

SCIENTIFIC ARTICLE

Selection of desert rose accessions with high ornamental potential

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Abstract

Adenium obesum belongs to the Apocynaceae family and is characterized as a succulent shrub with a multitude of botanical and morphological features of ornamental interest. The aim of this study was to evaluate the genetic dissimilarity of 28 accessions of *A. obesum* using morphological descriptors and multivariate techniques with the aim of pre-selecting the genotypes with the greatest ornamental potential. The distribution of the number of flowers throughout the year showed two flowering peaks in January and September. Twenty-one petal pigmentation patterns were identified, and 50% of the accessions had double-petal arrangement. The Gower's algorithm and the UPGMA-generated dissimilarity matrix indicated the formation of three groups. While Tocher's clustering method separated the accessions into eight groups showing greater ability to distinguish the evaluated genotypes. In conclusion, the multivariate analyses applied were effective in accessing the genetic diversity among the 28 accessions evaluated. The accessions ICA001, ICA005, ICA006, ICA018, ICA019, and ICA027 were preselected to compose the germplasm collection due to their high ornamental potential.

Keywords: desert rose, genetic variability, morphological markers, ornamental plants.

Resumo

Seleção de acessos de rosa-do-deserto com alto potencial ornamental

Adenium obesum, conhecida popularmente como rosa-do-deserto, pertence à família Apocynaceae e caracteriza-se por ser um arbusto suculento, com uma infinidade de aspectos botânicos e morfológicos de interesse ornamental. Objetivou-se no presente estudo avaliar a dissimilaridade genética de 28 acessos de *A. obesum* por meio de descritores morfológicos e técnicas multivariadas com objetivo de pré-selecionar os genótipos com maior potencial ornamental. A distribuição do número de flores durante os meses do ano demonstrou dois picos de florescimento em janeiro e em setembro. Vinte e um padrões de pigmentação petalar foram identificados e 50% dos acessos apresentaram 10 pétalas por flor (arranjo petalar duplo). Considerando os dados mistos, o algoritmo de Gower juntamente com a matriz de dissimilaridade gerada pelo método UPGMA indicou a formação de três grupos. O agrupamento de Tocher separou os acessos em oito grupos. Conclui-se as análises multivariadas aplicadas foram eficazes em acessar a diversidade genética entre os 28 acessos avaliados. Os acessos ICA001, ICA005, ICA006, ICA018, ICA019 e ICA027 foram pré-selecionados para comporem a coleção de germoplasma por apresentarem alto potencial ornamental.

Palavras-chave: marcadores morfológicos, plantas ornamentais, rosa-do-deserto, variabilidade genética.

Introduction

Popularly known as desert rose, *Adenium obesum* (Forssk.) Roem. & Schult. is an ornamental species with great potential for landscaping that has gained prominence for its high resistance to full sun and low water requirements. In addition, the plant presents a structure called the caudex that, besides having a sculptural shape, acts as a water storage organ (Santos et al., 2020). Other ornamental aspects also draw much attention from

landscapers, collectors, and floriculturists: the variability in color, and the shape and arrangement of the flower petals (Ramos et al., 2022).

A number of steps need to be taken to develop a new variety in plant breeding, with germplasm development is being considered one of the most important at the initial phase of the pre-breeding phase (Faleiro et al., 2008). During the germplasm evaluation is possible select superior genotypes and support the practical use of genetic resources, contributing to expanding the genetic base of

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breeding programs (Salgrota and Chauhan, 2023). At this stage, adequate characterization of the genetic diversity needs to be performed through the evaluation of phenotypic (agronomic and morphological descriptors) and molecular characteristics (Faleiro et al., 2008).

Estimating the genetic diversity through morphological markers and using biometrics is relatively simple and efficient for characterizing genotypes, selecting individuals to be allocated to germplasm banks, and assisting in the choice of parents for crossbreeding (Swarup et al., 2021). Multivariate techniques are indispensable for this process because they make it possible to group similar individuals, revealing the differences between the groups (Cruz and Regazzi, 2020). Estimates of genetic distances between individuals using appropriate techniques, such as Euclidean distance, Mahalanobis distance, and Gower's algorithm or distance, are among the most widely indicated (Andrade et al., 2020, Cruz and Regazzi, 2020).

