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Selection indexes and principal components for agronomic and bromatological traits in forage cactus

Índices de seleção e componentes principais para caracteres agronômicos e bromatológicos em palma forrageira

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ABSTRACT - The objective of the present work was to compare selection indexes focused on the selection of forage cactus (*Opuntia ficus-indica*) accessions at initial generations. Sixty-five accessions from different locations in the semiarid region of the state of Bahia, Brazil, were evaluated in a randomized complete block design with three replications. Agronomic and bromatological traits were evaluated. The genetic parameters were predicted by using mixed models (REML/BLUP). The linear correlation degree between variables was estimated through Pearson's correlation analysis. Selection gains were predicted using four selection indexes: Smith-Hazel index, with two combinations of economic weights; rank sum index of Mulamba and Mock; and Elston's multiplicative index. The selection intensity applied was 30%, which allowed the selection of the 20 best accessions. The analysis of deviance showed significant effect for all traits. The estimate of genetic parameters evidenced the existence of genetic variability for the *O. ficus-indica* accessions. The Smith-Hazel index (combination 1) was important for primary (fresh weight and cladode dry weight) and bromatological traits (acid detergent fiber and neutral detergent fiber), expressing higher selection gains than the other indexes. The rank sum and multiplicative indexes resulted in selection gains for most evaluated traits. The results of accessions 2, 4, 5, 7, 9, 11, 14, 15, 18, 26, 27, 34, 37, 38, 39, 41, 45, 49, 51, 52, 53, and 58 were promising for their inclusion in breeding programs, as they were selected by at least two of the four selection indexes used.

Keywords: *Opuntia ficus-indica* Mill.. Semiarid. Characterization. Breeding. Forage plants.

RESUMO - O objetivo do trabalho foi comparar índices de seleção com foco na seleção de palma forrageira (*Opuntia. ficus-indica*) nas gerações iniciais. Sessenta e cinco acessos de diferentes localidades da região Semiárida do estado da Bahia, Brasil, foram avaliados em um delineamento de blocos ao acaso com três repetições. Características agronômicas e bromatológicas foram avaliadas. Os parâmetros genéticos foram preditos usando modelos mistos (REML / BLUP). O grau de correlação linear entre as variáveis foi estimado por meio da análise de correlação de Pearson. Os ganhos de seleção foram preditos usando quatro índices de seleção: índice Smith-Hazel, com duas combinações de pesos econômicos; soma do índice de classificação de Mulamba e Mock; e o índice multiplicativo de Elston. A intensidade de seleção aplicada foi de 30%. As estimativas dos parâmetros genéticos evidenciaram a existência de variabilidade genética para os acessos de *O. ficus-indica*. O índice Smith-Hazel (combinação 1) foi importante para as características primárias (peso verde e peso seco do cladódio) e bromatológicas (fibra em detergente ácido e fibra em detergente neutro), expressando ganhos de seleção superiores aos demais índices. A soma dos *ranks* e índices multiplicativos resultou em ganhos de seleção para a maioria das características avaliadas. Os resultados dos acessos 2, 4, 5, 7, 9, 11, 14, 15, 18, 26, 27, 34, 37, 38, 39, 41, 45, 49, 51, 52, 53 104 e 58 foram promissores para sua inclusão no programa de melhoramento, uma vez que foram selecionados em pelo menos dois dos quatro índices de seleção utilizados.

Palavras-chave: *Opuntia ficus-indica* Mill.. Semiárido. Caracterização. Melhoramento. Plantas forrageiras.

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INTRODUCTION

The forage cactus specie *Opuntia ficus-indica* Mill. is native to Mexico and was introduced into Brazil in the late nineteenth century (LEITE, et al., 2014). Its morphophysiological traits contributed to its local adaptation and made possible its use as a forage resource in a large area of the Northeast region of Brazil (PAIXÃO, et al., 2011).

Forage cactus breeding has involved crossings and selections of more vigorous clones in several countries, such as Mexico, the United States, and South Africa. The State University of Feira de Santana, in the state of Bahia, Brazil, has conducted a breeding program that includes evaluation and selection of genotypes adapted to the region, and has a collection of accessions from different regions of the Northeast of Brazil.

The genetic and environmental contributions to the expression of phenotypes are explained by the analysis of genetic parameters (SALES, et al., 2013), which is indispensable for the conduction of breeding programs, as it provides data about heritability, amplitude of genetic variation, and prediction of selection gains, allowing the measurement of a population's potential and the obtaining of higher efficiency in the selection process (VIANA; RESENDE, 2014). Important information is also obtained through genetic correlations by assessing whether a change in a variable is proportionally correlate to a change in other (NARDINO et al., 2016). These data contribute to obtain selection gains for a trait through indirect selection of another correlated trait, as well as to discard redundant traits (CRUZ; REGAZZI, 2012).

However, the selection for quantitative traits is not an easy task for a breeding program, considering that they have complex dynamics, are highly affected by the environment, and can be strongly interrelated, making the selection for a trait to change another. The use of selection indexes is a strategy used by breeders to mitigate this problem, and has been proposed for plant and animal breeding programs to select quantitative traits simultaneously.

