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Original Article

Characterization of yellow pitahaya (*Selenicereus megalanthus* Haw.) genotypes under two productive systems in Colombia

Caracterização de genótipos de pitaia amarela (*Selenicereus megalanthus* Haw.) a partir de dois sistemas produtivos na Colômbia

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Abstract

Selenicereus megalanthus Haw. It is an exotic fruit tree, with productive and nutritional potential. In Colombia, there is a great phenotypic and genotypic diversity, but its genetic studies are scarce. The objective was to characterize morphologically 15 selected yellow pitahaya genotypes, under two productive systems in the open field and under cover, in the municipalities of Miraflores and Zetaquira, in Boyacá, Colombia. Quantitative characters were evaluated: plant height (PH), number of vegetative sprouts (NVS), sub-sprouts (SS), longest sprouts length (LSL), distance between areoles (DBA), width of the ribs in the apical region (WRA), width of the ribs in the middle region (WRM), width of the ribs in the basal region (WRB), height of undulations between successive areoles in a rib (HUA), number of spines per areole (NSA) and longest spine length (LSP). The results showed under the two productive systems and the evaluated localities that the variables with the highest coefficient of variation (greater than 90%) were the number of sub-sprouts, height of the undulations between successive areoles (HUA) and the longest spine length (LSP). High positive correlations were obtained between the distances areoles, the width of the ribs and the length of the spines (r>0.7). The conglomerate showed that the characteristics that define the groupings are height of the plant, the texture of the cladodes, the width of the ribs and the height of the undulations. Characters associated with the shoots and cladodes were identified, which directly influence the vegetative propagation and therefore the yield of the yellow pitahaya.

Keywords: *Selenicereus megalanthus*, phenotypic variation, cladode, sprouts characteristics.

Resumo

Selenicereus megalanthus Haw. é uma fruteira exótica, com potencial produtivo e nutricional. Na Colômbia existe uma grande diversidade fenotípica e genotípica, mas seus estudos genéticos são escassos. O objetivo deste trabalho foi caracterizar morfologicamente 15 genótipos selecionados de pitaya amarela, a partir de dois sistemas produtivos em campo aberto e sob cobertura, nos municípios de Miraflores e Zetaquira, em Boyacá, Colômbia. Foram avaliados os caracteres quantitativos: altura da planta (PH), número de brotos vegetativos (NVS), sub-brotos (SS), maior comprimento dos brotos (LSL), distância entre aréolas (DBA), largura das nervuras na região apical (WRA), largura das costelas na região média (WRM), largura das costelas na região basal (WRB), altura das ondulações entre aréolas sucessivas em uma costela (HUA), número de espinhos por aréola (NSA) e maior espinha comprimento (LSL). Os resultados mostraram nos dois sistemas produtivos e nas localidades avaliadas que as variáveis com maior coeficiente de variação (maior que 90%) foram o número de sub-brotos, altura das ondulações entre aréolas sucessivas (HUA) e o maior comprimento do espinho (LSL). Altas correlações positivas foram obtidas entre as distâncias entre as aréolas, a largura das costelas e o comprimento dos espinhos (r > 0.07). O conglomerado mostrou que as características que definem os agrupamentos são a altura da planta, a textura dos cladódios, a largura das nervuras e a altura das ondulações. Foram identificados caracteres associados à brotação e aos cladódios, que influenciam diretamente na propagação vegetativa e, consequentemente, na produção da pitaya-amarela.

Palavras-chave: *Selenicereus megalanthus*, variação fenotípica, cladódio, características dos brotos.

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1. Introduction

Yellow pitahaya is a member of the Cactaceae family and native to the tropical forest regions of southern Mexico, Central America, and northern South America. The crop adapts to different ecological conditions ranging from very dry regions to wet one receiving more than 3.500 mm of rainfall per year (Goenaga et al., 2020). It is an exotic fruit tree with great popularity in the national and international market due to the appearance of its fruits and its physicochemical, nutritional characteristics and bioactive components, being widely used for its organoleptic characteristics and for its added commercial value (Verona-Ruiz et al., 2020).

It is considered a colorful and attractive food, it arouses the curiosity of the palate favored by the natural color, in addition to the considerable sugar content of the fruit. Another relevant aspect is the composition of bioactives such as phenolic compounds, flavonoids and vitamin C, with quantitative concentrations, in addition to the high fiber composition (Al-Mekhlafi et al., 2021). When consumed, it can provide functional actions, supporting immunity and performing antimicrobial, antioxidant, hepatoprotective, hypoglycemic, healing and antiproliferative activities (Quispe Lupuche et al., 2021).

The dragon fruit cultivation area is expanding rapidly in many countries due to its economic potential and nutritional benefit (Hossain et al., 2021), attracting interest from countries such as the United States, Australia, Southeast Asia, Israel, and other regions (Jalgaonkar et al., 2022). Pitahaya mayor importers are the United States, Japan, European Union and Canada, while major exporters are: Israel, Mexico and Nicaragua, in addition, Colombia participate with 38% of the international exportations (AGRONET, 2022). *Selenicereus* production reaching 9.93 t/ha during 2020, the principal production departments include Huila, Boyacá, Santander and Valle del Cauca (AGRONET, 2022). Boyacá is one of the departments of Colombia, where the cultivation of yellow pitahaya has the productive potential and the edaphoclimatic conditions for its production, in addition to the fact that there are producer associations that encourage its planting (Morillo et al., 2022b). Despite the productive potential, a limiting factor in the development of this crop in Colombia is the incidence of pest and diseases, low quality of the fruit, the technological level, mechanical damage during shelf life and the lack of cultivated material which generates considerable economic losses (González-Trujillo et al., 2019; Morillo et al., 2021; Álvarez-Herrera et al., 2023).

Worldwide, morphological characterization studies on yellow pitahaya have found great morphological and genetic heterogeneity in many of this fruit's characteristics, such as sweetness, size, shape, color, and number of bracts, resulting from intra- or interspecific hybridizations between different cultivated and wild materials, which make it difficult to raise quality standards for the export market, posing serious problems when it comes to improving yield and post-harvest shelf-life (Abirami et al., 2021). Studies carried out by Abirami et al. (2021) through morphological, biochemical, and molecular characterizations allowed the correct identification of four *Hylocereus* species. The authors of Leovika et al. (2019) determined in Pangadaran that differences in the morphological, physiological, and anatomical structures of the plants allowed them to adapt to different agroclimatic conditions. A previous study showed that morphoagronomic characterizations could be used to determine the variation in natural pitahaya populations (Abirami et al., 2021). Sibut et al. (2023) evaluated yield capacity of six superior pitaya genotypes under edaphoclimatic conditions of the Federal district in Brazil, found genotypes with good physical characteristics, performance and adapted to local conditions.

In Colombia, knowledge of this crop mainly comes from the empirical processes of farmers who are motivated by the prices that fruits can fetch in some of the months of the year; however, increased penetration into international markets requires research on the processes of propagation, obtaining elite material, and resistance to biotic and abiotic factors, among other topics (Caetano et al., 2013). However, one of the bigger limitations is the broad morphological variation seen in the vegetative structures, which leads to confusion in identifying each species, with a lack of consensus (Gómez-Hinostrosa et al., 2014), where classification is mainly based on the number of areola ribs, the contour of the stem, the relative firmness of the stem and the size and color of the fruits; in addition, various studies on domesticated cactus species have demonstrated variations in fruit characteristics related to the domestication process, resulting in a lack of a taxonomic database (Jalgaonkar et al., 2022). Morphological and molecular characterization studies carried out on the germplasm at the Department of Boyacá have shown that there is genetic diversity in the province of Lengupá, which is the basis for the establishment of any selection process that would identify elite materials that respond to the needs of the farmer, producers, and consumers. *Selenicereus megalanthus*, or yellow pitahaya, a native fruit tree, constitutes a key product for the fruit and vegetable sector, with significant demand for its flavor, appearance, quality, and nutraceutical properties (Morillo et al., 2021, 2022a, b). In addition, it has market potential, both domestically and internationally. However, the prospects for the international market require research to raise the fruit quality and to supply elite genotypes for planting and managing the production chain with added value.

