth, and Guerra (2005), the production demand of ruderal Cucurbitaceae species can be supplied through extractive processes and intercrop managements. Considering the scarcity of commercial bitter melon crops in Brazil, extractivism is probably the main current form of production of this species. However, extractive practices for bitter melon production may decrease its genetic basis over the years in Brazil. Therefore, there is an increasing demand for researches focused on gather information about the genetic diversity of this species, which is important for plant breeding programs.

Information on genetic variation is essential for selection of superior genotypes (TWUMASI et al., 2017; KUNDU et al., 2012). However, estimating it requires the implementation of conserved germplasm characterization activities. According to Allard (1966), the maintenance of a germplasm bank consists of a set of activities focused on making it useful for the breeder.

Despite the medicinal importance of bitter melon in Brazil, as far as is known to date, little efforts have been made towards the conservation and gathering of information about genetic diversity of this germplasm in Brazil. Consequently, the breeding of species focused on supplying the national demand has also not advanced. Information contained in official Brazilian governmental websites confirms the previous reports; the Allele Genetic Resource Platform (Plataforma Alelo Recursos Genéticos) shows the conservation of only 11 bitter melon accessions (EMBRAPA, 2022), whereas the Web Cultivar System of the Brazilian Ministry of Agriculture shows the record of only four bitter melon cultivars recommended for planting in Brazil (BRASIL, 2022). However, these records are from almost 20 years back.

In this context, considering the conservation of bitter melon and the agricultural development of this crop in Brazil, the objectives of this work was to organize a germplasm collection of the species and characterize it based on morpho-agronomic variables to understand and discuss the clustering pattern of the germplasm; estimate the genetic diversity between and within plant collection groups, estimating the relative contribution of the most important variables for the determination of genetic diversity; and identify, in the collection, the genotypes of interest to be included in breeding programs for the species.

MATERIAL AND METHODS

Study site and experimental conditions

The data were obtained from the analysis of 88 genotypes of bitter melon (*Momordica charantia* L.) belonging to the germplasm collection of the Department of Crop Science of the Federal Rural University of Rio de Janeiro (UFRRJ), Seropédica campus, Rio de Janeiro, Brazil (22°44'29"S, 43° 42'19"W). The climate of the region is tropical (Aw), characterized by rainy summers and dry winters (KÖPPEN, 1948).

The seedlings were grown in 128-cell expanded polystyrene trays containing a commercial substrate (MacPlant®). The seedlings were transplanted at 45 days after sowing, using one plant per 18-liter pot containing a Typic Hapludoll soil with pH of 5.47, 4.76 mgL^{-1} of Na, 26.0 mgL^{-1} of K, 7.0 mgL^{-1} of P, and 2.57% organic matter. The plants were trellised using bamboo stakes and sisal ropes. The irrigation was carried out using a drip system.

Plant material

The genotypes were identified with a UFRRJ MSC accession code, as shown in Table 1. All genotypes were originated from open pollination in their respective municipalities of origin.

Table 1. Origin of the bitter melon (*Momordica charantia* L.) genotypes from the germplasm collection of the Department of Crop Science of the Federal Rural University of Rio de Janeiro (UFRRJ).

Origin	Accession code	Number of genotypes
Seropédica, RJ	MSC001/ MSC002/ MSC003/ MSC012/ MSC013/ MSC014/ MSC015/ MSC016/ MSC022/ MSC023/ MSC024/ MSC025	12
Bom Jesus do Itabapoana, RJ	MSC017/ MSC018/ MSC019/ MSC20/ MSC021	5
Lavras, MG	MSC026/ MSC027/ MSC028/ MSC029/ MSC030	5
Diamantina, MG	MSC051/ MSC052/ MSC053/ MSC054/ MSC055	5
Monte Azul, MG	MSC056/ MSC057/ MSC058	3
Carangola, MG	MSC036/ MSC037/ MSC038/ MSC039/ MSC040	5
Jerônimo Monteiro, ES	MSC084/ MSC085	2
Vargem Alta, ES	MSC083	1
Dourado, SP	MSC071/ MSC072	2
São Paulo, SP	MSC046/ MSC047/ MSC048/ MSC049/ MSC050	5
Ribeirão Preto, SP	MSC031/ MSC032/ MSC033/ MSC034/ MSC035	5
Presidente Castelo Branco, SC	MSC007/ MSC008/ MSC009/ MSC010/ MSC011	5
Timbó, SC	MSC068/ MSC069/ MSC070	3
Mandaguaçu, PR	MSC041/ MSC042/ MSC043/ MSC044/ MSC045	5
Ivaiporã, PR	MSC004	1
Três Lagoas, MS	MSC064 / MSC065/ MSC066/ MSC067	4
Paulista, PE	MSC059/ MSC060/ MSC061/ MSC062/ MSC063	5
Ibiara, PB	MSC086/ MSC087/ MSC088	3
João Pessoa, PB	MSC005/ MSC006	2
Governador Dix, RN	MSC078/ MSC079/ MSC080/ MSC081/ MSC082	5
Guanambi, BA	MSC073/ MSC074/ MSC075/ MSC076/ MSC077	5