Selection indexes were first described by Smith (1936) to maximize the correlation between the index and the genotypic value of individuals. Subsequently, Smith (1936) and Hazel and Lush (1943) adapted them to animal breeding programs and, thus, some authors termed it Smith-Hazel index; however, it requires the establishment of economic weights, which can hinder the selection due to the expression of negative selection gains in the traits (FARIAS et al., 2016).

The multiplicative index, also known as weight-free index, was developed by Elston (1963) and is characterized by not requiring the establishment of economic weights for the several traits and for estimation of phenotypic and genotypic variances and covariances. The rank sum index (MULAMBA; MOCK, 1978) is characterized by ranking genotypes based on their relation to each trait and in an order favorable to the breeder's goals and, similarly to the multiplicative index, it does not require the estimation of phenotypic and genotypic variances and covariances and the establishment of economic weights (FARIAS et al., 2016). Studies using selection indexes have been conducted successfully for different crops, such as eucalyptus (KRAUSE et al., 2021), herbaceous cotton (FARIAS et al., 2016), and sour passion fruit (DALBOSCO et al., 2019).

Considering the lack of studies using selection indexes for forage cactus, the objective of the present work was to compare selection indexes to indicate the best methods for selection of the most promising accessions.

MATERIAL AND METHODS

The experiment was implemented at the Rio Seco Experimental Station, which belongs to the State University of Feira de Santana, in the municipality of Amélia Rodrigues, Bahia, Brazil (12°23'30"S, 38°45'24"W, and altitude of 217 m). The experiment period had a rainfall depth of 1,270 mm, and a mean temperature of 24.6 °C (INMET, 2017). The climate of Amélia Rodrigues was classified as Af, tropical wet, according to the classification of Köppen.

The accessions were collected in 13 municipalities of the state of Bahia: Caetité, Vitória da Conquista, Ruy Barbosa, Feira de Santana, Jeremoabo, Ipirá, Morro do Chapéu, Riachão do Jacuípe, Valente, Juazeiro, Senhor do Bonfim, Jaguarari, and Irecê. A randomized complete block design was used, with 65 treatments, three replications, and plots composed of three plants.

One cladode per pit was used for planting; it was planted in an upright position, with the cut end pointing downwards into the soil, deep enough to prevent lodging, with spacing of 1.0 m between rows and 0.5 m between plants.

The agronomic performance was evaluated by measuring the following traits: plant height (PH; cm); plant width (PW; cm); total number of cladodes (TNC); cladode length (CL; cm); cladode width (CW; cm); cladode diameter (CD; mm); cladode fresh weight (CFW; g); cladode dry weight (CDW; g); dry matter yield (DMY; %), calculated by the expression $DMY\ (\%) = CDW/CFW\ x\ 100$. Cladode area (CA) was determined using the expression $CA = CL\ x\ CW\ x\ 0.632$. Cladode total photosynthetic area (CTPA) was calculated by the expression $CTPA = CA\ x\ TNC$. The measurements were carried out using a tape ruler, a caliper, and a precision balance.

One first-order and one second-order cladode were collected from each plant for bromatological analysis. The cladodes were dehydrated in a forced air circulation oven at 65 °C for approximately 15 days. The samples were then ground in a Willey mill, homogenized, and analyzed. Cladode gross protein (CGP) content was obtained by the Kjeldahl method (AOAC, 2019); acid detergent fiber (ADF) and neutral detergent fiber (NDF) were estimated by the methodology of AOAC (2019); and ethereal extract (EE) was obtained by the Soxhlet method. Total digestible nutrient (TDN; %) contents were estimated by the expression $TDN\ (\%) = 87.84 - (0.70\ x\ ADF\ (\%))$; and non-fibrous carbohydrates (NFC) were obtained by the expression $NFC\ (\%) = (100 - CGP - EE - ash - NDF)$.

The data were analyzed using the methodology of mixed linear models (restricted maximum likelihood/best linear unbiased prediction– REML/BLUP). The estimates of genetic parameters were obtained by REML approach and the prediction of genetic values of the accessions, for each characteristic, was obtained by BLUP. The following statistical model was used: $y = Xr + Zg + e$, where y is the vector of the data, r is the vector of the effects of replication (fixed effects) added to the overall mean, g is the vector of the effects of accessions (random effects), e is the vector of residues (random), and X and Z are the incidence matrices for fixed and random effects. The analysis of deviance was carried out to test the significance of the effects of accessions using the LRT (likelihood ratio test). The following equation was used: $D = -2LogL$, where D is the deviance and L is the maximum point of the residual likelihood function (VIANA; RESENDE, 2014). The estimates of the components of variance were obtained by the equations: $h_g^2 = \sigma_g^2/\sigma_f^2$, where h_g^2 is the individual heritability per plot in the broad sense, σ^2_g is the genetic variance of the accessions, σ^2_f is the phenotypic variance; and $h^2_{mg} = \sigma^2_g / \sigma^2_g + \frac{\sigma^2_e}{b}$, where h^2_{mg} is the heritability in the broad sense for the means of accessions, σ^2_e is the residual variance, and b is the number of replications (blocks) used for the evaluation of the accessions. The REML/BLUP analyses were carried out using the Selegen-REML/BLUP program (RESENDE, 2016).