Despite its great ornamental potential, scientific information about the genetic resources of the desert rose is still scarce. Therefore, there are limitations in the genetic improvement of the species, as it is the starting point for enabling the breeder to define which accessions will enter the stages of genitor selection, artificial hybridization, and the development of segregating populations.

This study aimed to evaluate the genetic dissimilarity of 28 accessions of *A. obesum* using morphological descriptors and multivariate techniques. The findings were discussed on the basis of the ornamental value for selection the most valuable genotypes for composing the germplasm collection.

Material and Methods

The 28 genotypes evaluated in the present study belong to two collectors located in the municipality of Montes Claros, Minas Gerais state, Brazil, located at latitudes 16°43'42" S and 43°52'03" W, respectively. The climate was classified as tropical savannah (Aw), according to Köppen, with a mean annual rainfall of > 1060 mm, dry winters and rainy summers (16° 41' S, 43° 50' W; 646.29 m asl). The plants were older than 12 months and were not in the juvenile phase, as they had presented at least one flowering period prior to the start of the evaluation. The plants were maintained in 4-liter pots containing the substrate Bioplant® (Ponte Nova, Brazil) and were placed outdoors in full sun. Irrigation was carried out twice per week, manually. Cultural treatments (fertilization, control of pests and diseases) were carried out following the recommendation of Mendes et al. (2021). The morphological traits were recorded monthly from December 2020 to September 2021.

The quantitative characteristics evaluated were: leaf length (LL, in cm), leaf width (LW, in mm), number of branches (NB), number of expanded leaves (NEL), number of flowers per plant (NFL), number of flowers per branch (NFLB), flower length (FL, in mm), flower width (FW, an average of 10 flowers per plant, in mm), number of petals (NP), number of days from flower bud opening to anthesis (ANT) and number of days from flower anthesis to flower senescence (SE). Regarding the qualitative characteristics, the following were evaluated: petal pigmentation (PP), anther position (AP) and anther coloration (AC).

The quantitative floral characters (NFL, FL, FW, NP, ANT and SE) were measured based on the average of all flowers on the branches at 30-day intervals over a 10-month period. The number of flowers per plant throughout the year was also accessed (ANF). The qualitative floral characters (petal and anther pigmentation and position of the anther) were evaluated in two blooms, using visual assessments as a parameter. The RHS (1995) color catalog was applied for the classification of petal pigmentation (PP). Petal pigmentation assessments were performed on all flowers during the flowering periods.

Statistical analyzes were carried out considering 28 treatments and 10 replications (months of evaluation). Descriptive analyzes were used and distances between individuals were calculated based on the means obtained for the 28 treatments and group analyzes were subsequently performed. Gower's algorithm (Gower, 1971) was utilized to estimate the distances between the genotypes using both quantitative and qualitative data simultaneously (mixed data). The UPGMA dendrogram and Mojena (1977) coefficient were used to represent the dissimilarity matrix and discriminate between groups, respectively. On the other hand, Mantel's Z test verified the existence of correlation between the dissimilarity matrices. Additionally, Tocher's clustering was used to discriminate between groups and determine the intra and intercluster distances. All the analyses were performed using the software program R (R Core Team, 2021).

Results and Discussion

Using the RHS color catalog, it was possible to detect a wide variability in flower colors (Table 1, Figure 1). Of the 28 accessions evaluated, six major color groups were recorded: white, yellow, red, magenta, pink, and violet, with 21 distinct codes according to the RHS catalog (Table 1). Regarding petal arrangements (NP), 41.6% of accessions had flowers with five petals, 50.0% had 10 petals, and only two with 15 petals were identified (Table 1). Another relevant observation was that all the plants presented petals with an apiculate apex and the anthers in the central position in relation to the stamens.

Table 1. Characterization of 24 accessions of *A. obesum*, based on petal pigmentation (PP) and number of petals per flower (NP), Montes Claros, MG, Brazil, 2021.