Variables analyzed

The data collection was carried out for 8 months, i.e., during the whole crop cycle. Thirty-eight quantitative morpho-agronomic variables related to fruits, flowers, leaves, seeds, and branches were analyzed, namely: number of fruits per plant (NFp), total fruit weight (g) (TFwe), mean fruit weight (g) (MFwe), total dry fruit weight (g) (TDFwe), mean dry fruit weight (g) (MDFwe), mean fruit length (cm) (MFle), mean fruit width (cm) (MFwi), mean fruit length to width ratio (MFlwr), pulp thickness (mm) (Pth), number of fruit protrusion rows (NFPro), number of aborted flowers and fruits (NAFLF), number of seeds per plant (NSp), mean number of seeds per fruit (MNSf), total seed weight (g) (TSwe), mean seed weight (g) (MSwe), mean seed length (cm) (MSle), mean seed width (cm) (MSwi), mean seed length to width ratio (MSlwr), mean aril weight (g) (MAwe), total dry fruit and dry seed weight (g) (TDFSwe), mean leaf length (cm) (MLle), mean leaf width (cm) (MLwi), mean leaf length to width ratio (MLlwr), mean number of lobules (MNLO), mean petiole length (cm) (MPle), petiole insertion angle (PIan), number of male flowers (NMFL), number of female flowers (NFFL), ratio between number of male and female flowers (NMFFLr), mean masculine floral peduncle length (cm) (MMFPle), mean female floral peduncle length (cm) (MFFPle), main stem length (cm) (MSTle), main stem diameter (cm) (MSTdi), number of base ramifications (NBR), mean internode length (cm) (MIle), number of internodes (NI), first branching height (cm) (FBhe), and number of fruits per plant per meter of main stem (NFp/MSTM).

Statistical analyses

The quantitative data were standardized, i.e., the value found was divided by the standard deviation of the corresponding variable. The matrix of data showed the need for discarding variables to minimize multicollinearity effects on the matrix. Thus, the data were subjected to Principal Component Analysis (PCA). Considering a minimum accumulation of 70.0% of total variance in the two first components, the cosine squared method was used to select the most important variables to reach the minimum accumulated variance in PC1 and PC2. The cosine squared shows the importance of a component for the observations (ABDI; WILLIAMS, 2010). The new matrix was used for a new PCA. A two-dimensional scattering was presented together with the k-means clustering analysis, making it possible to observe, simultaneously, the dispersion and the clustering pattern of the genotypes.

The means and standard deviations of each variable with high importance for PC1 and PC2 were estimated based on the clustering pattern of the genotypes through PCA/k-means. These variables were used to estimate the populational diversity indexes Shannon (H') and Pielou (J'). The diversity indexes between and within k-means groups were estimated through analysis of similarity (anosim).

The most important variables for PC1 and PC2 were subjected to analysis of relative importance (SINGH, 1981). All statistical

procedures were conducted using the R4.1.3 program (R CORE TEAM, 2022).

RESULTS AND DISCUSSION

According to the Principal Component Analysis (PCA), the two first Principal Components (PC) accumulated 72.80% of the variance (Figure 1). This estimate was only reached after the exclusion of 17 redundant variables from the 38 quantitative morpho-agronomic variables analyzed. Figure 2 shows the 21 most important variables in the two first PC, which were listed for subsequent analyses.