The correlation between traits was estimated using the predicted genetic values (BLUP) of each accession, added to the overall mean of the experiment, resulting in the mean genotypic values. The analysis was carried out using the corrgram package of the R 3.5.1 program (R CORE TEAM DEVELOPMENT, 2018).

The selection gains were predicted using four indexes: Smith-Hazel (SMITH, 1936; HAZEL; LUSH, 1943), with two combinations, varying the economic weights; rank sum index (MULAMBA; MOCK, 1978); and multiplicative index (ELSTON, 1963). Several combinations of economic weights were tested for the index that required them, focused on selecting the accessions with the best combinations regarding bromatological and morphological traits, for a selection intensity of 30%, allowing the selection of 20 accessions by all indexes used. The following economic weights were used for the Smith-Hazel index (Table 1). The indexes were calculated using the Selegen program (RESENDE, 2016).

Table 1. Economic weights assigned to bromatological and morphological traits by the Smith-Hazel selection index, in combinations 1 and 2.

	Economic weights	
Trait	Combination 1	Combination 2
Plant height (cm)	1	0
Plant width (cm)	1	0
Total number of cladodes	10	0
Cladode length (cm)	1	0
Cladode width (cm)	1	0
Cladode diameter (mm)	1	0
Cladode fresh weight (g)	5	0.9
Cladode dry weight (g)	10	0.9
Dry matter yield (%)	10	0.2
Cladode area (cm^2)	1	0.2
Cladode photosynthetic area	1	0.4
Gross protein (%)	10	0.5
Acid detergent fiber (%)	10	0
Neutral detergent fiber (%)	10	0.2
Ethereal extract (%)	5	0
Total digestible nutrients	5	0.2
Non-fibrous carbohydrates	5	0

RESULTS AND DISCUSSION

According to the analysis of deviance, the effect of accessions was significant for all evaluated traits (Table 2), denoting the existence of genetic variability among accessions and, therefore, the possibility of selection. The experimental precision through the selection accuracy results ($\hat{r}_{\hat{g}g}$) varied according to the characteristic evaluated. Considering the classification of Resende and Duarte (2007) for experimental evaluations, PH, PW, CD, CFW, ADF, NDF, and NFC had very high accuracy (above 90%); CL, CA, and CTPA had high accuracy (between 70% and 89%); CW, DMY, and TDN had moderate accuracy (between 41% and 69%); and TNC, CDW, CGP, and EE had low accuracy (below 40%) (Table 3).

The estimates of the coefficient of genetic variation were below 25% for all traits, except for CGP (53.83%) (Table 3). Seven traits had coefficient of genotypic variation to coefficient of residual variance ratio (CVg/CVe) higher than one (PH, PW, CD, CFW, ADF, NDF, and NFC) (Table 3).

The h^2_{mg} values were higher than 0.80 for PH, PW, CD, CFW, ADF, NDF, and NFC (Table 3). CL, CW, DMY, CA, and CTPA had h^2_{mg} between 0.28 and 0.61; h^2_{mg}; low magnitude estimates (<0.18) were found for TNC, CDW, CGP, and TDN.

Table 2. Analysis of deviance for the effects of accessions and the complete model, and maximum likelihood ratio test for agronomic and bromatological traits of 65 accessions of *Opuntia ficus-indica*.

Trait	Deviance		LRT (chi-square)
	Accessions	Complete Model	
Plant height (cm)	1480.92	1306.96	173.96**
Plant width (cm)	1547.88	1432.88	115.00**
Total number of cladodes	673.84	656.76	17.08**
Cladode length (cm)	1043.67	1022.80	20.87**
Cladode width (cm)	822.67	813.56	9.11**
Cladode diameter (mm)	1147.32	1029. 12	118.20**
Cladode fresh weight (g)	2424.03	2338.00	86.03**
Cladode dry weight (g)	1482.45	1377.96	104.49**
Dry matter yield (%)	446.52	310.48	136.04**
Cladode area (cm^2)	2078.48	2063.20	15.28**
Cladode photosynthetic area	2907.65	2889.00	18.65**
Gross protein (%)	1528.02	399.72	1128.30**
Acid detergent fiber (%)	840.25	430.88	409.37**
Neutral detergent fiber (%)	905.79	225.14	680.65**
Ethereal extract (%)	1205.09	470.48	734.61**
Total digestible nutrients	675.50	180.74	494.76**
Non-fibrous carbohydrates	1018.72	612.92	405.80**

LRT = maximum likelihood ratio test for chi-square with degree of freedom of 1.

The genetic variance, confirmed by the significant effects of accessions found for all evaluated traits and expressed by the analysis of deviance, indicated that the collection of accessions in different regions of the state of Bahia contributed to the wide genetic variance found among the 65 forage cactus accessions evaluated.

The estimates of genetic parameters showed that a reliable selection can be done for the traits PH, PW, CW, CD, CFW, ADF, NDF, and NFC (Table 3). These traits had individual heritability in the broad sense (h^2g) and heritability at genotype level (h^2mg) above 60%, with a high accuracy (above 0.90). Paixão et al. (2011) evaluated eight forage cactus genotypes of the genera *Opuntia* and *Nopalea* and found significant genetic variations among the clones for plant height and width and cladode length and width, with heritability estimates above 88%, denoting good genetic control for all traits. Similar results were found in the present work for these traits, except for cladode width, which expressed low heritability.