Accessions	Color group (catalog)	Color code (PP) (RHS catalog)	Number of petals/flower (NP)
ICA001	Magenta-XI	68B	5 petals
ICA002	White-I	NN155D	5 petals
ICA003	Yellow-V	9C	10 petals
ICA004	Red-III	N34C	10 petals
ICA005	Red-III	37A	10 petals
ICA006	Red-III	53D	15 petals
ICA007	Red-III	69A	10 petals
ICA008	Magenta-XI	67B	15 petals
ICA011	Violet-X	N81A	5 petals
ICA013	Violet-X	N80B	10 petals
ICA015	Red-III	45B	10 petals
ICA016	Violet-X	79B	10 petals
ICA017	Magenta-XI	68B	10 petals
ICA018	Yellow-V	1D	10 petals
ICA019	Pink-II	67B	5 petals
ICA020	Magenta-XI	58A	10 petals
ICA021	Red-III	58D	10 petals
ICA022	Magenta-XI	61D	5 petals
ICA023	Magenta-XI	58B	5 petals
ICA024	Magenta-XI	58D	10 petals
ICA025	Red-III	47C	5 petals
ICA026	Magenta-XI	67B	5 petals
ICA027	White-I	NN155C	5 petals
ICA028	Yellow-V	3B	5 petals

RHS: Royal Horticultural Society

A wide variation in petal pigmentation was identified from the results of the present study. Confirming the existence of variability for this trait and reinforces the possibility of using these genotypes in crosses to increase variations in flower colors. However, this character was not

the most important factor in discriminating the genotypes. Although there are no studies on consumer preference regarding flower color patterns in *A. obesum*, it is notable that the rarer and more different the genotype, the greater its ornamental value (Singh et al., 2019).



Figure 1. Variations in petal pigmentation according to the Royal Horticultural Society color catalog observed in *A. obesum* (A) ICA007-69A, (B) ICA016-79B, (C) ICA015-45B, (D) ICA008-67B, (E) ICA0013-N80B, (F) ICA011-N81A, (G) ICA017-68B, (H) ICA019-67B, (I) ICA002-NN155D, and (J) ICA006-53D, Montes Claros, MG, Brazil, 2021.

The vast range of flowers colours relies on four major pigment classes: chlorophylls, carotenoids, flavonoids, and betalains (Narbona et al., 2021). Besides solid colors, desert rose may also exhibit variegations with whitish, yellowish, or reddish and purplish areas of different intensities (Ramos et al., 2022). A study with gerberas showed that the red colors in the flowers are produced by flavonoids, while the yellow ones are derived from carotenoids. The authors also pointed out that these colors come from two biochemical pathways, probably involving distinct genes (Tyrach and Horn, 1997).

Considering the mixed data (quantitative and qualitative), Gower's dissimilarity and the UPGMA dendrogram were determined, and the Mojena coefficient was used to differentiate between groups (Figure 2). The groupings shown in Figure 2 correspond to the individuals with the highest averages for the characters evaluated. The cophenetic correlation was 0.8371**, and the p-value for the significance of the cophenetic correlation by Mantel's Z test was 0.001, thus confirming a minor distortion of the graphical values relative to the estimated distances of the genotypes.