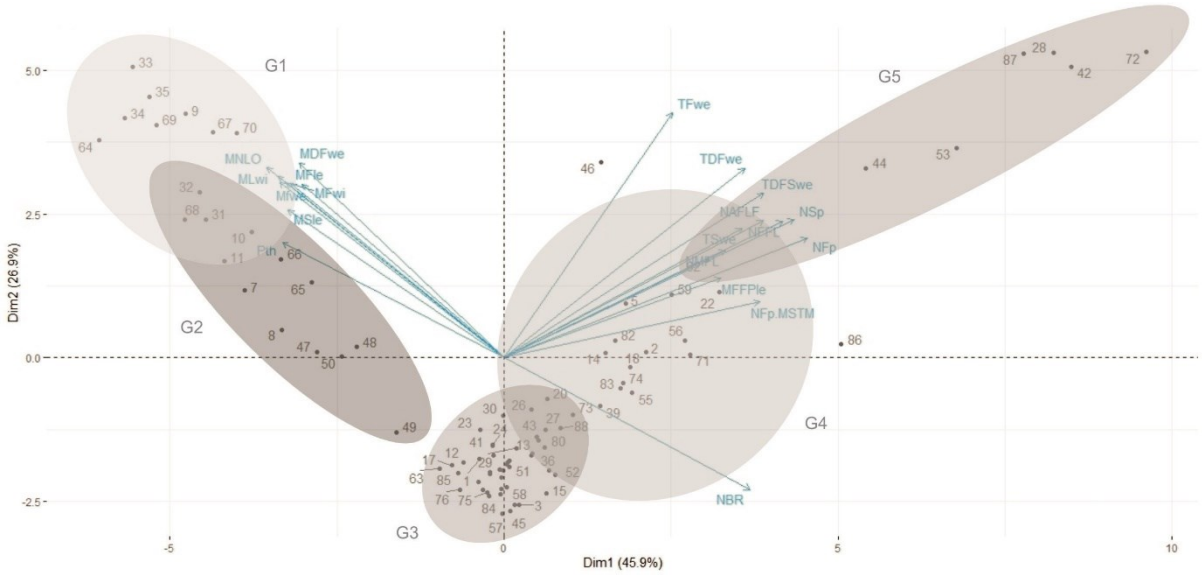

Figure 1. Principal Components Analysis (PCA) and k-means clustering analysis (groups G1, G2, G3, G4, and G5, left to right) based on 21 morpho-agronomic variables measured in 88 bitter melon (*Momordica charantia* L.) genotypes.

