

Characterization of genetic diversity of bird-of-paradise accessions⁽¹⁾

ALESSANDRO APARECIDO DOS SANTOS^{(2)*}, VALDETE CAMPOS AMBROZIO⁽²⁾, MARCO ANTONIO APARECIDO BARELLI⁽³⁾, THALLITA SANTOS GUIMARÃES⁽²⁾, PETERSON BAPTISTA DA LUZ⁽³⁾

ABSTRACT

This study aimed to characterize genetic diversity in the bird-of-paradise (*Strelitzia reginae*) collection at the Universidade do Estado de Mato Grosso Carlos Alberto Reyes Maldonado (UNEMAT) by estimating genetic divergence among genotypes based on agronomic characteristics. Seven agronomic characters were evaluated with average Euclidean distance. The UPGMA (Unweighted Pair Group Method with Arithmetic Mean) hierarchical clustering method was used between groups, as well as Tocher's optimization clustering method and principal component analysis (PCA), in order to classify the genotypes with maximum similarity between groups. Measures of genetic dissimilarity with average Euclidean distance verified the existence of genetic variability among accessions since the amplitude of dissimilarity values ranged from 1.09 to 36.97. Tocher's clustering method verified the formation of two distinct groups. UPGMA hierarchical clustering, based on the dissimilarity matrix, verified the formation of three groups with 30% cutoff point. Based on the main components analysis, we verified genetic divergence between the bird-of-paradise accessions in the UNEMAT Collection. The most promising combinations for future crosses in breeding programs comprise accessions 1, 11, and 23 and accession 1 as the most divergent among the accessions evaluated.

Keywords: *Strelitzia reginae*, main components, cluster methods, divergence, tropical flowers.

RESUMO

Caracterização da diversidade genética de acessos de ave-do-paraíso

Este trabalho foi realizado com o objetivo de caracterizar a divergência genética de acessos de ave do paraíso da coleção de mudas da UNEMAT com base em características agrônomicas. Foram avaliadas sete características agrônomicas, com emprego da distância Euclidiana Média, foram utilizados os métodos de agrupamento médio entre grupos (UPGMA), o método de agrupamento de Otimização de Tocher, além da análise de componentes principais, a fim de classificar os genótipos que apresentassem a máxima similaridade entre os grupos. As medidas de dissimilaridade genética em relação às características avaliadas, fazendo uso da distância Euclidiana Média, demonstraram a existência de variabilidade genética entre os acessos avaliados, uma vez que a amplitude dos valores de dissimilaridade foi de 1,09 a 36,97. Na análise de agrupamento com a utilização do método de Otimização Tocher verificou-se a formação de dois grupos distintos. No agrupamento hierárquico UPGMA, fundamentado na matriz de dissimilaridade, apresentou a formação de três grupos com o ponto de corte a 30%. Com base na análise dos componentes principais pode-se observar que houve divergência genética entre os acessos de ave do paraíso avaliados.

Palavras-chave: *Strelitzia reginae*, componentes principais, métodos de agrupamento, divergência, flores tropicais.

1. INTRODUCTION

Tropical ornamental plants and flowers are gaining importance in floriculture owing to the attractiveness of the flowers and leaves, as well as their exotic colors, shapes, sizes and durability. Among tropical species, bird of paradise (*Strelitzia reginae*) has been cultivated for cut flowers based on their exotic colors and shapes, as well as vase life (durability), length of stems, and plant resistance to pests and diseases (WOOD, 1995; MACNISH et al., 2010; TERAO et al., 2005). Bird of paradise plants are frequently used in landscaping, but they are more attractive and exotic as cut flowers in arrangements and for decoration.

The bird of paradise tends toward polymorphism; thus, each plant originated from seed presents its own

characteristics, especially as reflected in plant height, shape and size of leaves, stem length, and flower size, among other characteristics (TERAO et al., 2005). Species characterization has been very important to breeding programs since they provide parameters by which to identify the parents, contributing to greater heterosis in the progeny and high probability of achieving superior genotypes in segregating generations, in addition to gaining increased knowledge about the genetic basis of plant populations as a whole (FERRÃO et al., 2002).