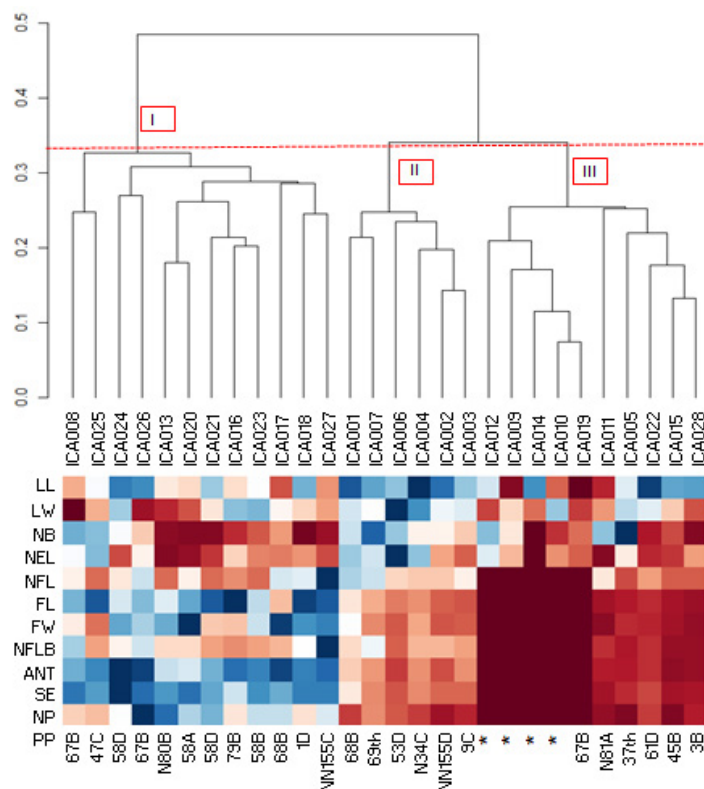


Figure 2. Representation of the dissimilarity among 28 accessions of *Adenium obesum* for morphological characters and group discrimination. Leaf length (LL, in cm), leaf width (LW, in mm), number of branches (NB), number of expanded leaves (NEL), number of flowers per plant (NFL), flower length (FL, in mm), flower width (FW, in mm), number of flowers per branch (NFLB), number of days from flower bud opening to anthesis (ANT), number of days from anthesis to flower senescence (SE), number of petals per flower (NP) and petal pigmentation (PP) according to RHS codes (67B, 47C, 58D, 67B, N80B, 58A, 58D, 79B, 58B, 68B, 1D, NN155C, 68B, 69th, 53D, N34C, NN155D, 9C, *, *, *, *, 67B, N81A, 37th, 61D, 45B, and 3B). The accessions with (*) did not flower during the period evaluated.

Table 2. Averages values for leaf length (LL, in cm), leaf width (LW, in mm), number of branches (NB), number of expanded leaves (NEL), number of flowers per plant (NFL), number of flowers per branch (NFLB), flower length (FL, in mm), flower width (FW, an average of 10 flowers per plant, in mm), number of petals (NP), number of days from flower bud opening to anthesis (ANT) and number of days from flower anthesis to flower senescence (SE) in 28 accessions of *A. obesum*, Montes Claros, MG, Brazil, 2021.

Accessions	LL	LW	NB	NEL	NFL	FL	FW	NFLB	ANT	SE	NP
ICA01	87.02	35.08	7.30	92.70	2.70	26.99	28.29	1.20	5.20	4.20	2.00
ICA02	83.80	32.70	6.00	50.00	1.50	12.73	10.51	1.00	2.40	2.00	1.00
ICA03	70.77	34.22	5.10	38.40	1.90	11.56	10.95	0.90	3.70	2.00	1.50
ICA04	92.29	43.40	6.00	95.00	1.50	17.03	17.19	1.00	3.70	2.50	2.00
ICA05	62.13	36.69	11.00	66.00	0.70	6.50	7.10	0.30	1.40	1.20	0.50
ICA06	71.47	51.18	8.10	128.90	1.60	15.18	10.88	0.60	2.10	1.80	2.50
ICA07	75.81	31.42	10.10	83.00	2.50	19.84	14.67	1.60	3.90	2.50	3.50
ICA08	44.91	11.76	8.60	73.70	1.90	45.68	25.21	2.00	10.20	8.20	5.00
ICA09	25.77	27.42	5.70	53.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ICA010	36.99	38.90	2.90	46.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ICA011	30.86	22.90	8.20	20.40	1.80	5.27	2.84	0.40	1.50	0.80	0.80
ICA012	63.91	18.11	8.30	80.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ICA013	53.59	16.50	2.10	20.00	0.90	35.33	41.95	1.20	8.40	7.50	11.50
ICA014	78.55	20.61	1.60	15.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ICA015	75.91	26.52	3.20	31.70	0.80	5.61	4.60	0.20	0.80	0.80	0.50
ICA016	51.46	39.60	2.80	59.10	1.10	62.40	20.10	0.80	12.00	5.70	5.60
ICA017	35.51	30.58	4.30	43.00	2.40	21.54	54.61	1.00	13.10	7.10	8.00
ICA018	74.07	27.22	1.80	46.70	2.30	60.12	44.70	1.50	11.50	8.00	5.50
ICA019	22.66	17.72	3.70	38.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ICA020	50.67	18.96	2.00	22.70	1.90	47.35	56.02	1.20	8.00	8.30	8.50
ICA021	70.33	28.84	2.00	31.80	0.90	57.33	20.53	0.90	10.10	7.20	9.50
ICA022	90.11	33.92	2.50	29.30	1.20	8.07	6.54	0.40	1.80	1.60	2.00
ICA023	57.61	40.49	3.40	43.90	0.90	39.14	33.90	0.90	11.40	7.60	8.00
ICA024	81.54	38.25	6.40	35.10	1.80	36.57	42.56	1.40	13.70	9.50	6.50
ICA025	58.43	24.55	8.30	96.70	0.90	57.50	12.70	0.90	11.30	7.40	4.50
ICA026	79.35	14.75	5.10	68.40	2.50	44.80	37.11	1.80	13.20	8.40	13.00
ICA027	42.13	23.40	2.30	34.90	4.10	57.34	47.05	3.00	12.20	8.00	7.50
ICA028	76.59	19.00	2.00	48.70	0.80	4.50	3.52	0.20	0.90	0.90	1.40