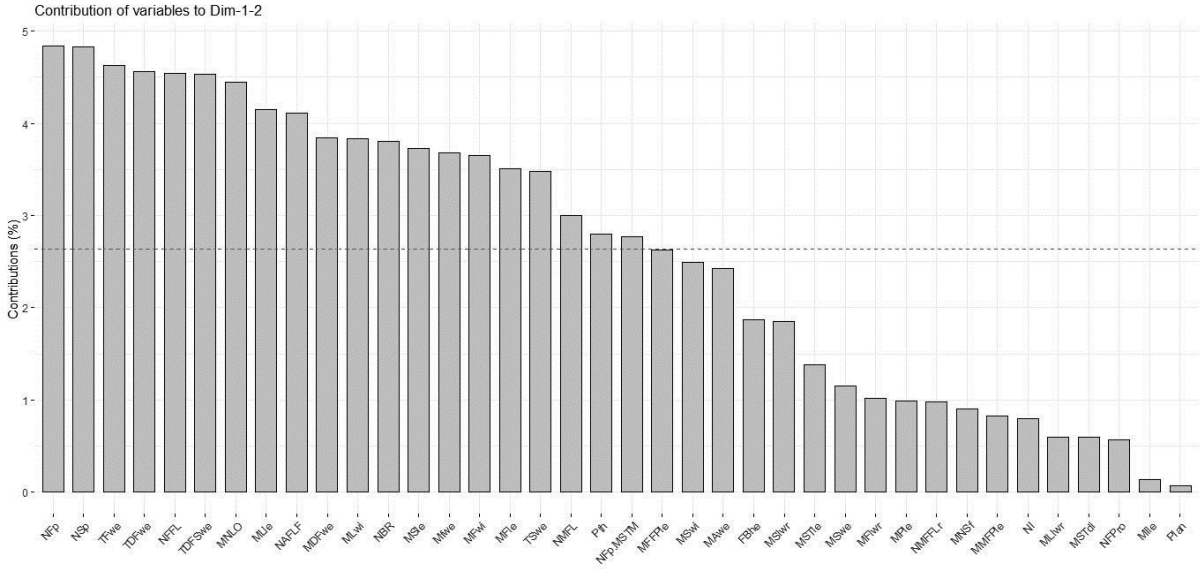

Figure 2. Relative individual contribution of morpho-agronomic variables to the two first Principal Components (PC1 and PC2). Bars below the cut point correspond to redundant variables that can be discarded. The variables were measured in 88 bitter melon (*Momordica charantia* L.) genotypes.

The PCA and k-means formed 5 groups of genotypes in the bitter melon germplasm collection (Figure 1): 9.09% of the genotypes were grouped in Group 1 (G1), 14.77% in Group 2 (G2), 51.14% (highest) in Group 3 (G3), 18.18% in Group 4 (G4), and 6.82% (lowest) in Group 5 (G5). The formation of groups had no correlation with the geographical origin of the genotypes (Table 1 and Figure 1). Maurya et al. (2018) also found no correlation between genetic diversity and geographical diversity.

Similar results were found by Singh and Kandasamy (2020), Kundu et al. (2012), and Singh, Singh, and Kumar (2013).

The groups formed by k-means showed a trend of decrease in the means of variables related to size of fruits (fruit length-MFle, fruit width-MFwi, and pulp thickness-Pth), seeds (seed length-MSle), and leaves (leaf length-MLle, leaf width-MLwi, and number of lobules-MNLO) (Table 2 and Figure 3) in the groups from G1 to G5. Contrastingly, an inverse trend was found from G1 to G5, with increases in fruit production (number of fruits per plant-NFp and total dry fruit weight-TDFwe), seed production (number of seeds per plant-NSp and total seed weight-TSwe) and flower production (number of male-NMFL and female-NFFL flowers) (Table 2 and Figure 3).

