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

ISSN 0100-316X (impresso)
ISSN 1983-2125 (online)
http://dx.doi.org/10.1590/1983-21252017v30n328rc

CHARACTERIZATION AND EARLY SELECTION OF SILK BLOSSOM (*CALOTROPIS PROCERA*) GENOTYPES WITH FORAGE POTENTIAL[1]

ISAIAS VITORINO BATISTA DE ALMEIDA[2]*, DIOGO GONÇALVES NEDER[2], FABIANE RABELO DA COSTA BATISTA[3], WELLISON FILGUEIRAS DUTRA[4]

ABSTRACT - This study aimed to characterize and select silk blossom genotypes (*Calotropis procera*) with forage potential. Between April and July 2014, we cultivated 89 genotypes in plastic tubes arranged in a randomized block design with three replications; each experimental plot was composed of 8 plants. The following characteristics were evaluated: plant height (PH), stem diameter (SD), number of leaves (NL), total leaf area (TLA), leaf fresh mass (LFM), stem fresh mass (SFM), root fresh mass (RFM), leaf dry mass (LDM), stem dry mass (SDM), and root dry mass (RDM). Significant differences ($p < 0.05$) among genotypes were observed for all characteristics, except for NL at 45 and 60 days after sowing (DAS) and for RFM at 60 DAS. Broad-sense heritability estimates and genotype means had medium and high values for most characteristics. Genetic variability among *C. procera* genotypes was observed. High gain selection was found for the characteristics TLA, PH, SFM, LFM, SDM, and LDM as the genotypes 79, 65, 48, 12, 51, 35, 63, 25, 1, and 46 are suitable for future breeding works to improve forage production.

Keywords: Xerophytic plant. Genetic improvement. Genetic parameters. Heritability.

CARACTERIZAÇÃO E SELEÇÃO PRECOCE DE GENÓTIPOS DE FLOR-DE-SEDA (*CALOTROPIS PROCERA*) COM POTENCIAL FORRAGEIRO

RESUMO - Objetivou-se caracterizar e selecionar genótipos de flor-de-seda (*Calotropis procera*) com potencial para forragicultura. Para tanto, 89 genótipos foram cultivados em tubetes organizados em blocos ao acaso com três repetições, no período entre abril e julho de 2014, sendo a parcela experimental composta por 8 plantas. Foram avaliadas as características: altura da planta (AP), diâmetro caulinar (DC), número de folhas (NF), área foliar total (AFT), massa verde das folhas (MVF), massa verde do caule (MVC), massa verde da raiz (MVR), massa seca das folhas (MSF), massa seca do caule (MSC) e massa seca da raiz (MSR). Houve diferença significativa ($p<0,05$) entre os genótipos para todos os caracteres, exceto para NF aos 45 e 60 dias após a semeadura (DAS) e MVR aos 60 DAS. As estimativas de herdabilidade no sentido amplo e de média de genótipos foram de média e alta magnitude na maioria dos caracteres. Existe variabilidade genética entre os genótipos de *C. procera.* Observou-se ganho elevado de seleção para AFT, AP, MVC, MVF, MSC e MSF. Os genótipos identificados como 79, 65, 48, 12, 51, 35, 63, 25, 1 e 46 são indicados para futuros trabalhos de melhoramento genético visando à produção de forragem.

Palavras chave: Planta xerófila. Melhoramento genético. Parâmetros genéticos. Herdabilidade.

---

*Corresponding author

[1] Received for publication in 03/24/2016; accepted in 12/07/2016.
Paper extracted from the masters dissertation of the first author.

[2] Department of Agroecology and Agriculture, Universidade Estadual da Paraíba, Campina Grande, PB, Brazil; isaiasvba@gmail.com, dgneder@hotmail.com.

[3] Genetic resources and plant breeding, Instituto Nacional do Semiárido, Campina Grande, PB, Brazil; fabiane.costa@insa.gov.br.