The municipality of Miraflores has the productive potential to make pitahaya an economically profitable crop, but first, it must generate strategies to promote cultivation in a technical way to position itself with the highest quality and develop research and technology for the yellow pitahaya production chain, therefore, two productive systems of yellow pitahaya have been implemented in the region in the open field and under cover, as alternatives to reduce the incidence and severity of phytosanitary problems, increase the quality of the fruit and yields, however, they do not studies have been carried out to determine the phenotypic differences of the productive systems. Therefore, the objective of this research was to morphoagronomically characterize yellow pitahaya genotypes grown in the open field and under cover in the municipality of Miraflores and Zetaquira, Boyacá in Colombia in order to identify those that present the best agronomic characteristics and can be a good production alternative under either of the two production systems.

2. Material and Methods

2.1. Vegetal material

Fifteen yellow pitahaya genotypes were evaluated, which were selected in an in situ morphoagronomic characterization study carried out in the main producing municipalities of the Lengupá province: Berbeo, Zetaquira, Paéz, San Eduardo and Miraflores (Morillo et al., 2021). The 15 genotypes were established in two experimental plots in the municipalities of Miraflores and Zetaquira under two production systems in the open field (8 genotypes) and under cover (7 genotypes), the experimental design was completely randomized, with 10 repetitions per genotype and in where the treatments corresponded to the 15 selected yellow pitahaya genotypes (Table 1, Figure 1).

2.2. Morphoagronomic characterization

The quantitative descriptors were evaluated *in situ*: plant height (PH), number of vegetative sprouts (NVS), sub-sprouts (SS), longest sprouts length (LSL), distance between areoles (DBA), width of the ribs in the apical region (WRA), width of the ribs in the middle region (WRM), width of the ribs in the basal region (WRB), height of undulations between successive areoles in a rib (HUA), number of spines per areole (NSA) and longest spine length (LSP). These descriptors have been used successfully in the evaluation of pitahaya germplasm in Colombia (Morillo et al., 2021).

2.3. Data analysis

For the analysis of the data obtained, an analysis of descriptive statistics was initially carried out. Then the normality assumptions for the parametric analyzes were verified and the analysis of variance (ANOVA) was performed. Pearson's correlation was estimated for variables, and the significance was evaluated using a t-test (the null hypothesis was H0: r = 0; 5% significance), and plotted using R package "corrplot": Visualization of a Correlation Matrix (Version 0.84) (Taiyun and Simko, 2017). A principal component analysis was performed between the variables using the correlation matrix between the characteristics, which were plotted on a two-dimensional plane to group the accessions with R Core Team Software (2020). For the clustering analysis, the Euclidean distance and Ward's minimum distance were taken into account using the algorithms in the Factoextra package of the R program (Kassambara and Mundt, 2020).

For the joint analysis of the qualitative and quantitative descriptors, a factorial analysis of mixed data was carried out with the Factoextra package of the R program. In addition, a dendrogram was generated using a hierarchical clustering method and the Euclidean distance of the minimum variance of Ward with the FactoMineR package (Le et al., 2008).

Table 1. Geographical location of the selected yellow pitahaya genotypes.

Under cover		
Genotype	**Municipality**	**Georeferencing**
Gen1	Miraflores	N 5°13'43,8 W 73°12'11,8"
Gen2	Miraflores	N 5°14' 09,4" W 73°12'15,3"
Gen3	Miraflores	N 5° 14' 09,2" W 73° 12' 15,3"
Gen4	Miraflores	N 5° 13' 03,3" W 73° 09'42,8"
Gen5	Berbeo	N 5° 11' 33.65" W 73° 03' 40,04"
Gen6	Berbeo	N 5° 08' 14,6" W 73° 03' 12,0"
Gen7	Miraflores	N 5° 14' 23" W 73° 10' 57.2"
Open field		
Genotype	**Municipality**	**Georeferencing**
Gen1	Miraflores	N 5° 12' 850" W 73° 09' 655"
Gen2	Berbeo	N 5° 17' 3065" W 73° 10' 153"
Gen3	Paez	N 5° 07' 57,5" W 73° 02' 57,9"
Gen4	Miraflores	N 5° 13' 46,5" W 73° 12' 23,2"
Gen5	Zetaquira	N 5° 14' 24,2" W 73° 12' 29,2"
Gen6	Miraflores	N 5° 14' 09,2" W 73° 11' 14,3"
Gen7	Miraflores	N 5° 14' 09,2" W 73° 11' 12,3"
Gen8	Paez	N 5° 14' 5´,56" W 73° 3',6"

3. Results

3.1. Morphoagronomic characterization using quantitative descriptors in the system under cover in the municipalities of Miraflores and Zetaquira

The evaluation of the descriptors associated with the seed and sprouts of the 7 yellow pitahaya genotypes in the system under cover in the municipalities of Miraflores and Zetaquira showed that the variables that presented a higher percentage of variation were: sub-sprouts (SS) with a coefficient of variation greater than 94%, followed by the height of the undulations between successive areoles in a rib (HUA) in the municipality of Zetaquira with 88.12% and in Miraflores the length of the longest sprouts (LSL) with 87.41%. While the least variable descriptor was the height of the plant (PH) with approximately 30%, in both municipalities. The average height of the average plants was 137 to 138 cm, the number of sprouts was 2 sprouts per plant (NVS), the number of thorns (NSA) per areola was 1 to 2, and the length of the largest thorn (LSL) was 0.2mm (Table 2).

The Pearson correlation analysis ($p \leq 0.05$) in the system under cover in the municipalities of Miraflores and Zetaquira showed positive correlations between all the variables, in the municipality of Miraflores high, significant and positive correlations were observed between rib width and width of the rib in the apical region (WRA) and longest spine length (LSP) with r= 0.93, the number of spines per areola (NSA) and longest spine length (LSP) (r= 0.91) and

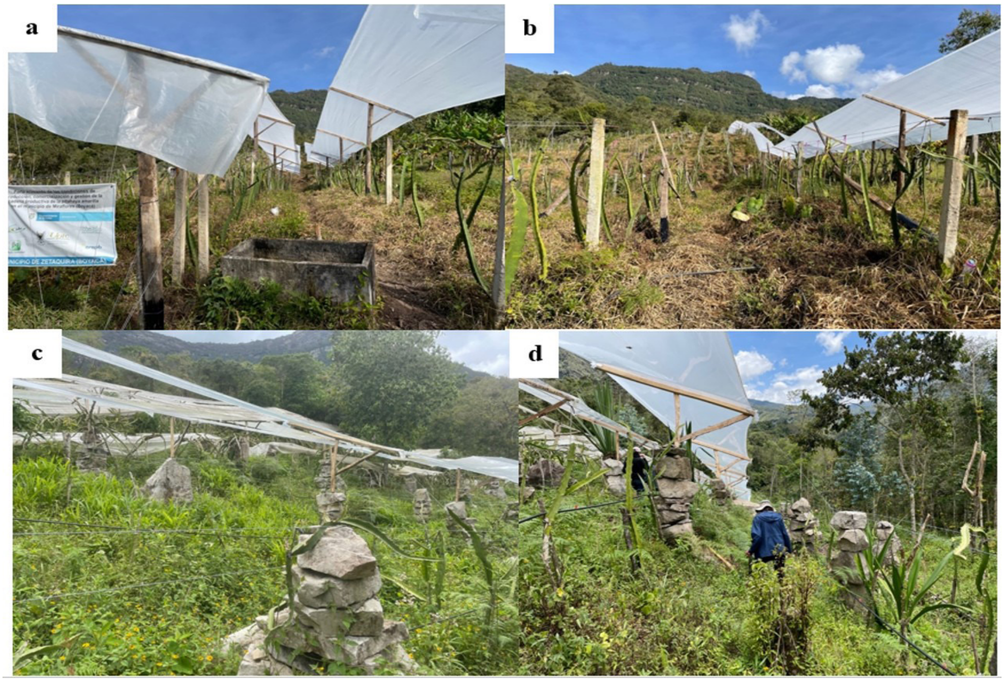

Figure 1. Experimental plots **a.** System under cover in the municipality of Zetaquira. **b.** Open field system in the Municipality of Zetaquira. **c.** System under cover in the municipality of Miraflores. **d.** Open field system in the Municipality of Miraflores.