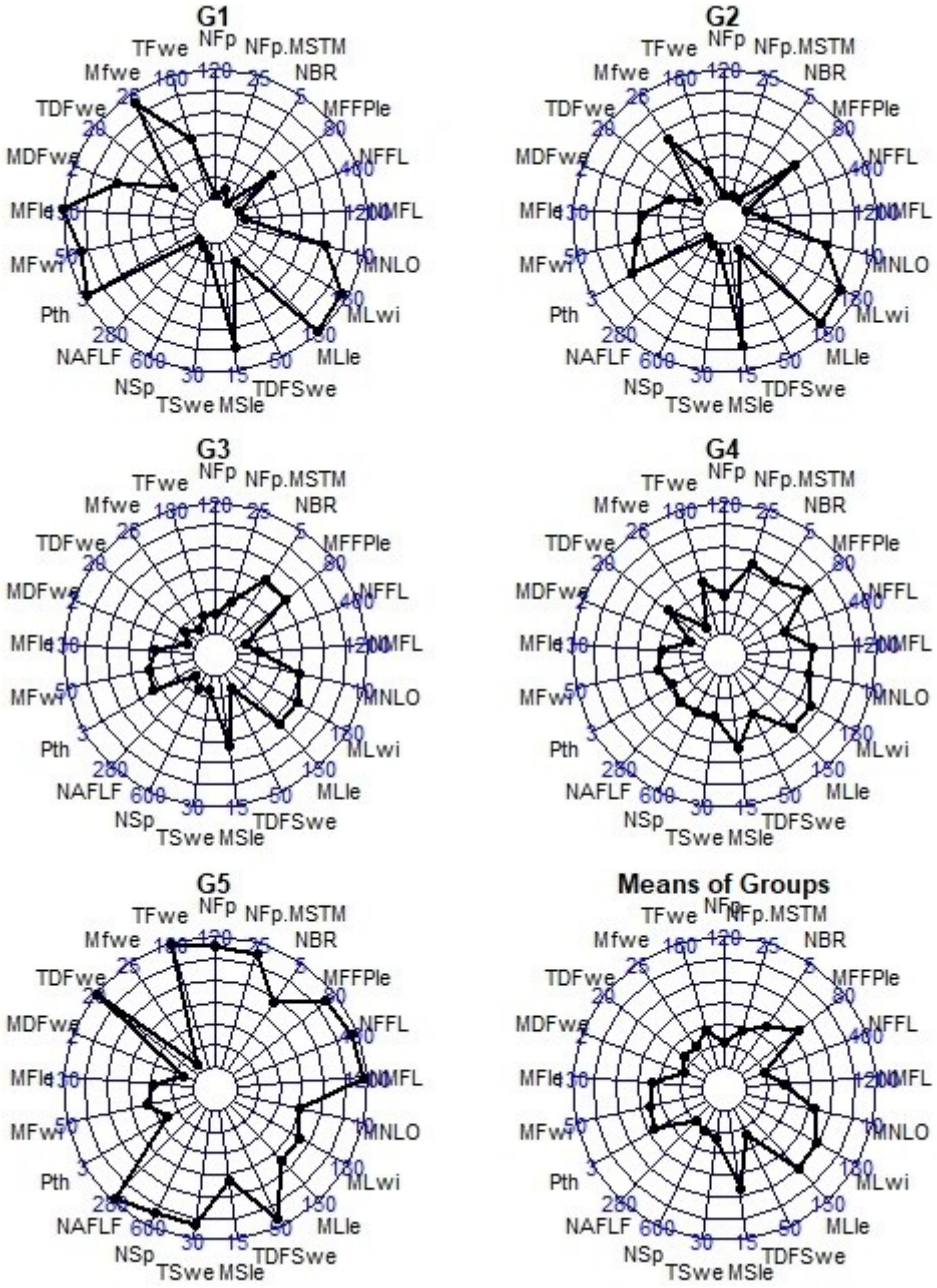

Figure 3. Means for 21 morpho-agronomic variables measured in 88 bitter melon (*Momordica charantia* L.) genotypes distributed into 5 groups (G1, G2, G3, G4 and G5), using, simultaneously, Principal Component Analysis (PCA) and k-means clustering analysis.

Table 2. Means and standard deviations for 21 morpho-agronomic variables measured in 88 bitter melon (*Momordica charantia* L.) genotypes distributed into 5 groups, using, simultaneously, Principal Component Analysis (PCA) and k-means clustering analysis.

Variable	Means ± standard deviation				
	Group 1	Group 2	Group 3	Group 4	Group 5
NFp	4.0 ± 1.70	3.31 ± 1.75	17.40 ± 7.28	32.88 ± 7.95	110.33 ± 27.27
TFwe	84.64 ± 22.94	37.83 ± 26.00	23.06 ± 11.97	69.08 ± 24.09	175.45 ± 49.42
MFwe	22.95 ± 5.47	10.66 ± 12.73	1.40 ± 0.40	2.23 ± 1.29	1.81 ± 0.40
TDFwe	5.40 ± 2.28	1.60 ± 1.16	2.09 ± 1.61	7.40 ± 3.06	19.47 ± 2.89
MDFwe	1.07 ± 0.48	0.53 ± 0.37	0.13 ± 0.08	0.24 ± 0.08	0.19 ± 0.04
MFle	13.49 ± 3.40	5.93 ± 2.16	3.78 ± 0.81	3.97 ± 0.59	3.93 ± 0.33
MFwi	4.37 ± 0.55	2.41 ± 0.71	1.74 ± 0.33	1.75 ± 0.20	1.86 ± 0.17
Pth	2.56 ± 1.52	1.50 ± 1.18	1.10 ± 0.26	0.86 ± 0.27	0.72 ± 0.09
NAFLF	6.88 ± 6.38	3.38 ± 3.33	13.78 ± 14.45	92.13 ± 50.70	271.33 ± 150.29
NSp	33.75 ± 20.08	21.31 ± 11.51	69.04 ± 33.25	179.06 ± 62.66	529 ± 71.72
TSwe	2.55 ± 2.06	1.95 ± 1.17	3.14 ± 1.47	8.91 ± 13.21	25.56 ± 4.91
MSle	1.24 ± 0.24	1.24 ± 0.25	0.84 ± 0.09	0.85 ± 0.12	0.82 ± 0.03
TDFSwe	9.28 ± 3.43	3.58 ± 1.92	5.36 ± 2.67	16.94 ± 13.06	45.09 ± 6.25
MLle	15.30 ± 1.67	13.30 ± 2.34	8.53 ± 1.13	8.40 ± 2.22	8.54 ± 0.53
MLwi	17.45 ± 2.31	15.15 ± 1.34	10.23 ± 1.47	10.43 ± 2.45	10.29 ± 0.72
MNLO	7.0 ± 0	6.38 ± 0.96	5.0 ± 0	5.13 ± 0.5	5.0 ± 0
NMFL	78.63 ± 42.17	162.08 ± 100.83	208.38 ± 47.13	734.0 ± 622.21	1159.17 ± 408.24
NFFL	10.88 ± 6.81	6.69 ± 3.22	31.18 ± 17.38	125.0 ± 49.76	381.67 ± 167.82
MFFPle	3.12 ± 1.01	4.14 ± 1.48	4.04 ± 0.87	5.10 ± 1.31	7.53 ± 1.04
NBR	0 ± 0	0.15 ± 0.55	2.60 ± 0.81	2.50 ± 0.82	3.17 ± 0.75
NFp/MSTM	2.31 ± 1.54	0.70 ± 1.22	5.91 ± 3.73	12.49 ± 9.37	19.62 ± 11.01