[4] Laboratory of Ecophysiology of Cultivated Plants, Universidade Estadual da Paraíba, Campina Grande, PB, Brazil; wfilgueiras@gmail.com.

INTRODUCTION

Frequent and long periods of water scarcity in Northeast Brazil have been regarded as the main limiting factor in animal production over the centuries. This is mostly due shortages in forage for ruminants during the dry season, a major factor in reducing production and productivity of Brazilian semi-arid livestock.

Due of the low and/or uneven rainfall distribution in this region, strategies to optimize northeastern livestock farming are currently explored, such as increasing the forage support, especially by growing xerophytic, drought-resistant crops. However, most of the caatinga native plants are not regularly cultivated as xerophytic crops because they are usually deciduous and lose their leaves during drought.

Silk blossom (*Calotropis procera* [Ait.] W.T. Aiton), a native species of Africa, Madagascar, Arabian Peninsula, Southeast Asia, India, and China to Malaysia, belongs to the Apocynaceae family and the Asclepiadoideae subfamily (RAHMAN; WILCOCK, 1991; SOBRINHO et al., 2013). It is alternatively used for forage production in the dry season due to its high protein content and its ability to stay green under normal drought conditions as well as in periods of prolonged droughts.

In Brazil, *C. procera* use has used as animal feed due to its high potential to produce green biomass (OLIVEIRA; SOUTO, 2009) and dry matter (COSTA, et al., 2009). However, its use is still limited, mainly due to toxic characteristics (MARQUES et al., 2008). However, the haymaking process promotes volatilization of toxic substances and allows the use of this species in ruminant nutrition (SILVA et al., 2010), particularly as forage replacement (MARQUES et al., 2008) and concentrate (COSTA et al., 2011), resulting in increased consumption and weight gain (SILVA et al., 2010).

Besides its forage production potential, silk blossom is used in medicine and pharmacology (YAO et al., 2015) and has biodiesel production potential (BARBOSA et al., 2014). These features have resulted in studies on characterization of fruits and on seed biometry (OLIVEIRA-BENTO et al., 2013), germination (SILVA et al., 2009; OLIVEIRA-BENTO et al., 2013), phenology (SOBRINHO et al., 2013; FARAHAT et al., 2015), growth (OLIVEIRA et al. 2009), bromatological composition (OLIVEIRA; SOUTO, 2009), oil and fatty acid content (BARBOSA et al., 2014), water-stress tolerance (BOUTRAA, 2010; RAMADAN et al., 2014), ecophysiology (FROSI et al. 2013), and seed storage (OLIVEIRA-BENTO et al., 2015).

Despite the existence of such research, Boutraa (2010) points out that most studies on *C. procera* are within the fields of pharmacology and medicine, while studies on plant growth are scarce. Similarly, Costa et al. (2009) emphasize that further studies on silk blossom production, especially for genetic improvement through the selection and spread of more productive plants, are needed.

Thus, considered the forage production potential in Brazilian semiarid regions, there is a need to deepen our knowledge about this species, especially in terms of production improvement. to the aim of this study was therefore to characterize and select silk blossom genotypes with forage potential.

MATERIAL AND METHODS

Seeds of 89 *C. procera* genotypes were collected in March 2014 in areas with natural occurrence in the State Paraíba, Brazil. The experiment was established and conducted in a greenhouse at the Paraíba State University (UEPB), Campina Grande city, Paraíba State (7º 12 '43.3 "S, 35 ° 54' 39.7" W and altitude 531 m), from April to July 2014.

Fruits with completed physiological maturity were collected, with open capsules and brown seeds. Seeds were extracted manually and dried in the shade. After drying, seeds were stored in paper bags prior to sowing. We used plastic tubes with a capacity of 280 cm³ and filled with a sandy loam soil with the following chemical composition: pH 5.1; 0.0 cmolc/dm^3 of Al^{+3}; 2.2 cmolc/dm^3 of Ca + Mg; 1.5 cmolc/dm^3 of Ca^{+2}; 0.7 cmolc/dm^3 of Mg^{+2}; 3.8 mg/dm^3 of P; 31 mg/dm^3 of K$^+$; 0.12% of N and 1.69 % of organic matter. Five seeds were sown in each plastic tube; irrigation was performed daily in the morning to enable drainage. Seedlings were thinned at 10 days after sowing (DAS), leaving only one seedling per tube.