The present study aimed to genetically characterize bird of paradise accessions from the UNEMAT Collection based on agronomic characteristics.

DOI: <http://dx.doi.org/10.14295/oh.v24i1.1132>

⁽¹⁾Received in 10/11/2017 and accepted in 09/04/2018

⁽²⁾ Universidade do Estado de Mato Grosso, Departamento de Agronomia, Cáceres-MT, Brazil. *Corresponding author: alessandro.agrocerrado@hotmail.com

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2. MATERIAL AND METHODS

In the present work, 27 accessions of birds of paradise from different regions of Brazil were used. Accessions 1 and 2 are from Cuiabá (MT); accession 3 is from Cáceres (MT); accessions 4, 5, 6, 7, 8 and 9 are from Limeira (SP); accessions 10, 11, 12, 13, 14, 17, 21 and 22 are from Acorizal (MT); accessions 15, 16, 18 and 20 are from São José do Rio Preto (SP); accessions 19, 26 and 27 are from Campo Verde (MT); accessions 23 and 24 are from Joinville (SC), and accession 25 is from Florianópolis (SC).

The accessions were evaluated according to agronomic characteristics, including plant height, as measured from the base of the soil to the tip of the last leaf extended, petiole length, length of leaves, leaf width, length/width ratio of leaf blades, diameter of the base of the petiole, diameter of the apex of the petiole and number of leaves.

Data were submitted to a multivariate analysis based on the Euclidean Mean distance to obtain the Matrix of Dissimilarity, using grouping methods, hierarchical linkage between groups (UPGMA) and Tocher's Optimization, in addition to an analysis of components to classify the genotypes that presented the highest similarity among groups. The statistical procedures were performed using the computational software GENES (CRUZ, 2013).

3. RESULTS AND DISCUSSION

Genetic dissimilarity, relative to the characteristics evaluated, using the average Euclidean distance, revealed the existence of genetic variability among the bird of paradise accessions. The values of amplitude of dissimilarity ranged from 1.09 to 36.97, indicating the presence of a broad spectrum of variability among the accessions (Table 1).