NFp = number of fruits per plant; TFwe = total fruit weight (g); MFwe = mean fruit weight (g); TDFwe = total dry fruit weight (g); MDFwe = mean dry fruit weight (g); MFle = mean fruit length (cm); MFwi = mean fruit width (cm); Pth = pulp thickness (mm); NAFLF = number of aborted flowers and fruits; NSp = number of seeds per plant; TSwe = total seed weight (g); MSle = mean seed length (cm); TDFSwe = total dry fruit and dry seed weight (g); MLle = mean leaf length (cm); MLwi = mean leaf width (cm); MNLO = mean number of lobules; NMFL = number of male flowers, NFFL = number of female flowers; MFFPle = mean female floral peduncle length (cm); NBR = number of base ramifications; NFp/MSTM = number of fruits per plant per meter of stem main.

Goo et al. (2016) reported bitter melon fruit lengths of 20.05 to 40.0 cm in an Indian germplasm. Alhariri et al. (2021), showed that the genotypes DBGS-7 and ArkaHarit, grown in central and west regions of India, present fruit lengths of 8.13 to 14.33 cm, respectively. In addition, Khan et al. (2015) reported fruit lengths of 15.55 to 21.59 cm; Kole et al. (2013) reported fruit lengths of 4.51 to 5.98 cm; and Assis et al. (2015) reported fruit lengths of 3.50 to 7.80 cm. Bitter melon fruits can be classified, based on their lengths, as: small (<10.0 cm), medium (10.0 to 20.0 cm), and large (> 20 cm). Based on in this classification, the germplasm collection analyzed presented genotypes containing medium- (group G1) and small-sized fruits (groups G5, G4, G3, and G2) (Table 2).

Considering that the genotypes were collected in 11 Brazilian states, the trend of production of small-sized fruits represents the variation of the Brazilian germplasm regarding fruit size. However, characterization and evaluation of collections in the field are necessary for more consistent conclusions. The results obtained by Assis et al. (2015) also denoted the occurrence of small fruits in Brazilian germplasms.

Regarding fruit production, genotypes in G5 produced, on average, 96.37% more fruits than genotypes in G1. The estimated mean number of fruits per plant (NFp) in these two groups was 110.33 and 4.0, respectively (Table 2). Khan et al. (2015) reported production ranging from 19.67 to 30.0 fruits for large-fruit plants in Dhaka, Bangladesh. Kole et al. (2013) reported production of 17.28 fruits per plant for the variety CBM12. Regarding medium-sized fruits, Singh and Kandasamy (2020), Maurya et al. (2018), and Kundu et al. (2012) reported productions higher than those found here (G1).

The number of male and female flowers of genotypes in G5 was, on average, 1159.17 and 381.67, respectively (Table 2). In this group, the estimated ratio between male and female flowers was 3.04. Considering the whole collection, the genotypes produced, on average, 4.22 male flowers for each female flower. According to Islam et al. (2014), increases in number of female flowers (NFFL) tend to decrease fruit size.