According to Viana and Resende (2014), heritability is expressed in percentages (0% to 100%.): heritability values from 0% to 20% are low, 20 to 40% are moderate, and above 40% are high. The higher the heritability of a trait, the more accurate its predicted genetic value, resulting in immediate selection gains for the trait.

However, selection accuracy $(\hat{r}_{\hat{g}g})$ lower than 40% was found for four traits (TNC, CDW, CGP, and EE). This estimate considers the genotypic variance (σ_g^2); thus, the low magnitude of the estimates of this parameter for the four traits may have reduced the experimental precision.

Contrastingly, a high coefficient of residual variance was found in the determination of phenotypic values, implying low heritability, for the traits TNC (0.11), CL (0.34), CW (0.21), CDW (0.03), DMY (0.12), CA (0.30), CTPA (0.32), CGP (0.02), EE (0.03), and TDN (0.07). Quantitative traits are the most interesting for breeding programs, but their analysis is difficult, as hereditary variations of quantitative traits are masked by greater non-hereditary variations, hindering the determination of genotypes values of individuals (SMITH, 1936). Therefore, the analyses indicate that these traits are expressed by a high number of alleles and are highly affected by the environment. The heritability of these traits can be increased by decreasing environmental variation, using more complete statistical designs and more adequate statistical analyses to mitigate environmental effects on the phenotype expression (LIMA NETO; SIQUEIRA, 2017).

Table 3. Estimates of components of variance and genetic parameters of 65 accessions of *Opuntia ficus-indica* by the REML/BLUP method.

	Parameter									
Trait	σ_g^2	σ_e^2	σ_f^2	h_g^2	h_{mg}^2	$\hat{r}_{\hat{g}g}$	$CVg\%$	$CVe\%$	CVg/CVe	OM
PH	99.82	18.99	118.80	0.84	0.94	0.97	16.08	7.01	2.29	62.12
PW	123.5	44.37	167.92	0.74	0.89	0.95	18.89	1.32	1.67	58.81
TNC	1.21	28.21	29.42	0.04	0.11	0.34	21.71	104.66	0.20	5.07
CL	5.02	9.65	14.67	0.34	0.61	0.78	9.13	12.66	0.72	24.53
CW	0.94	3.56	4.51	0.21	0.44	0.66	6.78	13.19	0.51	14.30
CD	15.81	5.92	21.73	0.73	0.88	0.94	18.40	11.26	1.63	21.61
CFW	10727.2	5986.93	16714.06	0.64	0.84	0.91	18.21	13.60	1.34	568.69
CDW	41.33	1307.50	1348.84	0.03	0.28	0.29	13.72	77.17	0.17	46.85
DMY	0.44	3.33	3.77	0.12	0.28	0.53	8.47	23.24	0.36	7.85
CA	841.24	1980.05	2821.29	0.30	0.58	0.75	12.99	19.92	0.65	223.27
CTPA	60530.85	129197.65	189728.50	0.32	0.58	0.76	22.90	33.46	0.68	1074.19
CGP	60.19	5175.70	5235.89	0.02	0.03	0.18	53.83	499.18	0.10	14.41
ADF	5.30	0.10	5.40	0.98	0.99	0.99	8.83	1.14	7.74	28.44
NDF	6.31	1.34	7.65	0.76	0.90	0.95	8.58	4.79	1.79	24.17
EE	0.09	2.88	2.97	0.03	0.08	0.29	7.38	41.99	0.17	4.05
TDN	1.71	22.41	24.12	0.07	0.18	0.43	1.89	6.85	0.27	69.04
NFC	11.30	3.19	14.49	0.78	0.91	0.95	7.68	4.08	2.29	43.76

σ_g^2 = genotypic variance; σ_e^2 = residual variance; h_g^2 = individual heritability in the broad sense; h_{mg}^2 = heritability in the broad sense for the means of the accessions; $\hat{r}_{\hat{g}g}$ = selection accuracy; $CVg\%$ = coefficient of genotypic variation; $CVe\%$ = coefficient of residual variance; CVg/CVe = coefficient of genotypic variation to coefficient of residual variance ratio; OM = overall genotypic mean; PH = plant height (cm); PW = plant width (cm); TNC = total number of cladodes; CL = cladode length (cm); CW = cladode width (cm); CD = cladode diameter (cm); CFW = cladode fresh weight; CDW = cladode dry weight ; DMY = dry matter yield (%); CA = cladode area (cm^2); CTPA = cladode total photosynthetic area (cm^2); CGP = cladode gross protein (%); ADF = acid detergent fiber (%); NDF = neutral detergent fiber (%); EE = ethereal extract (%); TDN = total digestible nutrients (%); NFC = non-fibrous carbohydrates.