Table 1. Genetic dissimilarity on seven characteristics of 27 bird of paradise accessions.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
1	0	28.7	30.8	30.4	28.4	28.5	35.5	24.5	28.4	31.7	36.4	32.5	27.1	29.2	35.2	31.5	32.6	33.5	30.0	32.3	27.0	30.2	37.0	35.2	33.7	26.4	30.7
2		0	9.3	2.7	2.5	2.6	8.6	6.4	9.3	5.2	9.3	10.8	2.7	4.8	8.7	4.0	4.3	5.3	4.7	4.0	3.2	4.5	10.3	7.4	6.6	4.7	2.7
3			0	11.0	8.2	10.0	6.7	14.4	18.2	5.9	8.5	19.7	9.2	13.7	6.2	6.6	8.6	8.3	7.6	8.6	8.0	5.1	7.4	9.1	6.7	6.6	8.7
4				0	3.8	4.6	8.8	7.5	9.0	6.4	9.4	9.3	4.7	4.0	9.1	4.9	4.1	5.0	6.3	4.0	5.5	6.0	10.6	7.3	7.2	7.3	3.6
5					0	4.5	8.2	7.7	10.9	4.8	9.0	12.1	2.4	6.2	8.1	4.0	4.5	5.5	4.6	4.3	2.5	3.8	10.0	7.7	6.5	4.4	3.3
6						0	9.5	5.6	8.5	5.7	9.7	10.6	3.3	4.9	9.5	5.1	5.4	6.4	4.1	4.9	3.7	5.6	11.1	7.5	7.0	4.9	3.4
7							0	14.8	16.7	4.4	3.1	16.7	9.7	11.8	1.2	4.6	5.1	3.9	7.2	5.5	9.2	5.3	1.8	4.0	3.0	9.3	6.8
8								0	5.7	11.0	15.1	9.6	6.0	5.5	14.9	10.2	10.3	11.4	9.0	9.9	6.9	10.3	16.5	12.9	12.5	8.0	8.3
9									0	13.4	16.2	4.8	9.4	5.6	17.0	12.8	11.8	13.0	11.4	11.5	10.6	13.5	18.3	13.8	14.4	12.5	10.2
10										0	4.9	14.3	5.7	8.8	4.3	2.1	3.2	3.4	3.0	3.4	5.1	2.3	5.9	4.1	2.4	5.5	3.4
11											0	15.9	10.0	11.7	3.3	5.9	5.3	4.8	6.9	5.9	9.7	6.8	3.4	2.8	3.6	10.4	6.9
12												0	11.3	6.8	17.0	13.5	11.8	12.9	12.8	11.7	12.6	14.7	18.1	13.6	14.7	14.9	11.0
13													0	5.6	9.6	5.4	5.6	6.9	4.1	5.3	1.4	5.1	11.4	8.5	7.4	4.1	3.6
14														0	12.2	7.9	7.0	8.1	7.5	7.0	6.7	8.7	13.5	9.5	9.9	8.7	5.7
15															0	4.8	5.3	4.4	7.0	5.6	9.0	5.3	2.1	4.3	2.8	9.1	6.9
16																0	2.5	2.4	4.1	2.5	5.0	1.9	6.4	4.6	3.1	5.4	2.9
17																	0	1.7	4.4	1.1	5.8	4.1	6.8	3.5	3.4	7.1	2.2
18																		0	5.4	2.1	6.9	4.2	5.6	3.2	3.0	7.7	3.7
19																			0	4.3	3.7	4.1	8.6	5.5	4.6	4.9	2.9
20																				0	5.5	4.1	7.1	3.9	3.4	6.8	2.1
21																					0	4.3	10.8	8.4	7.0	2.9	3.9
22																						0	7.0	6.0	4.0	4.1	3.9
23																							0	5.0	4.4	10.8	8.5
24																								0	2.7	9.2	5.0
25																									0	7.4	4.5
26																										0	5.6
27																											0

The most divergent accessions showed the highest dissimilarity (d_{ii}) of 36.97 and 36.38%, with the most divergent combinations for accessions 23 and 1 and 11 and 1, respectively. Therefore, these accessions present the highest divergence relative to all accessions evaluated. Based on the results, future genetic improvement programs can be suggested for these accessions showing high genetic divergence since their progeny would have greater genetic variability, which is desirable for plant crossings. According to Kvitschal (2009), the plant descendants of hybrids can generate seedlings with agronomic characteristics of interest and high production potential.

The combinations with the smallest distance magnitude based on values of d_{ii} were accessions 20 and 17, 21 and 14, 15 and 7, 18 and 17, 23 and 7, and 22 and 16 with d_{ii} values of 1.09, 1.39, 1.19, 1.72, 1.82 and 1.90%, respectively. These results indicate lower divergence relative to all evaluated accessions. Consequently, these accessions should not be recommended for genetic improvement

programs since their progenies would generate low heterosis, thereby reducing the possibility of genetic gains with these combinations.

Cluster analysis using Tocher's Optimization (Table 2) revealed the formation of two distinct groups. Group I was the most numerous with 96.30% of the 27 accessions evaluated. Group II was formed by accession 1 alone, representing 3.70% of the accessions evaluated, suggesting that this group is the most divergent and, consequently, the most suitable for future genetic improvement of bird of paradise. The results of this study were similar to those obtained by Zuin et al. (2009), who evaluated the genetic divergence among cassava accessions (*Manihot esculenta* Crantz) in the municipality of Cianorte (PR) and verified the distribution of the most divergent accessions using Tocher's method. Puiatti et al. (2014) evaluated the productivity of garlic accessions through morphological characteristics and observed that Tocher's method divided 60 accessions into eight different groups.

Table 2. Representation of Tocher's method based on genetic dissimilarity of seven characteristics on 27 accessions of bird of paradise.