Based on the analysis of similarity (anosim), the estimates of diversity within k-means groups were different from each other (Figure 4) (R = 0.807

and P = 0.001). The Shannon and Pielou indexes estimated collection diversity of 2.25 and 0.74, respectively. These estimates denote a high populational diversity. The existence of high genetic diversity in bitter melon was also reported by Maurya et al. (2018), Khan et al. (2015), Singh, Singh, and Kumar (2013), and Kundu et al. (2012).

According to Singh and Kandasamy (2020) and Kundu et al. (2012), this high genetic diversity in bitter melon may be due to the occurrence of high cross-pollination rates resulted from its monoicous condition. The results obtained through the analysis of similarity denoted that G4 and G5 were the groups with the highest diversity magnitudes (Figure 4); whereas G3, G1, and G2 presented the lowest diversity estimates, which were below the mean (Figure 4).

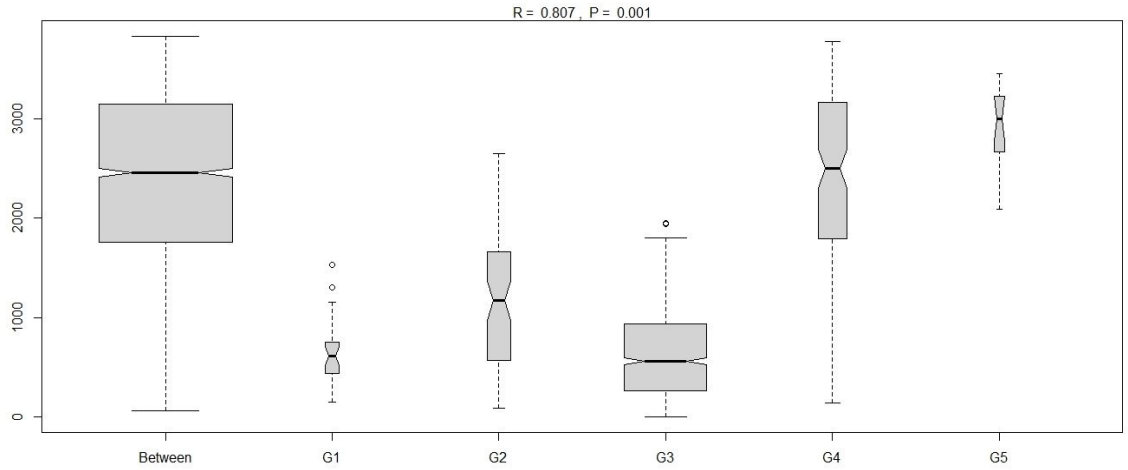

Figure 4. Box plots representing the genetic diversity through analysis of similarity (anosim) between and within 5 groups (G1, G2, G3, G4 and G5) of bitter melon (*Momordica charantia* L.) genotypes belonging to the germplasm collection of the Federal Rural University of Rio de Janeiro (UFRRJ).

The present work showed the existence of a trend of lower genetic diversity within groups of bitter melon genotypes with larger fruits, seeds, and leaves. Most germplasms analyzed presented small fruits, i.e., below 7.0 cm (MFle) (G3, G4, and G5; Table 2 and Figure 3).

Figure 5 shows the relative contribution of each one of the 21 variables for the estimation of genetic diversity, according to Singh (1981). The 6 first variables are highlighted, presenting relative contributions above 5.0%, namely: number of male flowers (NMFL) (22.0%), number of seeds per plant (NSp) (21.0%), number of female flowers (NFFL) (14.0%), total fruit weight (TFwe) (10.0%), number of aborted flowers and fruits (NAFLF) (8.0%), and mean fruit length (MFle) (7.0%). Together, these variables concentrated 82.0% of the relative contribution for the estimation of diversity. In addition, they correspond to characteristics connected to flowers (NMFL and NFFL), seeds (NSp), and fruits (TFwe, NAFLF and MFle).