Table 2. Quantitative descriptors evaluated under cover in the municipalities of Miraflores and Zetaquira.

Genotype	PH	NVS	SS	LSL	DBA	WRA	WRM	WRB	HUA	NSA	LSP
Miraflores											
Gen1	125.80	1.60	0.20	28.20	2.18	1.30	2.15	1.98	0.30	1.50	0.23
Gen2	157.60	2.10	1.40	36.30	2.81	1.29	2.27	1.37	0.29	1.50	0.22
Gen3	128.10	1.80	0.70	27.70	1.83	0.98	1.85	1.35	0.20	1.10	0.14
Gen4	117.70	2.40	0.60	32.60	1.71	1.02	1.92	1.44	0.25	1.20	0.19
Gen5	161.30	2.70	1.80	53.70	3.22	1.79	3.11	2.29	0.35	1.80	0.28
Gen6	113.60	1.80	1.20	22.65	2.18	1.12	2.44	1.56	0.15	1.30	0.17
Gen7	168.60	2.40	2.80	64.00	3.94	2.15	3.31	2.19	0.38	1.90	0.33
Mean	138.96	2.11	1.24	37.88	2.55	1.38	2.44	1.74	0.27	1.47	0.22
CV	29.75	76.20	94.00	87.41	68.93	68.52	72.72	73.30	74.14	67.19	66.24
Zetaquira											
Gen1	145.60	1.90	0.00	22.60	1.70	1.08	2.40	1.60	0.14	1.30	0.18
Gen2	150.10	2.00	0.10	32.30	2.68	1.67	3.24	2.12	0.26	1.60	0.28
Gen3	142.20	3.20	0.30	38.20	2.75	1.34	2.68	2.09	0.27	1.80	0.24
Gen4	126.80	2.44	0.80	15.40	1.13	0.79	1.36	1.07	0.12	0.80	0.11
Gen5	91.10	1.22	0.10	10.90	0.73	0.52	0.74	0.53	0.11	0.60	0.12
Gen6	160.74	3.50	1.20	34.55	3.23	2.12	3.90	2.20	0.23	2.00	0.29
Gen7	142.40	4.56	1.70	37.00	2.56	1.17	3.65	2.10	0.34	1.80	0.26
Mean	137.02	2.69	0.60	27.28	2.11	1.24	2.57	1.67	0.21	1.41	0.21
CV	30.49	65.51	96.08	75.86	71.15	73.69	72.38	71.94	88.12	67.56	72.27

PH: Plant height; **NVS:** Number of vegetative sprouts; **SS**: Sub-sprouts; **LSL**: Longest sprouts length; **DBA**: Distance between areoles; **WRA**: Width of the ribs in the apical region; **WRM**: Width of the ribs in the middle region; **WRB**: Width of the ribs in the basal region; **HUA**: Height undulations between successive areoles in the ribs; **NSA**: Number of spines per areole; **LSP**: Longest spine length; **CV:** Coefficient of variation.

distance between areoles (DBA) and number of spines per areola (NSA) with r= 0.9 (Figure 2a).

In the municipality of Zetaquira, high, significant and positive correlations were observed between the distance between areoles (DBA) and the width rib of mid region (WRM) (r= 0.93), between the number of spines per areole (NSA) and the distance between areoles (DBA) (r= 0.92) and between number of spines per areola (NSA) and width rib in apical region (WRA) (r= 0.92) (Figure 2b).

The analysis of mixed factors in the system under cover in the municipality of Miraflores showed that 82.81% of the total variance is explained in the first two components (PC1=70.89% and PC2= 11.92%) (Figure 3a). The variables that make the greatest contribution to the variation of CP1 are plant height, number of spines per areola, and width of the rib in the apical region. While the number of sub-sprouts and the width of the rib in the basal region contribute to CP2. A cluster is observed between genotypes 3, 4 and 6 (Figure 3b).

The analysis of mixed factors in the system under cover in the municipality of Zetaquira showed that 87% of the total variance is explained in the first two components (PC1= 72.95% and CP2= 14.05%) (Figure 4a). The variables that make the greatest contribution to the variation of CP1 are distance between areoles, longest spine length, width of the rib in the basal region. While the number of sprouts and sub-sprouts and the width of the rib in the apical region contribute to CP2. A cluster is observed between genotypes 2, 3 and 6 (Figure 4b).

The cluster analysis of the 7 genotypes evaluated in the municipalities of Miraflores and Zetaquira in the system under cover grouped the genotypes into four clusters (Figure 5a, Figure 5b). Genotype 1 remained independent in a cluster in both municipalities, this genotype was characterized by presenting 1 to 2 sprouts, and without sprouts. In a cluster genotypes 2 and 3 are grouped in both municipalities, however, in Miraflores genotype 4 was added to this cluster, while genotype 6 was added in Zetaquira. In Miraflores genotype 6 remained in an independent cluster because This genotype stood out for presenting the lowest plant size with 113.60 cm, the shortest sprouts length with 22.65 cm and the shortest

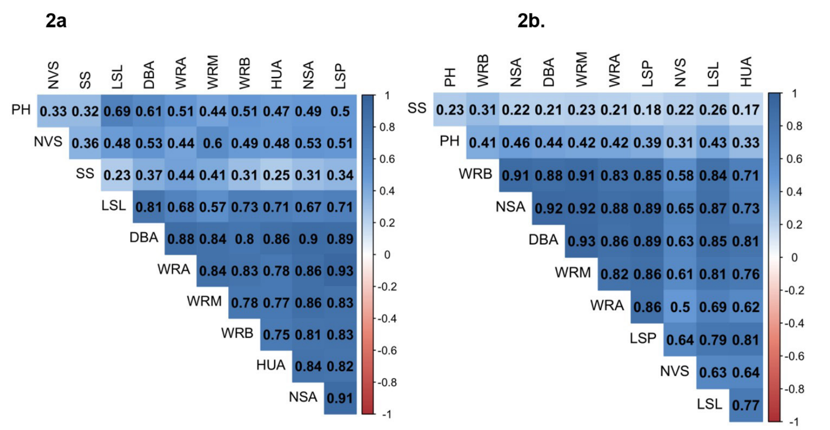

Figure 2. Pearson correlation analysis (p≤0.05) between the quantitative variables evaluated in the genotypes of yellow dragon fruit under cover. **a.** Miraflores. **b.** Zetaquira.