Groups	Accessions	%
I	17, 20, 18, 16, 27, 10, 25, 22, 19, 24, 2, 5, 21, 13, 6, 4, 26, 7, 15, 11, 23, 3, 14, 8, 9 e 12	96.29
II	1	3.7
Total	27	100

Intergroup analysis (Table 3) revealed that the highest values of genetic divergence occurred between groups

I and II and that group I presents the smallest intergroup distance.

Table 3. Mean intra- and intergroup distances estimated by Tocher's method based on the dissimilarity matrix of seven characteristics on 27 accessions of bird of paradise.

GRUPOS	I	II
I	7.14	31.05
II		-

Figure 1 shows that the UPGMA hierarchical grouping method, which is based on the dissimilarity matrix, resulted in the formation of of three groups with the cutoff point at 30%.

The first group consisted of a large number of accessions, with 23 of the 27 accessions evaluated. Group II consisted of three accessions. Group III consisted of only one accession.

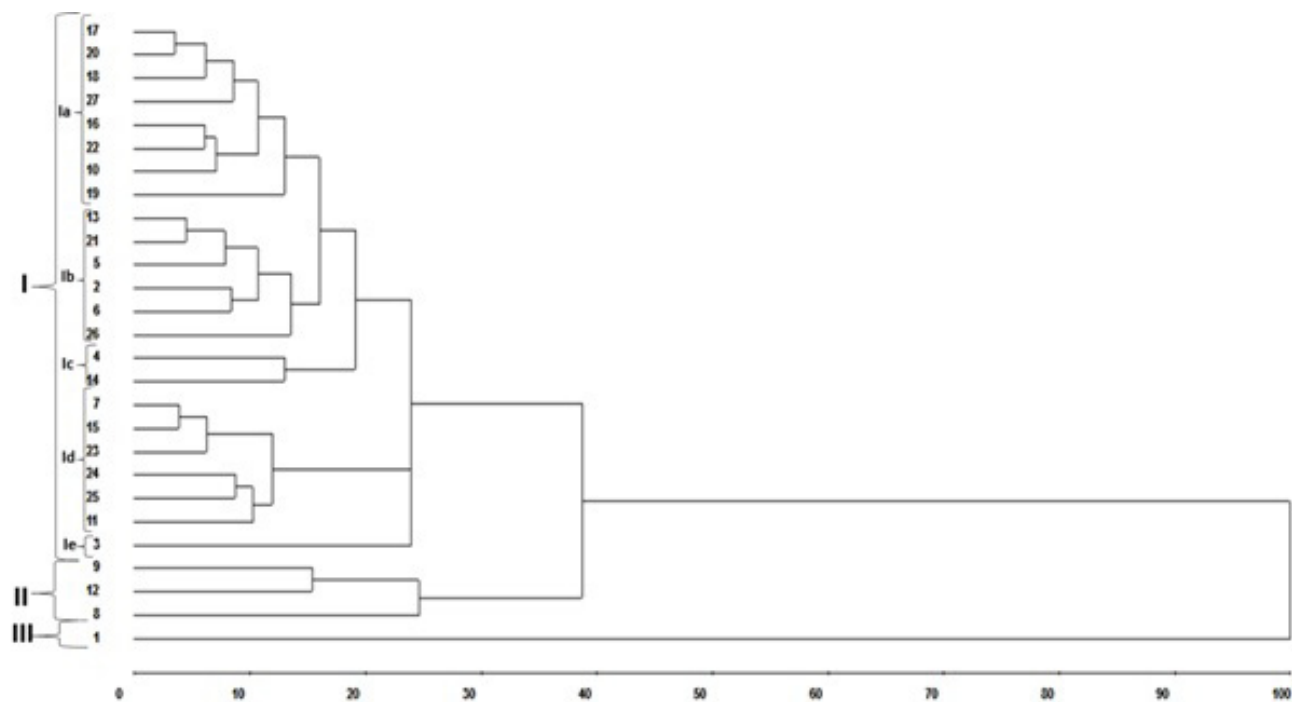


Figure 1. Dendrogram of the genetic divergence among the 27 accessions of birds of paradise obtained by the UPGMA method based on dissimilarity matrix of seven characteristics.