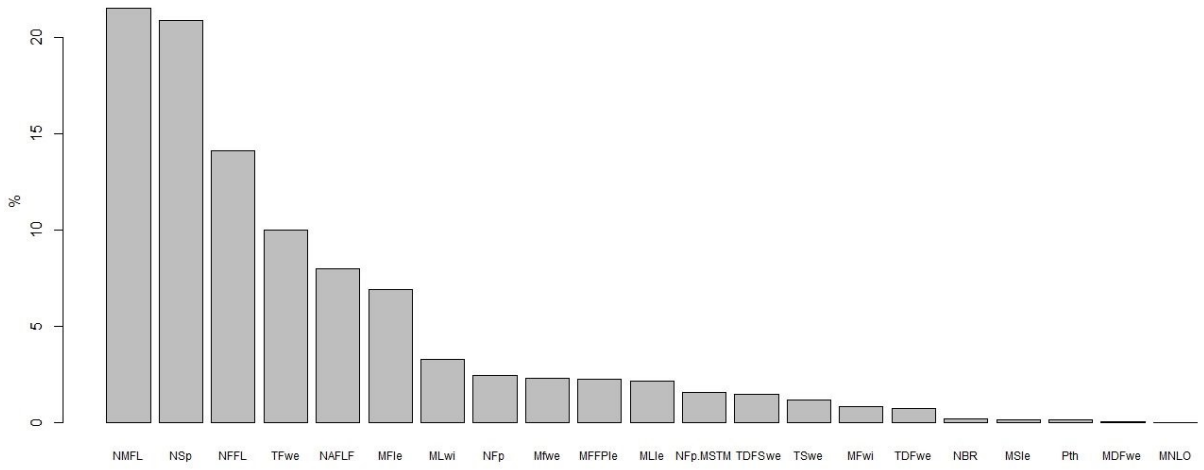

Figure 5. Relative contribution of 21 quantitative morpho-agronomic variables used for estimation of genetic diversity of *Momordica charantia* L. in the germplasm collection of the Federal Rural University of Rio de Janeiro (UFRRJ).

The genotypes UFRRJ MSC072 (146 fruits), UFRRJ MSC028 (128 fruits), UFRRJ MSC087 (118 fruits), and UFRRJ MSC042 (106 fruits) stood out for number of fruits produced. These genotypes belong to the same k-means group (G5, Figure 1), are from different origins (Table 1), and presented small fruits (Figure 1). Considering genotypes with medium-sized fruits (G1, Table 2 and Figure 3), UFRRJ MSC070 presented a production of only 7 fruits. Despite the crop was grown in a greenhouse, the production of this genotype can be considered very low, based on the literature (SINGH; KANDASAMY, 2020; MAURYA et al., 2018; KHAN et al., 2015; KUNDU et al., 2012). The results found here show that the scarcity of germplasm in Brazil for production of plants with medium-sized fruits can be partly explained by the low genetic diversity of the genotypes of this group. No large fruit genotype (> 20.0 cm length) was found in the collection.

Considering these results, in the context of bitter melon breeding, new Brazilian germplasm collections with medium- and large-sized fruits are needed, as well as the insertion of germplasm from other producing countries, such as India, Bangladesh, Philippines, and China.

CONCLUSION

The genotypes of bitter melon (*Momordica charantia* L.) analyzed were grouped into 5 statistically different groups. Group G1 encompassed genotypes with medium-sized fruits and low production of fruits and flowers. Groups G3, G4 and G5 encompassed genotypes whith greater number of fruits and smaller fruit size than G1 and G2. G5 grouped the most productive genotypes.

The genetic diversity of the collection was high. However, the estimates of intra group diversity showed a low genetic diversity among genotypes with medium-sized fruits. Variables related to flowers (number of male-NMFL and female-NFFL flowers), seeds (number of seeds per plant-NSp), and fruits (total fruit weight-TFwe, number of aborted flowers and fruits-NAFLF, and mean fruit length-MFle) had greater relative contribution to definition of the clustering pattern.

Regarding the fruit production, four genotypes are recommended to be included in bitter melon breeding programs, namely: UFRRJ MSC072, UFRRJ MSC028, UFRRJ MSC087, and UFRRJ MSC042. These genotypes presented small fruits. No genotype stood out for production of medium-size fruits. Large fruit genotypes were not found in the germplasm collection analyzed.

ACKNOWLEDGEMENTS

The authors thank the Brazilian National Council for Scientific and Technological Development (CNPq) for the financial support (Process 405926/2018-9), and the Brazilian Coordination for the Improvement of Higher Education Personnel (CAPES) (Financing Code 001) for granting study scholarship.

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