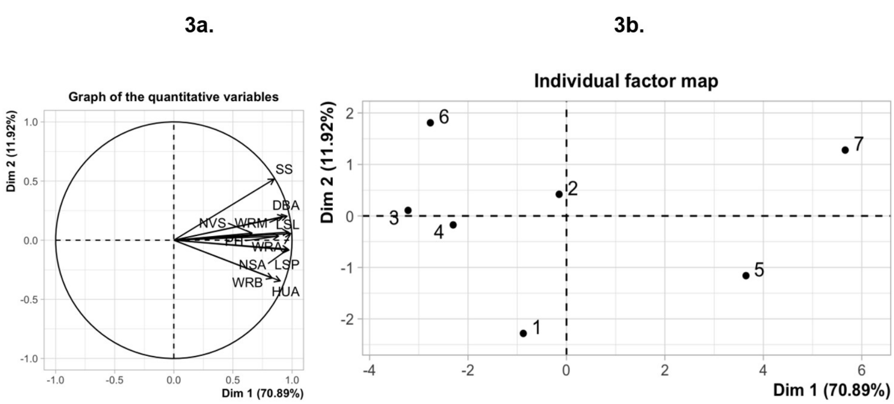

Figure 3. Analysis of mixed factors, considering quantitative and qualitative variables evaluated in the seven genotypes of yellow pitahaya in the Miraflores municipality under cover. **a.** Contribution of the variables to the first two components. **b.** Distribution of the genotypes in the first two components.

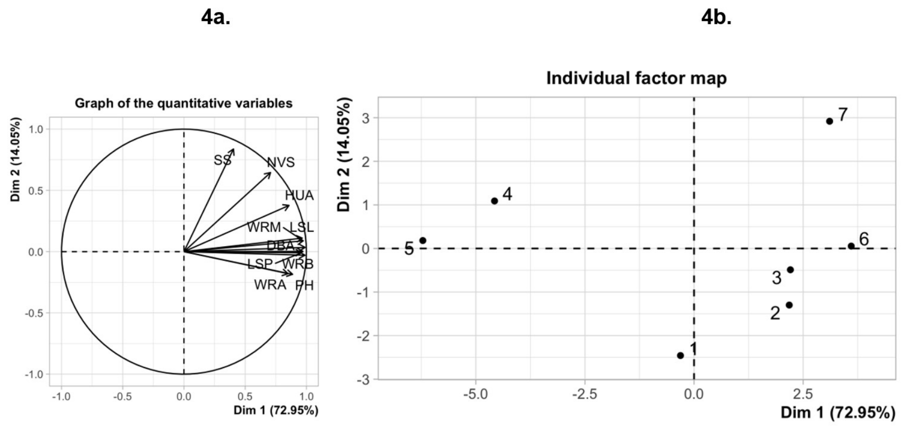

Figure 4. Analysis of mixed factors, considering quantitative and qualitative variables evaluated in the seven genotypes of yellow pitahaya in the municipality of Zetaquira under cover. **a.** Contribution of the variables to the first two components. **b.** Distribution of the genotypes in the first two components.

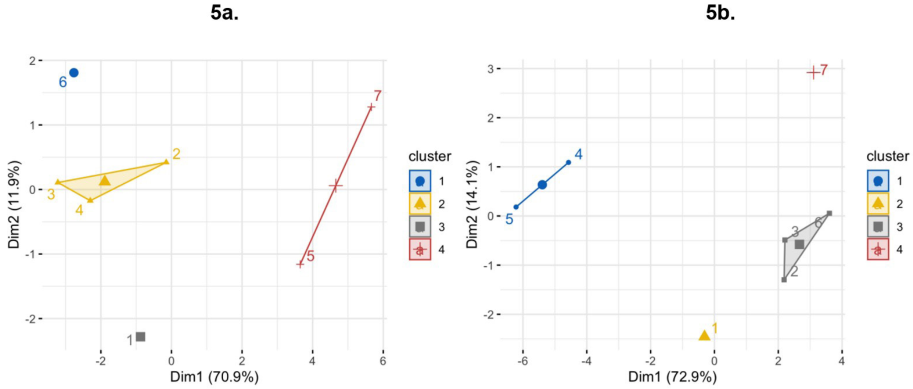

Figure 5. Analysis of hierarchical clusters of the yellow pitahaya genotypes of the municipalities of Miraflores and Zetaquira in the productive system under cover. **a.** Miraflores. **b.** Zetaquira.

height of the undulations between areolas with 0.15 cm. While in Zetaquira genotype 7 was grouped into a cluster, this genotype was characterized by presenting the highest number of sprouts with an average of 4.56 sprouts per plant, the highest number of sub-sprouts with approximately 2 sub-sprouts and a height of the undulations between successive areoles in an upper rib with 0.34 cm. A high incidence of pests and diseases, smooth cladodes texture, concave margin shape, and brown spine color were observed in both municipalities.

3.2. Morphoagronomic characterization using quantitative descriptors in the open field in the municipalities of Miraflores and Zetaquira

The evaluation of the descriptors associated with seed and sprouts of the 8 genotypes of yellow pitahaya in the open field in the municipalities of Miraflores and Zetaquira showed that the variables that presented a higher percentage of variation were: sub-sprouts (SS) with a coefficient of variation greater than 97%, followed by the height of the undulations between successive areoles in a rib (HUA) in Zetaquira with 97.48% and longest spine length with 89.33%. While the least variable descriptor was the height of the plant (PH) with approximately 35%, in both municipalities (Table 3). The average height of the average plants is 140-156 cm, the number of sprouts is 2-3 sprouts per plant (NVS), the number of spines (NSA) per areole is 1-2, and the length of the largest spine (LSP) between 0.26 to 0.52 mm.

The Pearson correlation analysis ($p \leq 0.05$) in the open field system in the municipalities of Miraflores and Zetaquira showed positive correlations between all the variables, in the municipality of Miraflores high, significant and positive correlations were observed between the distance between areoles (DBA) and number of spines per areola (NSA) with r = 0.89, between the number of spines per areola (NSA) and longest spine length (LSP) (r = 0.84) and the apical rib width (WRA) and number of spines per areola (NSA) with r= 0.83 (Figure 6a).

Table 3. Quantitative descriptors evaluated in the open field in the municipalities of Zetaquira and Miraflores.

Genotype	PH	NVS	SS	LSL	DBA	WRA	WRM	WRB	HUA	NSA	LSP
Miraflores											
Gen1	102.50	2.40	1.60	40.64	2.58	1.26	2.19	1.93	0.20	1.50	0.19
Gen2	164.90	2.70	0.70	44.80	3.13	1.49	2.91	2.42	0.22	1.50	0.28
Gen3	155.00	2.40	0.70	49.20	3.82	1.52	4.61	2.18	0.52	1.80	0.30
Gen4	212.30	3.10	2.50	62.10	3.74	1.66	3.88	2.53	033	1.90	0.27
Gen5	130.90	2.50	0.60	32.10	2.75	1.63	2.29	1.54	0.19	1.20	0.21
Gen6	192.30	2.70	2.80	52.10	3.17	1.40	3.51	2.27	0.22	1.50	0.24
Gen7	125.80	2.20	0.80	40.30	2.79	1.54	2.32	1.76	0.40	1.50	0.26
Gen8	164.40	3.00	1.50	58.40	3.93	1.86	2.87	2.78	0.64	1.80	0.35
Mean	156.01	2.63	1.49	47.46	3.24	1.55	3.07	2.18	0.34	1.59	0.26
CV	38.19	57.62	97.31	77.35	55.21	58.23	85.87	61.06	79.36	54.62	58.88
Zetaquira											
Gen1	129.00	2.40	0.20	15.30	1.20	0.83	1.35	1.02	0.05	0.70	0.12
Gen2	132.20	3.20	0.40	26.60	1.82	1.11	2.15	1.69	0.15	1.20	0.02
Gen3	132.00	2.70	0.60	27.90	2.06	1.78	1.86	1.86	0.09	1.40	0.17
Gen4	153.20	2.90	0.40	30.40	2.92	1.85	3.20	2.68	0.20	1.50	0.29
Gen5	165.30	3.80	0.50	30.10	2.90	2.44	3.47	3.10	0.12	2.10	0.29
Gen6	107.70	1.90	0.20	13.30	1.09	0.70	1.34	1.31	0.08	0.80	0.10
Gen7	160.00	3.60	3.00	39.80	3.54	1.88	3.97	2.99	0.20	2.00	0.63
Gen8	146.00	2.40	0.60	20.50	1.57	1.16	2.12	1.74	0.09	1.20	0.55
Mean	140.68	2.86	0.74	25.49	2.14	1.47	2.43	2.05	0.12	1.36	0.52
CV	33.50	75.55	98.10	83.42	73.84	87.54	78.13	74.71	97.48	69.33	89.33