The accessions were grouped into three groups. Group I comprised the accessions ICA008, ICA025, ICA024, ICA026, ICA013, ICA020, ICA021, ICA016, ICA023, ICA017, and ICA018. These accessions presented the highest averages, during the period observed, for the following characteristics: number of flowers (NFF), average leaf length (LL), flower width (FW), number of flowers per branch (NFLB), number of days from emission of the flower bud to anthesis (ANT), number of days from anthesis to senescence (SE), and number of flowers per plant (NFL) (Figure 2 and table 2).

Group II comprised the accessions ICA001, ICA007, ICA006, ICA004, ICA002, and ICA003, with a higher mean for the vegetative trait of leaf length (LL) and a lower mean for the floral traits such as average flower length (FL), flower

width (FW), number of flowers per plant (NFL), number of flowers per branch (NFLB), and number of days from anthesis to flower senescence (SE). In addition, this group had the greatest variation in petal pigmentation (PP) (Figure 2).

Group III comprised the accessions ICA012, ICA009, ICA014, ICA010, ICA019, ICA011, ICA005, ICA022, ICA015, and ICA028, which also showed lower means for the characteristics associated with flowering: flower length (FL), flower width (FW), number of flowers per plant (NFL), number of flowers per branch (NFLB) and number of days from anthesis to flower senescence (SE) when compared to group I. Although the variables indicate that group III was comprised of flower plants with the lowest mean values for length and width, these individuals were the earliest to flower (Figure 2).

The distribution of the number of flowers throughout the year can be seen in Figure 3. Two flowering peaks were recorded: one in January and the other in September 2021. However, as can be seen from the points in (x), many genotypes did not flower in both periods. The genotypes ICA001, ICA006, ICA007, ICA011, ICA018, ICA020, and ICA027 produced the highest average number of flowers throughout the year. In accessions ICA001 and ICA006, flowering was highest in September, while in the others, flowering was highest in January.

Considering the quantitative characteristics, we can highlight some of the descriptors associated with flowers and flowering characters that are considered very

relevant by the flower production segment, such as the number of flowers per plant, average flower length, the number of flowers per branch, and the number of days from anthesis to flower senescence. In relation to these descriptors, accessions ICA001 and ICA018 stood out. It is also worth noting that ICA001 showed the highest peak flower production in September and had petal pigmentation described as magenta. In contrast, ICA018 showed peak flower production in January, and had yellow petals. These results indicate that, besides being ideal candidates to compose a germplasm collection, these two accessions could also be used as genitors in future hybridizations.