Heritability impacts of traits on the selection have been studied, showing that predictive models work relatively well, even for low-heritability traits (TOEBE et al., 2017). Grattapaglia and Resende (2011) reported that the accuracy increased by only 10-20% as the heritability increased from 0.2 to 0.6, regardless of the population size, indicating greater individual selection gains even for low-heritability traits. According to Toebe et al. (2017), tests with high selection accuracy present lower residual variance and greater genetic variance.

The analysis of the coefficient of genotypic variation (CVg) showed the amplitude of genetic variability in the studied population. Paixão et al. (2011) found higher CVg for CW (24.52%), and Santos et al. (1994) found CVg of 14.2% for CGP, 1.5% for gross fiber content, and 0.3% for phosphorus content. These results and the information about origin, introduction, and propagation mode of *O. ficus-indica* denote genetic variability, allowing the selection of accessions with the best allelic combinations for the evaluated traits.

Cladode gross protein (CGP) showed a low genetic variance and a high error variance, resulting in low estimates of heritability and accuracy. CGP is an important bromatological component related to the nutritional quality of *O. ficus-indica* cactus forage; adequate CGP contents are above 7% (AOAC, 2019). The low accuracy probably hindered the obtaining of selection gains because the CGP variation in the accessions was above 7% (9-18%).

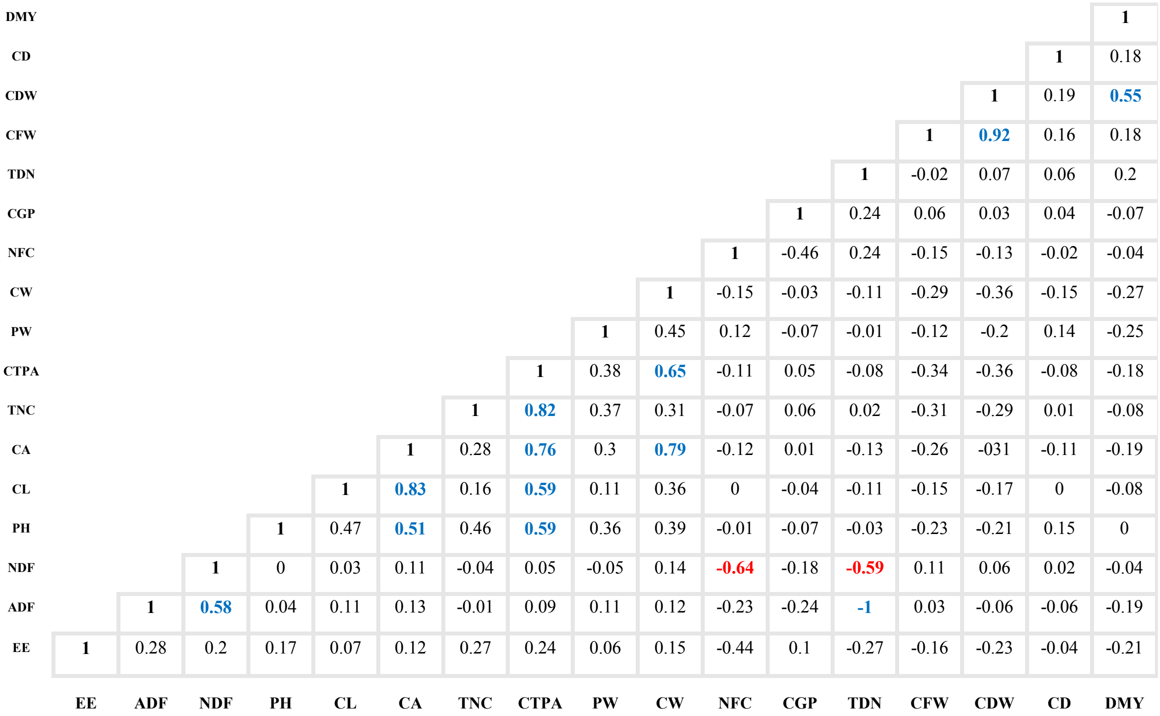
Genetic correlations

Positive correlations of high magnitude were found for ADF × NDF (0.58), CA × CL (0.83), CA × CTPA (0.76), CA × PH (0.51), TNC × CTPA (0.82), CA × CW (0.79), CTPA × CW (0.65), CTPA × PH (0.59), CTPA × CL (0.59), CDW × DMY (0.55), and CDW × CFW (0.92). Positive correlations of medium magnitude were found for CL × PH (0.47), TNC × PH (0.46), CTPA × PW (0.38), PW × PH (0.36), PW × TNC (0.37) CW × PH (0.39), CW × CL (0.36), CW × TNC (0.31), and CW × PW (0.45). Negative correlations of high magnitude were found for the bromatological traits ADF × TDN (-1.00), NDF × NFC (-0.64), and NDF × TDN (-0.59). Negative correlations of medium magnitudes were found for NFC × CGP (-0.46), and NFC × EE (-0.44), CTPA × CDW (-0.36), CTPA × CFW (-0.34), CDW × CW (-0.36), and CA ×

CDW (-0.31) (Figure 1).

The results indicated a perfect negative correlation for ADF × TDN, which hindered the obtaining of simultaneous selection gains for these traits. Contrastingly, the correlations CFW × CDW (92%) and CTPA × TNC (89%) favored an indirect selection, increasing cladode fresh weight and light interception, resulting in increases in CDW and, consequently, in cladode production.