The experimental design was a randomized block design with three replications and 8 plants per plot, totaling 24 plants per genotype. Non-destructive evaluations of plant height (PH, cm), stem diameter (SD, mm), number of leaves (NL, unit), and total leaf area (TLA, cm^2) were performed at 45, 60, 75, and 90 days after sowing (DAS), three useful plants were considered per plot. Leaf fresh mass (LFM, g), stem fresh mass (SFM, g), root fresh mass (RFM, g), leaf dry mass (LDM, g), stem dry mass (SDM, g), and root dry mass (RDM, g) were obtained by collecting two plants per plot at 60 and 90 DAS.

Plant height was obtained by measuring the distance from the stem base to the apical bud with a graduated ruler (in cm). For measuring stem diameter (measured at the base of the stem corresponding to the neck of the plants), we used a digital caliper. For number of leaves, we only considered permanent leaves (no cotyledons); measurements of leaf length (L) (cm) and width (W) (cm) were performed using a graduated ruler (in cm).

Individual leaf area was obtained from the model LA (cm²) = L x W x 0.75 proposed by Moreira Filho et al. (2007) for *C. procera* and TLA was obtained from the sum of all leaf areas.

To obtain RFM and RDM values, we immersed the tubes in water to remove the substrate and avoid damage to the root system. The plants were placed in paper bags and immediately taken to the Laboratory of Ecophysiology of Cultivated Plants (ECOLAB) in UEPB, located in the vicinity of the experimental area.

The plants were then partitioned in leaves, stems, and roots and weighed on an analytical balance (e = 0.0001 g) for determination of RFM, SFM, and LFM. For the evaluation of RDM, LDM, and SDM, the same material was placed in a forced air oven at 65°C for 48 hours and then weighed on an analytical balance.

Data were subjected to analysis of variance using the F test ($p < 0.05$). Based on the mean square expected values, we estimated the following genetic parameters: genetic variance (σ_g^2), phenotypic variance (σ_f^2), and environmental variance (σ_e^2); broad sense heritability (h^2) and genotype mean heritability (h^2mg); coefficient of environmental variation (CV*e*) and coefficient of genetic variation (CV*g*), relationship (CV*g*/CV*e*), and overall mean, using the R software (TEAM, 2015).

For estimation of genetic gains, we used the Mulamba and Mock (1978) selection index. From the classification order of the genotypes, the 10 best performing materials were selected and we estimated the genetic gain of each character.

RESULTS AND DISCUSSION

Overall, there was a significant difference between the 89 *C. procera* genotypes, except for NL at 45 and 60 DAS and for RFM at 60 DAS ($p > 0.05$), and the significant F test at 5% or 1% probability for the other parameters. The absence of significance for the NL character may be explained by the slow initial growth of the species, particularly related to reduced assimilate allocation for issuing leaves. After this period, there was a significant increase in leaf number, with greater values 75 and 90 DAS. The other genotype characteristics differed in the first assessment (45 DAS). Thus, genetic parameters were estimated in order to select material based on these characters. According to Bárbaro et al. (2009), estimates of genetic parameters plays an important predictive role in targeting improvement programs in relation to the selection process of the most promising genotypes.