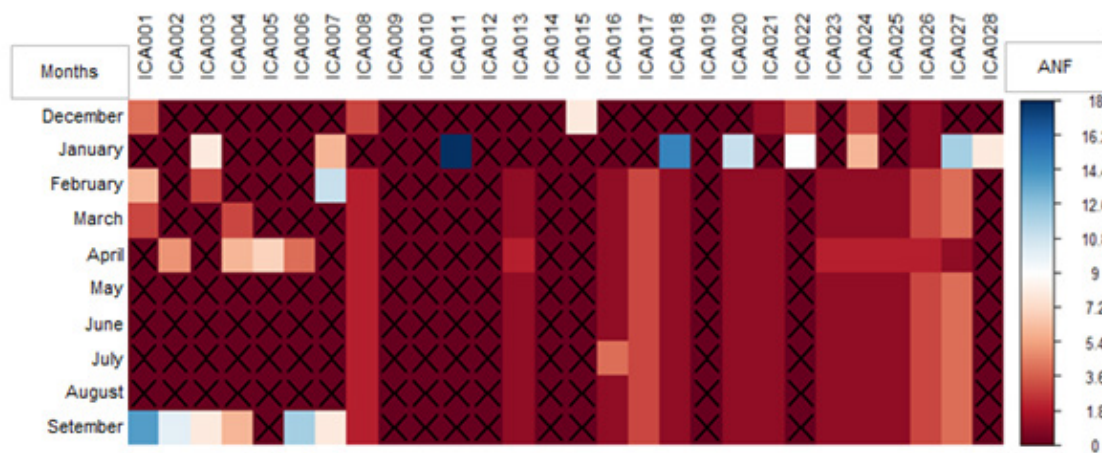


Figure 3. Average number of flowers (ANF) distribution in 28 accessions of *Adenium obesum* in the period December 2020 to September 2021, Montes Claros, MG, Brazil, 2021.

Some authors reported a close genetic correlation between leaf number traits and flower number (Pnueli et al., 1998; Azimi and Alavijeh, 2020). In Figure 2, it can be observed that the five accessions that did not flower during the evaluation period presented the lowest averages for vegetative characteristics such as number of leaves and/or leaf length and width. This indicates that these plants may not have reached sufficient vegetative conditions to flower that year. The transition from vegetative to reproductive meristem in higher plants is controlled by internal and environmental cues (Corbesier et al., 2007). According to Gaarslev et al. (2021) floral activation and repressing complexes, which contain florigen (STF) or antiflorigen (SP), are believed to regulate the expression of floral identity genes to ensure a timely transition to flowering.

For the quantitative descriptors of the vegetative part, particularly leaf length, width, and the number of branches, important variations were also observed among the

accessions evaluated. For leaf width, accessions ICA001 and ICA006 showed the smallest and largest widths, respectively. For leaf length, ICA004 and ICA019 had the largest and smallest lengths, respectively, and for the number of branches, ICA005 had the highest number. The number of branches is one of the characteristics that may be influenced by several environmental factors, as well as plant management, but a genotype with good branch production capacity should be considered because the greater the ramification, the better the chances of obtaining a plant with good conformation and a good number of flowers (Mendes et al., 2021)

Based on Gower's dissimilarity index, the Tocher's clustering method provided the formation of eight distinct clusters (Table 3), of which the inter and intracluster distances are shown in table 4. The formation of eight clusters validates the existence of variability among the phenotypes studied.

Table 3. Clusters formed by Tocher's grouping method of 28 accessions of *Adenium obesum* evaluated from December 2020 to September 2021, Montes Claros, MG, Brazil.

Cluster 1: ICA010 ICA019 ICA014 ICA009 ICA012 ICA015 ICA028 ICA011 ICA005 ICA022

Cluster 2: ICA002 ICA003 ICA004 ICA007 ICA001 ICA006

Cluster 3: ICA013 ICA020 ICA021 ICA023 ICA016 ICA018

Cluster 4: ICA008 ICA025

Cluster 5: ICA017

Cluster 6: ICA024

Cluster 7: ICA026

Cluster 8: ICA027

Table 4. Intra and intercluster distances of Tocher's clustering of 28 accessions of *Adenium obesum* evaluated from December 2020 to September 2021, Montes Claros, MG, Brazil.