Positive correlations of low magnitudes were found for CTPA × ADF and NDF × EE, showing the importance of selecting alleles that increase light interception capacity of the plant and, consequently, its photosynthetic potential, increasing forage yield and quality in *O. ficus-indica* plants.



	EE	ADF	NDF	PH	CL	CA	TNC	CTPA	PW	CW	NFC	CGP	TDN	CFW	CDW	CD	DMY
DMY																	**1**
CD																**1**	0.18
CDW															**1**	0.19	**0.55**
CFW														**1**	**0.92**	0.16	0.18
TDN													**1**	-0.02	0.07	0.06	0.2
CGP												**1**	0.24	0.06	0.03	0.04	-0.07
NFC											**1**	-0.46	0.24	-0.15	-0.13	-0.02	-0.04
CW										**1**	-0.15	-0.03	-0.11	-0.29	-0.36	-0.15	-0.27
PW									**1**	0.45	0.12	-0.07	-0.01	-0.12	-0.2	0.14	-0.25
CTPA								**1**	0.38	**0.65**	-0.11	0.05	-0.08	-0.34	-0.36	-0.08	-0.18
TNC							**1**	**0.82**	0.37	0.31	-0.07	0.06	0.02	-0.31	-0.29	0.01	-0.08
CA						**1**	0.28	**0.76**	0.3	**0.79**	-0.12	0.01	-0.13	-0.26	-031	-0.11	-0.19
CL					**1**	**0.83**	0.16	**0.59**	0.11	0.36	0	-0.04	-0.11	-0.15	-0.17	0	-0.08
PH				**1**	0.47	**0.51**	0.46	**0.59**	0.36	0.39	-0.01	-0.07	-0.03	-0.23	-0.21	0.15	0
NDF			**1**	0	0.03	0.11	-0.04	0.05	-0.05	0.14	**-0.64**	-0.18	**-0.59**	0.11	0.06	0.02	-0.04
ADF		**1**	**0.58**	0.04	0.11	0.13	-0.01	0.09	0.11	0.12	-0.23	-0.24	**-1**	0.03	-0.06	-0.06	-0.19
EE	**1**	0.28	0.2	0.17	0.07	0.12	0.27	0.24	0.06	0.15	-0.44	0.1	-0.27	-0.16	-0.23	-0.04	-0.21

PH = plant height (cm); PW = plant width (cm); TNC = total number of cladodes; CL = cladode length (cm); CW = cladode width (cm); CD = cladode diameter (cm); CFW = cladode fresh weight; CDW = cladode dry weight ; DMY = dry matter yield (%); CA = cladode area (cm^2); CTPA = cladode total photosynthetic area (cm^2); CGP = cladode gross protein (%); ADF = acid detergent fiber (%); NDF = neutral detergent fiber (%); EE = ethereal extract (%); TDN = total digestible nutrients (%); NFC = non-fibrous carbohydrates.

Figure 1. Coefficients of genetic correlation for 17 agronomic and bromatological traits of 65 accessions of *Opuntia ficus-indica.*

Silva et al. (2020) evaluated forage cactus clones (*O. ficus-indica* and *Nopalea cochenillifera*) and found correlations of high and medium magnitudes for the traits plant height, dry weight, and plant and cladode widths, indicating the need to prioritize selection of clones that have taller and wider plants to increase dry matter yield (Mg ha^{-1}). Similar results were found in the present work.

Pinheiro et al. (2014) found that the cladode area of the forage cactus clones IPA-Sertânia (*N. cochenillifera*) and Orelha-de-Elefante-Mexicana (*O. stricta*) expressed high and positive correlation to total number of cladodes. Similar results to the present study were reported by Guimarães et al. (2018), who also found increases in forage cactus yield due to an increased plant photosynthetic area.

Considering the need to optimize the research work and the positive correlations of high and high magnitudes found, it would be more feasible and practical for the study to measure only cladode dry weight, as the plant material is weighing on a precision balance after drying in an oven; whereas fresh weight may vary depending on the moment of collection until the packaging and transport of the material for weighing, impairing the sampling for these data. Therefore, the obtaining of fresh weight can be excluded from the analysis, proceeding immediately to the drying of cladodes, saving time and labor.

The importance of a large cladode photosynthetic area which results in greater plant yield, the easy measurement of cladode length and width when compared to the great complexity of measuring cladode area, and the positive correlations of high magnitudes between these traits make it possible to suggest a simple collection of data related to cladode dimensions to evaluate plant production. However, the data collection should be wider for taller plants, as they have greater number of cladodes and a higher plant yield.

Thus, it is suggested to exclude from the analysis the determination of cladode total photosynthetic area and cladode area.

Bromatological traits are correlated to each other and to other traits in a varied way, however, they are directly related to cladode dry weight. In this sense, cladode gross protein (CGP), non-fibrous carbohydrates (NFC), and ethereal extract (EE) area are negatively correlated to each other. Forage cactus plants do not meet adequate contents of these components, thus needing to be associated with other sources of energy, in addition to fiber, minerals, and concentrates. The limitations are great, however, increases in chemical and organic fertilizations may increase the contents of these sources, possibly, allowing for changes in the association of forage cactus with other sources of energy.