The results of the estimates of genetic parameters for the 10 characteristics are described in Table 1. The coefficient of environmental variation (CV*e*) showed a good precision for PH, SD, NC, SFM, and SDM at 60 DAS and a low precision for SFM, LFM, RFM, TLA, LDM, and RDM at 90 DAS. According to Ramalho, Ferreira and Oliveira (2000), CV*e* classification, despite widely used, does not take into account the studied culture and especially the considered character. Thus, the parameters used must be associated with other characteristics, such as heritability, coefficient of genetic variation (CV*g*), and relationship CV*g*/CV*e*, as these are parameters used in plant breeding programs to verify genetic variability access in addition to supporting the selection of promising material (FALCONER; MACKAY, 1996; VENCOVSKY, 1987). Estimation of these parameters in *C. procera* characteristics results in the most reliable genotype selection, favoring future studies with access to greater genetic potential in species breeding programs.

Table 1. Estimates of genetic parameters: phenotypic variance (σ_f^2), environmental variance (σ_e^2), and genotypic variance (σ_g^2); broad sense heritability (h^2); genotype mean heritability (h^2mg); coefficient of environmental variation (CV*e*), coefficient of genetic variation (CV*g*) and the relationship (CV*g*/CV*e*); and overall average of 89 silk blossom genotypes.

Genetic parameters	PH (cm)				SD (mm)			
	----------------DAS---------------				----------------DAS---------------			
	45	60	75	90	45	60	75	90
σ_f^2	0.23	0.33	0.64	2.31	0.05	0.05	0.06	0.2
σ_e^2	0.18	0.27	0.55	1.46	0.04	0.04	0.03	0.14
σ_g^2	0.05	0.06	0.08	0.85	0.01	0.01	0.02	0.06
h^2 (%)	0.21	0.18	0.13	0.37	23.0	15.0	43.0	31.0
h^2mg (%)	45.45	40.00	30.38	63.59	42.86	42.86	66.67	56.25
CV*e* (%)	12.0	12.0	12.0	13.0	9.0	8.0	6.0	11.0
CV*g* (%)	6.0	5.0	5.0	10.0	5.0	3.0	5.0	7.0

DAS – days after sowing; PH - plant height; SD - stem diameter; TLA - total leaf area; NL - number of leaves; SFM - stem fresh mass; LFM - leaf fresh mass; RFM - root fresh mass; SDM - stem dry mass; LDM - leaf dry mass; and RDM - root dry mass (RDM).

Table 1. Continuation.

Genetic parameters	PH (cm)				SD (mm)			
	----------------DAS---------------				----------------DAS---------------			
	45	60	75	90	45	60	75	90
CV*g*/CV*e*	0.51	0.46	0.39	0.76	0.54	0.42	0.87	0.67
Mean	3.45	4.4	6.26	9.57	2.18	2.48	2.85	3.48

Genetic parameters	TLA (cm^2)				NL (unit)			
	----------------DAS---------------				----------------DAS---------------			
	45	60	75	90	45	60	75	90
σ_f^2	9.21	31.82	493.68	868.66	0.87	1.08	2.43	5.75
σ_e^2	6.47	22.1	282	496.96	0.84	1.06	1.87	4.14
σ_g^2	2.74	9.71	211.68	371.7	0.03	0.02	0.56	1.61
h^2 (%)	30.0	31.0	43.0	43.0	3.0	2.0	23.0	28.0
h^2mg (%)	55.96	56.86	69.25	69.17	9.68	5.35	47.32	53.85
CV*e* (%)	23.0	21.0	29.0	29.0	20.0	14.2	16.0	17.8
CV*g* (%)	15.0	14.0	25.0	25.0	4.0	-	9.0	11
CV*g*/CV*e*	0.65	0.66	0.87	0.86	0.18	-	0.55	0.62
Mean	11.18	22.05	57.55	75.67	4.58	7.33	8.75	11.43