PH: Plant height; **NVS:** Number of vegetative sprouts; **SS**: Sub-sprouts; **LSL**: Longest sprouts length; **DBA**: Distance between areoles; **WRA**: Width of the ribs in the apical region; **WRM**: Width of the ribs in the middle region; **WRB**: Width of the ribs in the basal region; **HUA**: Height undulations between successive areoles in the ribs; **NSA**: Number of spines per areole; **LSP**: Longest spine length; **CV:** Coefficient of variation.

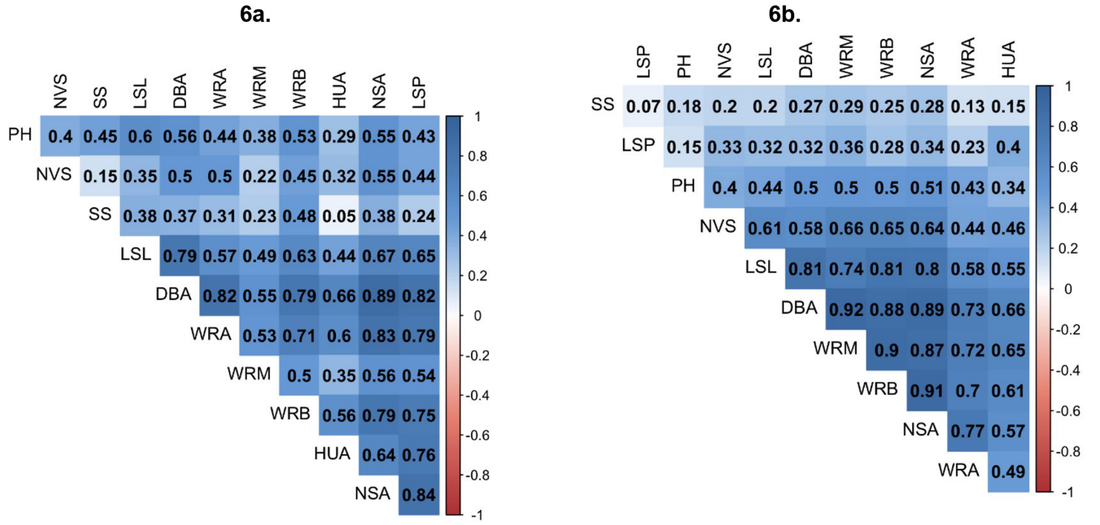

Figure 6. Pearson correlation analysis (p≤0.05) between the quantitative variables evaluated in the open field yellow pitahaya genotypes. **a.** Miraflores. **b.** Zetaquira.

In the municipality of Zetaquira, high, significant and positive correlations were observed between the distance between areolas (DBA) and apical rib width (WRA) (r = 0.92), between the number of spines per areola (NSA) and rib width. of basal thickness (ACGB) (r = 0.91) and between medium thickness rib width (ACGM) and basal rib width (WRB) (r = 0.9) (Figure 6b).

The analysis of mixed factors in the system under cover in the municipality of Miraflores showed that 66.19% of the total variance is explained in the first two components (PC1= 48.19% and CP2= 18.00%) (Figure 7a). The variables that make the greatest contribution to the variation of CP1 are the basal rib width, the average width of ribs and number of spines per areola. While the number of sub-sprouts, the height of the plant and the height of the undulations between areoles contribute to CP2. A cluster is observed between genotypes 1, 5 and 7 (Figure 7b).

The analysis of mixed factors in the system under cover in the municipality of Zetaquira showed that 74.66% of the total variance is explained in the first two components (PC1=61.74% and PC2= 12.92%) (Figure 8a). The variables that make the greatest contribution to the variation of the CP1 are the height of the plant, the length of the longest sprouts and the basal ribs width. While the length of the largest spine and the number of sub-sprouts contribute to CP2. A cluster is observed between genotypes 8, 2 and 3 and the cluster of genotypes 6 and 1 (Figure 8b).

The cluster analysis of the 8 genotypes evaluated in the Miraflores and Zetaquira municipalities in the open field system grouped the genotypes into four clusters (Figure 9a, Figure 9b) in the Miraflores municipality and into three clusters in the Zetaquira municipality. In Miraflores genotypes 6 and 2 each formed a cluster. Genotype 6 was characterized for being the genotype with the highest

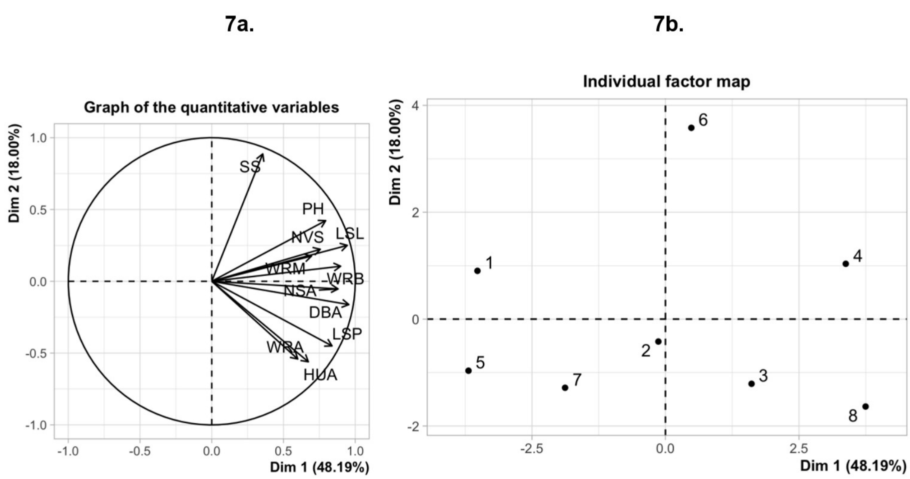

Figure 7. Analysis of mixed factors, considering quantitative and qualitative variables evaluated in the seven genotypes of yellow pitahaya in the municipality of Miraflores in the open field. **a.** Contribution of the variables to the first two components. **b.** Distribution of the genotypes in the first two components.