Selection of accessions

The first combination of economic weights of the Smith-Hazel index showed positive selection gains for PH, CD, CFW, CDW, ADF, NDF, and EE (0.15%, 3.82%, 17.54%, 1.81%, 1.76%, 1.83%, and 0.04%, respectively) (Table 4). The other traits presented negative selection gains.

The second combination of economic weights of the Smith-Hazel index was evaluated considering the association between traits. The highest values found for traits of greater economic and agronomic impacts for forage cactus and neutral values for those that were directly correlate with these traits were used to reach the highest selection gains. Six traits presented positive selection gains, namely TNC (0.19%), CFW (11.49%), CDW (0.24%), DMY (0.55%), CGP (0.09%), and EE (0.03%) (Table 4). The other traits expressed negative selection gains when using this selection criterion. These results did not significantly favor selection gains for most traits when compared to the first combination. A small increase in traits of great impact was found for dry matter yield (DMY) and cladode gross protein (CGP).

The rank sum index (MULAMBA; MOCK, 1978) expressed positive selection gains for the traits PH, CL, CW, CD, CFW, CDW, DMY, CA, CTPA, NDF, and TDN (1.25%, 1.41%, 0.06%, 0.53%, 7.49%, 0.05%, 0.17%, 1.79%, 2.49%, 0.27%, and 0.04%, respectively) (Table 4). This index also stood out, with some exceptions, in percentage terms.

The multiplicative index (ELSTON, 1963) showed positive selection gains for most traits, similarly to the rank sum index; these indexes presented positive selection gains for bromatological traits, which are the most agronomically important traits. Probably, some correlations contributed to these increases. The highest selection gains were found for CFW (11.37%), CD (2.87%), CTPA (2.31%), CA (1.28%), CL (1.16%), NDF (0.38%), DMY (0.13%), CDW (0.09%), ADF (0.06%), and TDN (0.02%). The other traits expressed negative selection gains (Table 4).

Table 4. Estimates of genetic gains for traits, in unit and percentage, by selection index methods.

Trait	Selection index			
	Smith-Hazel (1)	Smith-Hazel (2)	Rank Sum	Multiplicative
PH	0.09 (0.15%)	-1.66 (-2.66%)	0.78 (1.25%)	-0.120 (-0.19%)
PW	-0.87 (-1.49%)	-1.07 (-1.82%)	-2.47 (-4.21%)	-0.349 (-0.59%)
TNC	-0.02 (-0.46%)	0.01 (0.19%)	-0.004 (-0.07%)	-0.004 (-0.07%)
CL	-0.02 (-0.09%)	-0.20 (-0.79%)	0.35 (1.41%)	0.285 (1.16%)
CW	-0.19 (-1.33%)	-0.02 (-0.16%)	0.01 (0.06%)	-0.010 (-0.07%)
CD	0.83 (3.82%)	0.00 (-0.01%)	0.11 (0.53%)	0.621 (2.87%)
CFW	100.20 (17.54%)	65.25 (11.49%)	42.60 (7.49%)	64.68 (11.37%)
CDW	0.80 (1.81%)	0.11 (0.24%)	0.03 (0.05%)	0.04 (0.09%)
DMY	-0.01 (-0.15%)	0.04 (0.55%)	0.01 (0.17%)	0.01 (0.13%)
CA	-4.65 (-2.07%)	-2.04 (-0.92%)	4.00 (1.79%)	2.86 (1.28%)
CTPA	-30.80 (-2.86%)	-9.47 (-0.88%)	26.78 (2.49%)	24.84 (2.31%)
CGP	-0.0024 (-0.03%)	0.01 (0.09%)	-0.004 (-0.03%)	-0.005 (-0.03%)
ADF	0.43 (1.76%)	-0.46 (-1.90%)	-0.45 (-1.87%)	0.015 (0.06%)
NDF	0.52 (1.83%)	-0.29 (-1.02%)	0.08 (0.27%)	0.109 (0.38%)
EE	0.0016 (0.04%)	0.00 (0.03%)	-0.001 (-0.03%)	-0.001 (-0.03%)
TDN	-0.05 (-0.07%)	-0.02 (-0.03%)	0.02 (0.04%)	0.013 (0.02%)
NFC	-0.64 (-1.46%)	-0.57 (-1.31%)	-1.45 (-3.32%)	-1.07 (-2.44%)

PH = plant height (cm); PW = plant width (cm); TNC = total number of cladodes; CL = cladode length (cm); CW = cladode width (cm); CD = cladode diameter (cm); CFW = cladode fresh weight; CDW = cladode dry weight ; DMY = dry matter yield (%); CA = cladode area (cm^2); CTPA = cladode total photosynthetic area (cm^2); CGP = cladode gross protein (%); ADF = acid detergent fiber (%); NDF = neutral detergent fiber (%); EE = ethereal extract (%); TDN = total digestible nutrients (%); NFC = non-fibrous carbohydrates.

The accessions selected for each selection index are presented in Table 5. Considering all indexes, three accessions were selected. However, the number of accessions increases when at least two of the four indexes used are considered, totaling 22, with three of them present in all selection indexes.