Genetic parameters	SFM (g)		LFM (g)		RFM (g)	
	------DAS-----		-----DAS-----		-----DAS-----	
	60	90	60	90	60	90
σ_f^2	0.0007	0.0808	0.0076	1.3607	0.0199	0.2191
σ_e^2	0.0004	0.0523	0.0054	0.9829	0.0179	0.14
σ_g^2	0.0003	0.0285	0.0022	0.3778	0.002	0.0791
h^2 (%)	43.0	35.0	29.0	28.0	11.17	36.0
h^2mg (%)	69.23	64.29	55.0	53.77	25.1	63.16
CV*e* (%)	16.06	27.19	22.0	28.0	38.0	31.0
CV*g* (%)	13.91	20.07	14.0	17.0	13.0	24.0
CV*g*/CV*e*	0.8661	0.74	0.64	0.62	0.33	0.75
Mean	0.1245	0.84	0.33	3.6	0.36	1.19

Genetic parameters	SDM (g)		LDM (g)		RDM (g)	
	------DAS-----		-----DAS-----		-----DAS-----	
	60	90	60	90	60	90
σ_f^2	0.0000225	0.0011	0.0000672	0.0125	0.0005	0.0038
σ_e^2	0.0000136	0.0008	0.0000502	0.0087	0.0004	0.0028
σ_g^2	0.00000897	0.0003	0.0000169	0.0038	0.0001	0.001
h^2 (%)	39.8	27.0	25.0	30.0	20.0	26.0
h^2mg (%)	66.43	52.94	50.25	56.71	42.86	51.72
CV*e* (%)	16.37	28.66	20.13	26.0	33.84	33.01
CV*g* (%)	13.52	17.55	11.71	17.0	16.92	19.73
CV*g*/CV*e*	0.8137	0.6124	0.5817	0.66	0.5	0.6
Mean	0.0225	0.0987	0.0352	0.35	0.0591	0.1603

DAS – days after sowing; PH - plant height; SD - stem diameter; TLA - total leaf area; NL - number of leaves; SFM - stem fresh mass; LFM - leaf fresh mass; RFM - root fresh mass; SDM - stem dry mass; LDM - leaf dry mass; and RDM - root dry mass (RDM).

Overall, mean and approximate values of CV*g* were observed for PH, SD, and NC at 75 and 90 DAS and for LFM, LDM, and RDM at 90 DAS. It is noteworthy that the largest CV*g* values were observed for SFM, SDM, TLA and RFM at 90 DAS (Table 1), which indicates the existence of significant genetic dispersion of genotype means in relation to the overall means of these characteristics. It is important to note that the CV*g* values express the magnitude of genetic variation in relation of the analyzed average of the variable (RESENDE, 2002).

Relationship values CV*g*/CV*e* near unit refer to 0.87 and 0.86 for TLA at 75 and 90 DAS; 0.76 for PH at 90 DAS; 0.87 for SD at 75 DAS; 0.81 for SDM at 60 DAS; 0.75 for RFM at 90 DAS and 0.86 and 0.74 for SFM at 60 and 90 DAS (Table 1), respectively, reflecting improved reliability compared to the findings of other reviews and reasonable conditions for genotype selection. According to Vencovsky (1987), when the CVg/CVe relationship approaches or exceeds 1, selection gain is successful. However, despite the favorable results, it is still necessary to carry out further researches under field conditions or using larger pots, thereby providing better conditions for plant growth and enabling more accurate evaluation of the characteristics of the best genotypes in other phenological phases. It is worth noting that early selection is an important step in plant breeding programs; it accelerates the program and eliminates unproductive material, even in the seedling stage.

However, genetics parameters (CV*e*, CV*g*, and CV*g*/CV*e*) should not be considered in isolation, and heritability is a better indicator of selection process success in breeding programs. This understanding strengthens the decision making about the best procedures and strategies to adopt at different stages in the cultivar development. We add that its relevance is in fact able to show how genetic effects are present in the individual's phenotype, since it is the genotypic value that influences the subsequent generation (FALCONER; MACKAY, 1996).

Heritability can be estimated based on data from a single plant, a plot, or a plot mean (BORÉM; MIRANDA, 2013). We estimated broad-sense heritability (h^2) based on plots, considering the genotypic and environmental variation value of characteristics without the repetition effect, and genotype mean heritability (h^2mg), which takes into account replications. These estimates are important in the selection of appropriate genotypes in plant breeding programs, especially when the experiment is conducted in blocks involving three or more repetitions (BORÉM; MIRANDA, 2013).