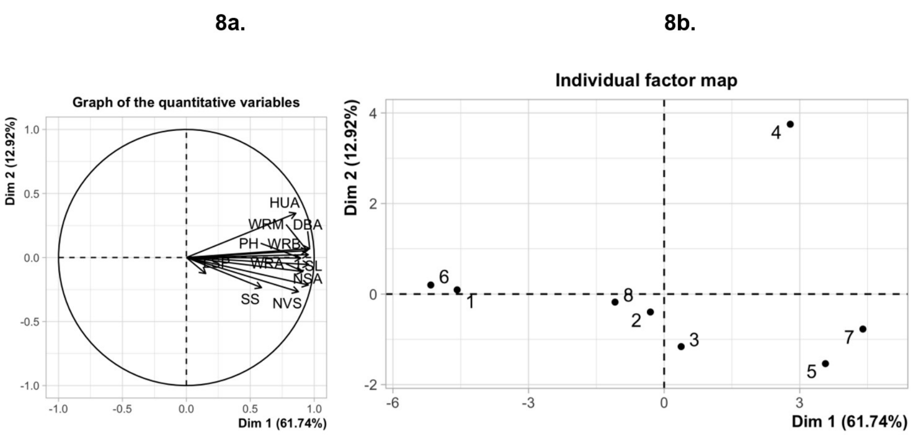

Figure 8. Analysis of mixed factors, taking into account quantitative and qualitative variables evaluated in the seven genotypes of yellow pitahaya in the municipality of Zetaquira in the open field. **a.** Contribution of the variables to the first two components. **b.** Distribution of the genotypes in the first two components.

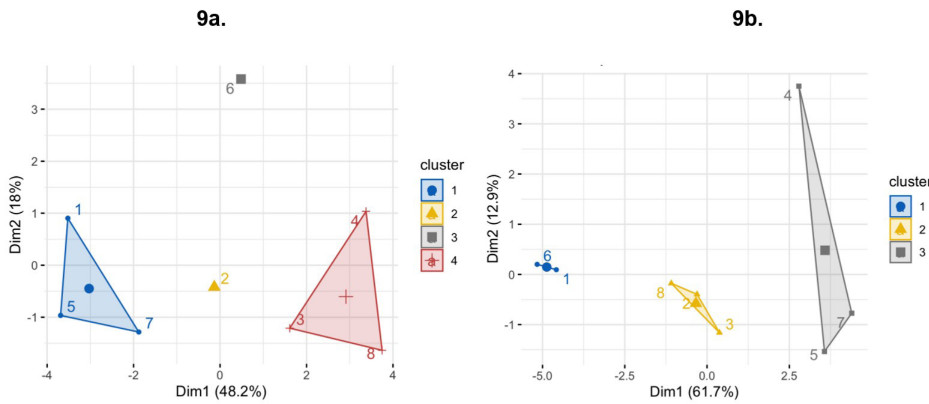

Figure 9. Analysis of hierarchical clusters of the yellow pitahaya genotypes of the municipalities of Miraflores and Zetaquira in the open field production system. **a.** Miraflores. **b.** Zetaquira.

number of sub-sprouts with an average of 2.8 and a higher than average plant height. Genotype 2 was characterized by presenting the lowest number of sub-sprouts with 0.70 and an average plant height of 164.90 cm.

Smooth cladodes texture, concave margin shape, and brown spine color were observed in both municipalities. In the municipality of Zetaquira, genotypes 1 and 6 were grouped because they presented the lowest size with 129.00 and 107.70 cm respectively, the lowest number of sprouts and sub-sprouts with 2.0 and 0.2 sprouts per plant. The cluster formed by genotypes 2, 3 and 8 presented genotypes with plant height of 132.00 cm and 146.00 cm and width of ribs with a basal thickness between 1.69 and 1.74 cm. Finally, genotypes 4.5 and 7 presented the tallest plants with heights of 153.20, 165.30 and 160.00 cm, average number of sprouts and sub-sprouts of 3.43 and 1.30 sprouts respectively.

4. Discussion

Pitahaya is an exotic fruit that has been cultivated on family farms since ancient times (Tel-Zur, 2022) and currently, given the physiological characteristics of cacti, such as adaptability to drought, they have made it an economically profitable crop option in many parts of the world., in addition to its appearance, flavor and consistency of the fruit that contribute to its economic value. This has encouraged a commercial market for exotic fruits in Europe, Asia and the Americas (Jalgaonkar et al., 2022), with these also being highly valued in national markets (González-Trujillo et al., 2019). It is mainly consumed as dried fruit and can be used in fruit salads, soft drinks, jams, beer, wine, among others (El Salous et al., 2020). The pitahaya fruit, given its physical and chemical features offer a wide market of exportation as a dry fruit, or frozen pulp and its ample and diverse forms of consumption, constitute productive and viable alternatives as long as the internal market is strengthened, promoting the habit of consumption (Quispe Lupuche et al., 2021).

The importance of the cultivation of *S. megalanthus* for their commercialization has allowed for the development of a wide variety of studies about the quality of the fruit, commercialization, nutritional composition, cultivation, phenology, organic fertilization, physical chemistry, genetics, postharvest management, morphology and production systems (Tel-Zur, 2022).

However, even today, it is difficult to clearly identify the species and varieties of dragon fruit, due to its high rate of inter- and intra-specific hybridization and the genotype-environment interaction that has led to some confusion at the national level taxonomic worldwide (Tel-Zur, 2022). The phenotypic and genetic variability in morphological characteristics associated with the plant such as height, width ribs of the cladode, distance between areoles, number of sprouts, length of the spines and sweetness, size and color of the fruit are the product of this natural hybridization process (Tel-Zur et al., 2011). makes it difficult to increase the quality standards for the exportation market because it posed serious problems in determining their performance in handling and shelf life (Álvarez-Herrera et al., 2023).

Conventionally, morphological traits had been used to differentiate plant germplasm/ species and to elucidate their genetic relationship (Sibut et al., 2023). As in this study, high values were observed in the coefficients of variation in the characteristics associated with the cladode and the sprouts, in the evaluated locations. Several authors suggest that cladode characters such as cladode width (mm), distance between areoles (mm), number of spines, length of areoles (mm), margin ribs of cladode and its waxiness could be used for identification of *Hylocereus* and *Selenicereus* spp. (Rodrigues et al., 2021; Mejía et al., 2013).

Abirami et al. (2021) in the morphological, biochemical and molecular characterization of three species of *Hylocereus* from India, found that cladode characters such as number of spines (Verona-Ruiz et al., 2020; Oliveira et al., 2020), length of areoles (mm) as 1–4, margin ribs of cladode (convex or concave) and its waxiness (weak or strong white waxy or light waxy) could be used for identification of three *Hylocereus* spp. In this study, the genotypes showed the shape of margin between areolas between concave and right, contrary to that reported in other studies on different species of *Hylocereus*, where the predominant forms were convex, with the presence of wax (Abirami et al., 2021). The cladode width and distance between areoles corresponded well with earlier studies from México (Castillo et al., 2005), India (Abirami et al., 2021), Puerto Rico and Colombia (Morillo et al., 2021; Betancur et al., 2020; Goenaga et al., 2020).

Multiple correspondence analyzes showed that the characteristics that most contributed to the phenotypic variation observed were the distance between areoles, the width of the ribs in the apical, middle, and basal region, and number of spines. Results that had already been reported in other studies in different countries where found high variation in characteristics of agronomic importance, even within the same species of *Hylocereus* and *Megalanthus* spp. (Goenaga et al., 2020; Abirami et al., 2021; Mejía et al., 2013), which is favorable for future breeding studies. The availability of this information would be of great assistance in developing an appropriate method for the cultivation of a particular species (Callejas-Chavero et al., 2021)

Among pitahaya propagation techniques, cutting stands out, as it enables the uniformity and quality of seedlings by cloning selected genotypes from mother plants in addition to eliminating the youth period (Zem et al., 2015). Rodrigues et al. (2021) evaluated the ideal size of white-fleshed red pitahaya cladodes and the time of their collection for crop propagation by cutting in view of the physiological quality of the produced clonal plants to enable more appropriate cultural management and increase the cultivation area. Analyzing only the cladode size, a positive relationship was observed between the number of sprouts and sprouting percentage in the cladodes of the greatest studied lengths. this result corroborates the analyses carried out by Moreira et al. (2017), who studied the determination of the cutting length for the production of clonal pitahaya plants (*Hylocereus costaricensis*) in protected environments and observed that clonal plants formed from cladodes of greater lengths presented higher reserves and stored nutrient availabilities (Delgado and Yuyama, 2010), mainly carbohydrates, which directly contribute to the formation and growth of sprouts and roots (Nicoloso et al., 2001).