The Smith-Hazel index showed positive selection gains and high absolute values for three primary traits (CD, CFW, and CDW), especially CFW, whose selection gain was 17.54%. Moreover, positive selection gains were found for two bromatological traits (ADF and NDF). Thus, the indirect selection may result in a population with more productive and nutritive plants in the next generation when growing under similar conditions to those found in Amélia Rodrigues. Negative correlation between DMY and nutritional parameters in plants was also reported by Santos et al. (1994), who found decreases in gross protein, phosphorus, potassium, and calcium contents at the expense of dry matter yield. The results indicated that breeding programs intended to increase DMY will demand greater inputs of fertilizers and improvements in cultural practices.

Table 5. Accessions selected by the selection indexes Smith-Hazel (SMITH, 1936; HAZEL; LUSH, 1943), Rank Sum (MULAMBA; MOCK, 1978), and Multiplicative (ELSTON, 1973).

Selection index	Accession Selected
Smith-Hazel (combination 1)	2 7 10 19 21 29 31 33 34 36 37 38 39 42 45 46 48 49 50 65
Smith-Hazel (combination 2)	37 26 41 4 49 39 11 2 53 35 38 5 52 27 15 14 51 9 18 54
Rank Sum	37 26 49 15 27 4 41 5 35 2 52 55 14 11 7 53 58 51 59 20
Multiplicative	37 26 41 35 49 52 11 15 4 39 2 27 9 5 58 18 51 45 53 7
Accessions selected by all indexes	2 37 49
Accessions selected by at least 2 indexes	2 4 5 7 9 11 14 15 18 26 27 34 37 38 39 41 45 49 51 52 53 58

The Smith-Hazel index (combination 2) presented positive selection gains for a smaller number of traits, despite the adjusts in the economic weights, indicating difficulties in establishing this parameter; CFW stood out with a selection gain above 11%. This was the only index that expressed positive selection gains, despite a low magnitude, for CGP and DMY, which presented negative (first combination) and positive selection gains, but lower than those found through the rank sum and multiplicative indexes. These traits are important for forage cactus and should be considered in breeding programs, considering their main use and the difficulties in obtaining genetic gains for them.

The use of combinations of economic weights for the Smith-Hazel index showed variation in selection gain for the traits and selected accessions. In general, the two combinations showed satisfactory selection gains for CFW, CDW, DMY, ADF, and NDF. The breeder's experience is an important factor to be considered in forage cactus breeding programs. Depending on the weights used, the breeder can improve the selection for several traits or only for a few traits.

The rank sum and multiplicative indexes presented positive selection gains for most traits, but with low magnitudes. These indexes do not require the establishment of economic weights, and in addition to encompassing more characters, although they presented less expressive selection gains, as they are quantitative traits that present mostly negative correlations, making adequate adjustments difficult. CFW had the highest selection gain in both indexes, presenting 7.49% (rank sum) and 11.37% (multiplicative), and should be considered, as this cactus is also used as fresh forage. Six traits presented negative selection gains by the rank sum index, showing that this index can be the most useful to increase selection gains for a larger set of forage cactus traits. The rank sum index stood out for primary traits, whereas the multiplicative index stood out for secondary traits (bromatological).

The use of selection indexes in forage cactus breeding programs should increase the efficiency of the selection process, as it helps the breeder to choose an adequate index for each situation. The use of constrained selection indexes is a desirable procedure for the selection of negatively correlated traits, as it contributes to prevent unfavorable changes in economically important traits.

Selection gains were different between indexes, denoting the need for determination of the most adequate index to the breeding program goals, population to be improved, and traits of greatest interest to the breeder. The evaluated accessions had positive selection gains for the most traits through the rank sum and multiplicative indexes. However, the Smith-Hazel index (combination 1) was important for primary (CFW and CDW) and bromatological (ADF and NDF) traits, showing higher selection gains than the other indexes.

Three accessions were selected by all selection indexes, and 22 of the 65 accessions were selected in at least two of the four indexes used (Table 5). The genotypes showed potential to be included in breeding programs for development of superior lines/hybrids.

The accessions evaluated in the present study are deposited in the collection of the Forest Garden Experimental Unit of the State University of Feira de Santana, Bahia, Brazil, which develops a forage cactus breeding program. New accessions from collections and seedlings produced via seeds also will be deposited in this collection to increase its genetic base, using hybridization to proceed with the cycles of evaluation and selection of superior individuals, focused on obtaining cultivars with improved morphological and bromatological traits.

CONCLUSIONS

The Smith-Hazel index (combination 1) was important for primary traits (fresh weight and cladode dry weight) and bromatological traits (acid detergent fiber and neutral detergent fiber), expressing higher selection gains than the other indexes. The use of the rank sum and multiplicative indexes resulted in positive selection gains for most evaluated traits. The results of the accessions 2, 4, 5, 7, 9, 11, 14, 15, 18, 26, 27, 34, 37, 38, 39, 41, 45, 49, 51, 52, 53, and 58 were promising for their inclusion in the breeding programs, as they were selected by at least two of the four selection indexes used.

The accessions 2, 37, and 49 were selected by all evaluated indexes.

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