Heritability estimates (h2) for SD and NL were low until 60 DAS, similar to PH at 75 DAS. However, h^2 was considered of high and medium magnitude for SD at 75 and 90 DAS and medium magnitude for NL at 75 and 90 DAS and for PH at 90 DAS (Table 1), respectively, indicating the period with greater genetic effect on characteristic expression. Heritability of the characteristics LFM, LDM, RFM, RDM, and SFM at 90 DAS, SDM at 60 and 90 DAS, and TLA at 45 and 60 DAS was considered to be of medium magnitude. For SFM at 60 DAS, TLA at 75 and 90 DAS, h^2 was considered high. These estimates indicate favorable conditions for selecting the plot level in the experiment and a great potential for high magnitude characters.

Predominance of genetic effects on the characteristic expressions of PH, SD, TLA, and NL at 75 and 90 DAS as well as of SFM, SDM, LFM, LDM, RFM, and RDM at 90 DAS was observed with the h^2mg estimates. The h^2mg values were classified as high, which enables efficient *C. procera* genotype selection for these traits (see CRUZ, 2005). Thus, all characteristics should be taken into consideration.

For examples plants with higher PH and SD values have greater vigor, which facilitates the establishment of young plants in the field. According to Tekrony and Egli (1991), seedling vigor can also influence crop productivity. In the case of *C. procera*, genotypes with greater height are favored by farmers due to easier transport and use in forage machines.

The low height reached by the genotypes in this study, possibly due to the slow growth of this species in the evaluation period, has also been observed in previous studies on initial succession of C. *procera* (OLIVEIRA et al., 2009; BOUTRAA, 2010). However, it is important that material is selected based on the PH and a number of other characters, considering the greatest growth potential in the early stage and the high heritability estimates obtained for all characters, except for PH at 75 DAS, NC at 45 and 60 DAS and for RFM at 60 DAS.

Variations in medium values of SD, SFM and SDM, ranging from 2.74 mm to 4.24 mm, 0.36 g to 1.38 g, and 0.0483 g to 0.1683 g at 90 DAS, respectively, indicate favorable genotype selection for these characters, considering genetic variability. The corticiforme stem of *C. procera* seems to be a large morphological adjustment which reduces excessive water loss to the middle part of the plant, also functioning as thermal insulation and protection from wind, as well as a serous stem which reduces insect attacks (COSTA et al., 2009). Thus, stem-related characteristics are important in genotype evaluation, especially from an agronomic point of view.

Calotropis procera is a perennial plant with an outstanding potential to adapt to arid and semi-arid regions, degraded soils, and low rainfall sites; it is drought-resistant and stays green throughout the year, even in the dry season, because of its ability to resist water deficits (MELO et al., 2001; COSTA et al., 2009). Thus, genotype selection based on leaf characteristics is of great importance in

C. procera genetic improvement, because these characteristics represent the plant´s potential for forage production. Selection for these characteristics directly benefits livestock in semiarid regions, where plants with greater leaf area and increased yields in LFM and LDM weight are of interest because of limited availability of bulky food in drought periods. Thus, selecting plants with higher forage potential results in expressive genetic gain and may minimize forage shortage problems in low rainfall years. However, future studies involving the best material to analyze the bromatological composition are necessary.

Mean TLA mean, ranging from 25.5 to 100.25 cm^2 at 75 DAS and from 32.5 to 132.61 cm^2 at 90 DAS, as well as variation in LFM and LDM values, ranging from 1.93 to 6.15 g and from 0.1933 to 0.5965 g at 90 DAS, respectively, indicate genetic variability among genotypes, which shows the importance of genotype selection.