Thus, in cases where there is greater availability of material, the use of larger cladodes is recommended, since according to Balaguera et al. (2011), a greater cladode length allows a plant to reach the apex of the tutor and begin emitting secondary branches more quickly, with adult plants forming earlier, initiating the reproductive stage. The size of cuttings is related to their nutritional condition, with the amount of reserves and the number of buds varying according to the length used; normally, cuttings with greater lengths may have higher carbohydrate and endogenous auxin contents (Mayer et al., 2002). Additionally, it is known that the presence of leaves and buds in cuttings plays a key role in the formation of new root systems, and these factors are responsible for the production of assimilates and substances such as auxins, which is synthesized in these locations (Taiz et al., 2017); this analysis shows the high capacity of pitahaya wood cladodes to remain alive.

In general terms, the morphological evaluation of the yellow pitahaya genotypes under the two productive systems in the municipalities of Miraflores and Zetaquira, show differences in the expression of the phenotypic characteristics associated with the cladodes and the sprouts, the above may be due to the factors agroclimatological present in the evaluated localities. Results similar to those obtained by Morillo-Coronado et al., 2021 in the morphoagronomic characterization of different genotypes in five municipalities of the province of Lengupá.

In Colombia, the morphoagronomic characterization studies of the yellow pitahaya germplasm have shown the existence of variability which can be used within improvement programs, considering the productive systems that farmers currently have, since this in one way or another is influencing the expression of desirable characters.

5. Conclusions

The morphoagronomic characterization of yellow pitahaya genotypes showed morphological differences in shoots and cladodes according to the site where they were evaluated. The existence of phenotypic variation allows carrying out selection processes that lead to the identification of elite genotypes that meet the needs of producers and are an economically profitable alternative.

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References

ABIRAMI, K., SWAIN, S., BASKARAN, V., VENKATESAN, K., SAKTHIVEL, K. and BOMMAYASAMY, N., 2021. Distinguishing three Dragon fruit (*Hylocereus* spp.) species grown in Andaman and Nicobar Islands of India using morphological, biochemical and molecular traits. *Scientific Reports*, vol. 11, no. 1, p. 2894. http://dx.doi.org/10.1038/s41598-021-81682-x. PMid:33536453.

AL-MEKHLAFI, N., MEDIANI, A., ISMAIL, N.H., ABAS, F., DYMERSKI, T., LUBINSKA-SZCZYGEŁ, M., VEARASILP, S. and GORINSTEIN, S., 2021. Metabolomic and antioxidant properties of different varieties and origins of Dragon fruit. *Microchemical Journal*, vol. 160, p. 105687. http://dx.doi.org/10.1016/j.microc.2020.105687.

ÁLVAREZ-HERRERA, J.G., BURGOS-CHINOME, D.Y. and JAIME-GUERRERO, M., 2023. Calidad de frutos de pitahaya (*Selenicereus megalanthus* Haw.) sometidos a diferentes recubrimientos durante el almacenamiento. *Entramado*, vol. 19, no. 1, pp. 1-12. https://doi.org/10.18041/1900-3803/entramado.1.8507.

BALAGUERA, H.E., MORALES, E.I., ALMANZA-MERCHÁN, P.J. and BALAGUERA, W.A., 2011. El tamaño del cladodio y los niveles de auxina influyen en la propagación asexual de pitaya (*Selenicereus megalanthus* Haw.). *Revista Colombiana de Ciencias Horticolas*, vol. 4, no. 1, pp. 33-42. http://dx.doi.org/10.17584/rcch.2010v4i1.1222.

BETANCUR, J.A., MURIEL, S.B. and GONZÁLEZ, E.P., 2020. Morphological characterization of the red dragon fruit—*Selenicereus undatus* (Haw.) D.R. Hunt—under growing conditions in the municipality of San Jerónimo (Antioquia, Colombia). *Revista Facultad Nacional de Agronomía*, vol. 73, no. 1, pp. 9019-9027. http://dx.doi.org/10.15446/rfnam.v73n1.77735.

CAETANO, C., ZAMBRANO, J., GÓMEZ, E., SUÁREZ, R., SANDOVAL, C., JIMÉNEZ, J. and PARRA, E., 2013. *Cartilla frutales: pitahaya amarilla*. Palmira: Universidad Nacional de Colombia.

CALLEJAS-CHAVERO, A., VARGAS-MENDOZA, C.F., GOMEZ-HINOSTROSA, C., ARRIOLA-PADILLA, V.J. and CORNEJO-ROMERO, A., 2021. Breeding system in a population of the globose cactus Mammillaria magnimamma at Valle del Mezquital, Mexico. *Botanical Sciences*, vol. 99, no. 2, pp. 229-241. http://dx.doi.org/10.17129/botsci.2654.

CASTILLO, R., LIVERA, M. and MÁRQUEZ, G., 2005. Caracterización morfológica y compatibilidad sexual de cinco genotipos de pitahaya (*Hylocereus undatus*). *Agrociencia*, vol. 39, no. 2, pp. 183-194.

DELGADO, J.P.M. and YUYAMA, K., 2010. Comprimento de estaca de camu-camu com ácido indolbutírico para a formação de mudas. *Revista Brasileira de Fruticultura*, vol. 32, no. 2, pp. 522-526. http://dx.doi.org/10.1590/S0100-29452010005000066.

EL SALOUS, A., ORDOÑEZ-ARAQUE, R., ZUÑIGA-MORENO, L., HUERTA, M. and MELENDEZ, J., 2020. Sensory and physicochemical characteristics of cookies made of yellow pitahaya (*Selenicereus megalanthus*) peel flour. *International Journal of Pharmaceutical Research*, vol. 12, no. 4, pp. 4179-4185. http://dx.doi.org/10.31838/ijpr/2020.12.04.575.

GOENAGA, R., MARRERO, A. and PÉREZ, D., 2020. Yield and fruit quality traits of dragon fruit cultivars grown in Puerto Rico. *HortTechnology*, vol. 30, no. 6, pp. 803-808. http://dx.doi.org/10.21273/HORTTECH04699-20.

GÓMEZ-HINOSTROSA, C., HERNÁNDEZ, H.M., TERRAZAS, T. and CORREA-CANO, M.E., 2014. Studies on Mexican Cactaceae. V. Taxonomic notes on *Selenicereus tricae. Brittonia*, vol. 66, no. 1, pp. 51-59. http://dx.doi.org/10.1007/s12228-013-9308-y.

GONZÁLEZ-TRUJILLO, M.M., PERAZA-ARIAS, A. and BROCHERO, H.L., 2019. Insectos asociados a cultivos de pitaya amarilla (*Selenicerus megalanthus*) en Inzá, Cauca, Colombia. *Revista Colombiana de Entomologia*, vol. 45, no. 2, p. e7961. http://dx.doi.org/10.25100/socolen.v45i2.7961.

HOSSAIN, F.M., NUMAN, S.M.N. and AKHTAR, S., 2021. Cultivation, nutritional value, and health benefits of dragon fruit (*Hylocereus* spp.): a review. *International Journal of Horticultural Science and Technology*, vol. 8, no. 3, pp. 259-269. http://dx.doi.org/10.22059/ijhst.2021.311550.400.