Clusters	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	0.226	0.341	0.491	0.486	0.512	0.543	0.576	0.635
Cluster2	0.341	0.230	0.433	0.386	0.428	0.390	0.464	0.557
Cluster3	0.491	0.433	0.244	0.311	0.285	0.291	0.316	0.310
Cluster4	0.486	0.386	0.311	0.248	0.367	0.341	0.319	0.377
Cluster5	0.512	0.428	0.285	0.367	0.000	0.275	0.320	0.296
Cluster6	0.543	0.390	0.291	0.341	0.275	0.000	0.270	0.353
Cluster7	0.576	0.464	0.316	0.319	0.320	0.270	0.000	0.338
Cluster8	0.635	0.557	0.310	0.377	0.296	0.353	0.338	0.000

Cluster 1, comprised of genotypes ICA010, ICA019, ICA014, ICA009, ICA012, ICA015, ICA028, ICA011, ICA005, and ICA022. This cluster showed greater distances (0.543, 0.576 and 0.635) in relation to clusters 6 (ICA024), 7 (ICA026), and 8 (ICA027), respectively (Table 4). Cluster 2 and 3 grouped six accessions each. Cluster 4 was formed by two accessions (ICA008 and ICA025) and the clusters 5, 6, 7 and 8 consisted in one genotype each (Table 3).

Considering the data obtained from UPGMA and Tocher's clustering methods is possible highlight some genotypes. The accession ICA027 (cluster 8) showed the highest mean values for the variables: average flower length (FL), flower width (FW), number of flowers per plant (NFL), number of flowers per branch (NFLB) and number of days from anthesis to flower senescence (SE) and for presenting higher distances in relation to cluster 1 and 2 (0.635 and 0.557, respectively) (Table 4).

Overall, both groupings successfully discriminated the desert rose genotypes, as at least three groups were formed considering the UPGMA method and eight groups considering the Tocher's method. This is a preponderant factor for subsequent steps in the improvement of the species. According to Cruz and Regazzi (2020), high mean values for the character of interest and genetic divergence are two key aspects for the exploration of heterosis in allogamous species, like the desert rose. Other authors have also achieved good estimates of genetic divergence using Gower's algorithm in different species, including safflower (Lira et al., 2022), and passion fruit (Machado et al., 2015).

Different methodologies for estimating genetic diversity

may differ for the same data set because each method has its particularities (Cruz and Regazzi, 2020). The Tocher's method adopts the criterion that the dissimilarity *within* each group should be less than that *between* any of the groups. Thus, it uses average measures of dissimilarity so that the most similar pair of individuals will form the initial group, and the addition of new individuals is evaluated by comparing the increase in the average distance within the group with a maximum allowable level. The UPGMA hierarchical method, on the other hand, uses the arithmetic (unweighted) averages of the dissimilarity measurements, thus avoiding characterizing the dissimilarity by extreme values (minimum and maximum) among the genotypes (Valadares et al., 2019).

The results indicate that some genotypes (ICA001 and ICA018) that stand out for their floral characteristics of interest and their divergent petal pigmentation should be considered strong candidates to compose the germplasm collection. Additionally, genotypes ICA005, ICA006, ICA019, and ICA027 stood out with respect to their vegetative characteristics. Finally, it is worth mentioning that ICA027 was grouped alone in cluster 8 by Tocher's method and exhibited, on average, the greatest distances in relation to the other clusters.

Although the two methods, UPGM and Tocher, distributed the 28 accessions into three and eight groups, respectively, the accessions pre-selected as being of greatest ornamental interest, were grouped within the same cluster (ICA019 and ICA005); while others were separated into distinct groups (ICA001, ICA018, ICA027

and ICA006), by both methods. Considering these findings, both multivariate analysis methods were effective in distinguishing the genotypes evaluated and are an important tool for plant breeders.

As the genotypes mentioned above are presented in groups with distinct dissimilarity, this being an indication of genetic diversity, the possibility of combinations between them can culminate in great gains for the genetic improvement of *Adenium obesum*. Therefore, these two groups can be explored in future crossings to increase these characteristics in future progeny.

Conclusions

The morphological descriptors evaluated and multivariate analysis applied indicate the existence of genetic variability in the accessions studied. Despite the great variability, petal pigmentation is not the most important factor in discriminating the genotypes. Accessions ICA001 and ICA018 stood out for their floral characteristics of interest as well as being allocated to different groups. On the other hand, accessions ICA005, ICA006, ICA019, and ICA027 stood out in relation to their vegetative characteristics of interest, indicating the possibility of their hybridization in the future.

Author Contribution

SN: conceptualization, methodology and editing. **MCRA:** investigation, Writing- original draft preparation. **NCV:** data curation, visualization. **RBM:** validation, data curation. **CCFP:** methodology, supervision and writing- reviewing.

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