Variations of 6.33 to 12.0 and 8.0 to 17.33 units were obtained for NL in evaluations carried out at 75 and 90 DAS, respectively. It is interesting to highlight that the genotypes with larger NL values, such as 94, 29, 91, 67, and 59, showed lower mean values of TLA, LFM, and LDM, which is an important factor to consider in forage production. Thus, genotype selection should be directed to the plants with the highest number of leaves, which also have larger TLA values and, consequently, higher fresh and dry mass yield, such as the genotypes 12, 79, 35, and 25.

Root-related characteristics are usually not used in genotype selection, mainly because the root system is difficult to study and needs to be evaluated via destructive methods (BRASIL et al., 2007) which require plant removal, resulting in to large volumes of excavated soil root loss. However, if the experiment is conducted in plastic tubes, root system assessment may become accessible and genotype selection could be based on root characteristics.

In the present study, genotype selection for *C. procera* by RFM and RDM can contribute to improvement of this species, whereas plants with greater pivoting roots as well as a greater number of secondary roots and absorbent root hairs might have a greater ability to establish themselves in the soil, along with a higher absorption capacity, which favors the uptake of water and nutrients from deeper soil layers, thereby increasing survival rates in droughts.

Mean RFM values were 0.36 g at 60 DAS and 1.19 g at 90 DAS; mean RDM values were 0.0591 g at 60 DAS and 0.1603 g at 90 DAS. However, the root system should not be considered in isolation, and shoot growth is another important characteristic. It is therefore necessary to take into consideration both the characteristics of the root and of the shoot system. Some genotypes use most of their photosynthesis products for root formation, for example the genotypes 81, 2, 22, 72, and 34, which expressed, as a result of this, lower shoot growth. Other genotypes showed better results in terms of the shoot and root development, for example the genotypes 48, 51, 79, and 25 genotypes, ranked among the 10 genotypes with the highest RDM values and obtained the best results in terms of TLA, SFM, LFM, SDM, and LDM (Table 2). We therefore suggest that these genotypes are important for future breeding programs, mainly because of the high root/ shoot relation, which proves to be the most effective method to adapt to stressful environments.

In order to select genotypes good germination qualities associated with high production and shoot development to forage use, in addition to roots with further water capture and use, Mulamba and Mock (1978) developed the selection index. Among the evaluated characteristics, EP, PH, TLA, SD, CR and LFM, SFM, RFM, LDM, SDM, and RDM were used for the development of this index.

Of the 89 *C. procera* genotypes evaluated, 10 were selected according to the established criteria (Table 2). Among the selected genotypes are the 10 genotypes with greater LDM values and the 7 with greater SDM values, indicating that the selection criteria used were adequate in the selection of genotypes with good forage use.

High gains for TLA (34.23%), SFM (28.17%), LDM (24.83%), LFM (21.97%), SDM (20.57%), RFM (17.25%), RDM (14.64%), and PH (10.85%) were observed. For other characteristics, the gains were lower, albeit still useful in the elimination of genotypes with unfavorable characteristics. These results demonstrate a potential of genetic improvement of *C. procera* for forage exploration, with improved earnings.

Cultivation of the 10 selected genotypes in future breeding programs of C. procera is recommended, for example in studies of genetic diversity, production, and field or greenhouse experiments to subsidize research of hybridization of different materials with forage potential.

Table 2. The best 10 genotypes, selected according to the Mulamba and Mock (1978) index, from the classification sum of eleven agronomic characters of silk blossom (*Calotropis procera*).

Ranking	Index	Genotypes	Characters										
			SE	PH	TLA	SD	RL	RFM	SFM	LFM	RDM	SDM	LDM
1	99	79	2	3	5	21	13	7	2	4	13	23	6
2	117	65	6	4	12	13	24	29	5	8	9	4	3
3	132	48	74	12	3	1	15	10	4	3	6	2	2
4	184	12	56	37	2	14	27	20	1	1	24	1	1
5	195	51	82	11	7	12	38	3	11	7	8	7	9
6	201	35	36	1	1	2	87	21	3	6	33	3	8
7	205	63	38	21	21	39	16	26	8	12	12	5	7
8	220	25	83	17	4	3	62	8	7	5	10	17	4
9	229	1	26	2	47	30	14	34	10	9	43	9	5
10	248	46	21	18	8	9	53	51	20	13	21	24	10

SE - Seedling emergence; PH - plant height; TLA - total leaf area; SD - stem diameter; RL - root length; RFM - root fresh mass; SFM - stem fresh mass; LFM - leaf fresh mass; RDM - root dry mass; SDM - stem dry mass; and LDM - leaf dry mass.