JALGAONKAR, K., MAHAWAR, M.K., BIBWE, B. and KANNAUJIA, P., 2022. Postharvest profile, processing and waste utilization of dragon fruit (*Hylocereus* Spp.): a review. *Food Reviews International*, vol. 38, no. 4, pp. 733-759. http://dx.doi.org/10.1080/87559129.2020.1742152.

KASSAMBARA, A. and MUNDT, F., 2020 [viewed 30 May 2023]. *Factoextra: extract and visualize the results of multivariate data analyses. R Package version 1.0.7* [online]. The R Project for Statistical Computing. Available from: https://cran.r-project.org/web/packages/factoextra/index.html

LE, S., JOSSE, J. and HUSSON, F., 2008. FactoMineR: an R package for multivariate analysis. *Journal of Statistical Software*, vol. 2008, no. 25, pp. 1-18.

LEOVIKA, A., SUMINAR, E., ISNANIAWARDHANI, V., QANIT, M., FAUZI, A. and MUBAROK, S., 2019. Morphological characterization and adaptation of four dragon fruit genotypes in pangandaran regency of Indonesia. *Asian Journal of Plant Sciences*, vol. 18, no. 1, pp. 21-25. http://dx.doi.org/10.3923/ajps.2019.21.25.

MAYER, N.A., PEREIRA, F.M. and NACHTIGAL, J.C., 2002. Efeito do comprimento de estacas herbáceas de dois clones de umezeiro (*Prunus mume* Sieb & Zucc.) no enraizamento adventício. *Revista Brasileira de Fruticultura*, vol. 24, no. 2, pp. 500-504. http://dx.doi.org/10.1590/S0100-29452002000200044.

MEJÍA, H.A., MURIEL, S.B., MONTOY, A.C.A. and REYES, C., 2013. In situ morphological characterization of Hylocereus spp. (fam.: Cactaceae) genotypes from Antioquia and Córdoba (Colombia). *Revista Facultad Nacional de Agronomía*, vol. 66, no. 1, pp. 6845-6854.

MOREIRA, A.R., SOUZA, F.L.B., SILVA, R.T.L., OLIVEIRA, R.L.L., ALONÇO, A.S., OLIVEIRA NETO, C.F. and SOUSA, S.K.A., 2017. Determinação do comprimento da estaca para produção de mudas de pitaia (*Hylocereus costaricensis*) em ambiente protegido. *Tecnologica*, vol. 21, no. 2, pp. 41-45. http://dx.doi.org/10.17058/tecnolog.v21i2.8734.

MORILLO, A.C., MORA, M.S. and MORILLO, Y., 2022a. Analysis of the genetic diversity of dragon fruit based on ISSR markers in Colombia. *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 82, p. e256451. http://dx.doi.org/10.1590/1519-6984.256451. PMid:35081251.

MORILLO, A.C., MANJARRES, E.H. and FORERO, L., 2021. Phenotypic diversity of morphological characteristics of pitahaya (*Selenicereus megalanthus* Haw) germplasm in Colombia. *Plants*, vol. 10, no. 11, p. 2255. http://dx.doi.org/10.3390/plants10112255. PMid:34834618.

MORILLO, A.C., MANJARRES, E.H., SAENZ, Ó.J. and MORILLO, Y., 2022b. Morphoagronomic evaluation of yellow pitahaya (*Selenicereus megalanthus* Haw.) in Miraflores, Colombia. *Agronomy*, vol. 12, no. 7, p. 1582. http://dx.doi.org/10.3390/agronomy12071582.

NICOLOSO, F.T., CASSOL, L.F. and FORTUNATO, R.P., 2001. Comprimento da estaca de ramo no enraizamento de ginseng brasileiro (*Pfaffia glomerata*). *Ciência Rural*, vol. 31, no. 1, pp. 57-60. http://dx.doi.org/10.1590/S0103-84782001000100009.

OLIVEIRA, M.M.T., SHUHUA, L., KUMBHA, D.S., ZURGIL, U., RAVEH, E. and TEL-ZUR, N., 2020. Performance of Hylocereus (Cactaceae) species and interspecific hybrids under high-temperature stress. *Plant Physiology and Biochemistry*, vol. 153, no. 1, pp. 30-39. http://dx.doi.org/10.1016/j.plaphy.2020.04.044. PMid:32474384.

QUISPE LUPUCHE, E., CHÁVEZ PÉREZ, J.A., MEDINA-PIZZALI, M.L., LOAYZA GUTIÉRREZ, L. and APUMAYTA SUÁREZ, E., 2021. Chemical characterization, polyphenol content and antioxidant capacity of two pitahaya ecotypes (*Hylocereus* spp.). *Revista Facultad Nacional de Agronomía*, vol. 74, no. 3, pp. 9723-9734. http://dx.doi.org/10.15446/rfnam.v74n3.92821.

R CORE TEAM SOFTWARE. (2020). *R: a language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing.

RED DE INFORMACIÓN Y COMUNICACIÓN DEL SECTOR AGROPECUARIO COLOMBIANO – AGRONET [online], 2022 [viewed April 2023]. Available from: https://www.agronet.gov.co/estadistica/Paginas/home.aspx?cod=1

RODRIGUES, M.G.F., FERREIRA, A.F.A., MALAGUTTI, E.S., PINTO, M.S., MONTEIRO, L.N.H. and SÁ, M.E., 2021. Cladode size and collection time for pitahaya propagation. *Ciência e Agrotecnologia*, vol. 45, no. 1, p. e004821. http://dx.doi.org/10.1590/1413-7054202145004821.

SIBUT, H.C.P., FALEIRO, F.G., OLIVEIRA, J.S., LUZ, A.L., CALIMAN NETO, D. and JUNQUEIRA, N.T.V., 2023. Yield capacity of six superior pitaya genotypes under edaphoclimatic conditions of the Federal District. *Revista Brasileira de Fruticultura*, vol. 45, p. e-025. http://dx.doi.org/10.1590/0100-29452023025.

TAIYUN, W. and SIMKO, V.R., 2017. Package "corrplot": visualization of a correlation matrix (version 0.84). *The Statistician*, vol. 56, p. e24.

TAIZ, L., ZEIGER, E., MOLLER, I.M. and MURPHY, A., 2017. *Fisiologia e desenvolvimento vegetal*. 6th ed. Porto Alegre: ARTMED, 888 p.

TEL-ZUR, N., 2022. Breeding an underutilized fruit crop: a long-term program for *Hylocereus. Horticulture Research*, vol. 9, p. uhac078. http://dx.doi.org/10.1093/hr/uhac078. PMid:35707296.

TEL-ZUR, N., MIZRAHI, Y., CISNEROS, A., MOUYAL, J., SCHNEIDER, B. and DOYLE, J.J., 2011. Phenotypic and genomic characterization of vine cactus collection (Cactaceae). *Genetic Resources and Crop Evolution*, vol. 58, no. 7, pp. 1075-1085. http://dx.doi.org/10.1007/s10722-010-9643-8.

VERONA-RUIZ, A., URCIA-CERNA, J. and PAUCAR-MENACHO, L., 2020. Pitahaya (*Hylocereus* spp.): culture, physicochemical characteristics, nutritional composition, and bioactive compounds. *Scientia Agropecuaria*, vol. 11, no. 3, pp. 439-453. http://dx.doi.org/10.17268/sci.agropecu.2020.03.16.

ZEM, L.M., WEISER, A., ZUFFELLATO-RIBAS, K., RANDOMSKI, M. and SOARES, K., 2015. Enraizamento de estacas semilenhosas de cataia coletadas em quatro estações. *Ciência Rural*, vol. 45, no. 10, pp. 1815-1818. http://dx.doi.org/10.1590/0103-8478cr20140534.