Cophenetic correlation coefficient (CCC) showed a significant value with $r = 0.95$ ($p < 0.01$), demonstrating reliability in the relationship between dissimilarity matrix and dendrogram, allowing inferences through visual evaluation and demonstrating reliability in the relationship between the dissimilarity matrix and the dendrogram generated by UPGMA. The CCC value of the dendrogram from 70% shows a good fit between the graphical representation of the distances and its original matrix, allowing the possibility of making inferences by visual evaluation (ROHLE, 2000). According to Monteiro et al. (2010), the representation of the similarity matrix of a dendrogram is better when it is closer to the unit.

Group I was formed by 85.18% of the accessions. This group was divided into subgroups Ia, Ib, Ic, Id and Ie. Subgroup Ia was formed by accessions 17, 20, 18, 27, 16, 22, 10 and 19. Subgroup Ib was formed by accessions 13, 21, 5, 2, 6 and 26. Subgroup Ic was formed by accessions 4, 5, 6, and 14. Subgroup Id was formed by accessions 7, 15, 23, 24, 25, and 11. Subgroup Ie was formed by accession 3 alone.

Group II consisted of 11.11% of the accessions, and this group was formed by accessions 9, 12 and 8. Group III was the most divergent, representing only 3.7% of the total accessions and was composed of accession 1. Even though group III was isolated from the other groups, accession 1 was still the most divergent among all accessions.

Comparing clustering methods, we observed that the UPGMA method formed more groups than Tocher's method. The UPGMA method offered a more detailed

presentation, allowing the visualization of the distances inside the group, thus complementing Tocher's method. Tocher's method provided different groups; however, the grouping methods were concordant in the way they grouped accession 1 isolated from the other accessions. Kvitschal et al. (2009), studying the characterization and genetic divergence of cassava germplasm from the urban region of Maringá (PR), also concluded that the combination of the two methods allows a better orientation by which to choose accessions. Gomes Filho et al. (2010) used RAPD molecular markers and morpho-agronomic characteristics to evaluate the genetic divergence between six cultivars and 19 accessions of guava trees, and they verified partial correlation among the cluster methods studied. Bonett et al. (2010) used multivariate techniques to evaluate the genetic diversity of 63 bean cultivars in 11 morpho-agronomic characteristics, and they concluded that UPGMA and Tocher's grouping methods were partially concordant in establishing the same number of groups. The authors stated that the UPGMA grouping method was more sensible or accurate than Tocher's method, essentially because it grouped the most similar accessions differently, indicating the higher efficiency of the method. However, both methods should be applied together for better results.

PCA also showed genetic divergence among the bird of paradise accessions (Table 4). Results show that the first two components explained about 96.83% of the total variation and that CP1 was responsible for 71.60% and CP2 for 25.24%, adapting, in this case, to a two-dimensional graphical representation (Figure 2).

Table 4. Eigenvalues and eigenvectors associated with seven morpho-agronomic characters on 27 accessions of bird of paradise.

Principal components	Root (%)	% Accumulated
Length of leaves	71.60	71.60
Diameter of the apex of the petiole	25.24	96.83
Petiole length	1.83	98.67
Length of leaves	0.89	99.56
Diameter of the base of the petiole	0.39	99.95
Plant height	0.05	99.99
Number of leaves	0.0001	100.00

In studies carried out by Rocha et al. (2013), who evaluated the quality of light guava nectars of different brands marketed in Lavras (MG), it was observed that the first two principal components explained about 84.08% of

the total variation. PCA is used when the first components involve at least 80% of the total variation, allowing evaluation of the importance of each studied character on the total variation among genotypes (CRUZ et al., 2012).

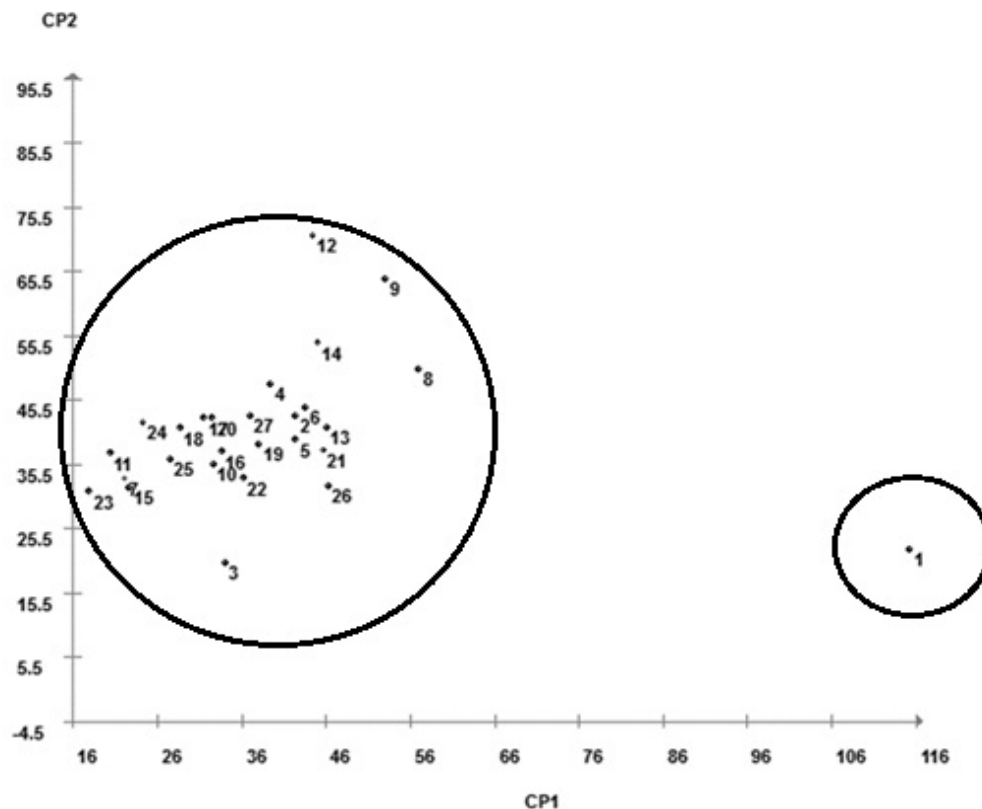


Figure 2. Graphical dispersion of the scores in relation to the representative axes of the first two main components (CP1 and CP2) of seven morpho-agronomic characters on 27 accessions of bird of paradise.

The graphical representation of genotype dispersion, which is based on the first two main components arranged in the two-dimensional space, revealed the formation of two small divergent groups, showing great similarity (Figure 2). Group I was formed by most accessions, and group II was only formed by accession 1 from Cuiabá, MT, indicating that this accession diverges from others in the study (most dissimilar) and is, therefore, the most suitable for genetic improvement programs. It is necessary to select parents who present a greater divergence in the characteristics in order to perform crosses between parents (HALLAUER and MIRANDA FILHO, 1981).

The intergroup space formed by the majority of the accessions in the dispersion graphic presented little dispersion, indicating, in turn, little divergence among them. A convergence was observed between the UPGMA and Tocher grouping methods with respect to the graphical representation of dispersion among the formed accession groups, indicating consistency in the results to identify divergent accessions. The graphical representation of dispersion simplified and complemented the interpretation of the other clustering methods used.

4. CONCLUSIONS

Our results show genetic variability among bird of paradise accessions in the plant collection of UNEMAT. The most promising combinations for future crosses in breeding programs comprise accessions 1, 11, and 23. Accession 1 is the most divergent among the accessions evaluated.

AUTHORS CONTRIBUTIONS

A.A.S.: main author of the manuscript, performing the analysis, tabulation of data and discussion of the results. **V.C.A.:** assistance in the implementation of the experiment, collection, tabulation and interpretation of data and construction of tables and graphs. **M.A.A.B.:** statistical analysis and discussion of results. **T.S.G.:** assistance in the implementation of the experiment and data collection. **P.B.L.:** writing and discussion of the results.

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