CONCLUSIONS

We found high heritability and variability between the studied genotypes of *C. procera* for all assessed characteristics, except for NL at 45 and 60 DAS and for RFM at 60 DAS. The use of the Mulamba and Mock selection index was adequate in the selection of the best *C. procera* genotypes with highest forage yield, enabling high gains. Based on our results, the genotypes 79, 65, 48, 12, 51, 35, 63, 25, 1, and 46 are suitable for future breeding works to improve forage production.

ACKNOWLEDGEMENTS

We thank the Paraíba State University (UEPB) for funding this research and the forest nursery of the Laboratory of Ecophysiology of Cultivated Plants (ECOLAB) in UEPB for providing the physical structure for this research.

REFERENCES

BÁRBARO, I. M. et al. Seleção em populações F3 de soja visando à resistência ao cancro da haste e bons atributos agronômicos. **Revista Ceres**, Viçosa, v. 51, n. 297, p. 619-634, 2004.

BRASIL, F. C. et al. Métodos de amostragem e quantificação para estudos do sistema radicular em condições de campo - Uma revisão crítica. **Revista Ciência da Vida**, Rio de Janeiro, v. 27, n. 2, p. 14-33, 2007.

BARBOSA, M. O. et al. Seed oil content and fatty acid composition from different populations of *Calotropis procera* (Aiton) WT Aiton (Apocynaceae). **Journal of the American Oil Chemists' Society**, New York, v. 91, n. 8, p. 1433-1441, 2014.

BORÉM, A.; MIRANDA, G. V. **Melhoramento de Plantas**. 6. ed. Viçosa, MG: UFV, 2013. 523 p.

BOUTRAA, T. Growth performance and biomass partitioning of the desert shrub Calotropis procera under water stress conditions. **Research Journal of Agriculture and Biological Sciences**, Faisalabad, v. 1, n. 6, p. 20-26, 2010.

COSTA, R. G. et al. Perspectivas de utilização da flor-de-seda (*Calotropis procera*) na produção animal. **Revista Caatinga**, Mossoró, v. 22, n. 1, p. 1-9, 2009.

COSTA, R. G. et al. Meat quality of lambs fed silk flower hay (*Calotropis procera* SW) in the diet. **Revista Brasileira de Zootecnia**, Viçosa, v. 40, n. 6, p. 1266-1271, 2011.

CRUZ, C. D. **Princípios da genética quantitativa**. 1. ed. Viçosa, MG: UFV, 2005. 394 p.

FALCONER, D. S.; MACKAY, T. F. C. **Introduction to quantitative genetics**. 4. ed. Essex: Longman, 1996. 464 p.

FARAHAT, Emad Abdelmoneim et al. Phenology, biomass and reproductive characteristics of Calotropis procera (Aiton) WT Aiton in South Cairo, Egypt. **Rendiconti Lincei**, Roma, v. 27, n. 2, p. 197-204, 2015.

FROSI G. et al. Ecophysiological performance of Calotropis procera: an exotic and evergreen species in Caatinga, Brazilian semi-arid. **Acta Physiologiae Plantarum**, Kraków, v. 35, n. 2, p. 335-344, 2013.

MARQUES, A. V. M. S. et al. Feno de flor de seda (*Calotropis procera Sw.*) em dietas de cordeiros Santa Inês: biometria e rendimento dos componentes não-constituintes da carcaça. AGRÁRIA. **Revista Brasileira de Ciências Agrárias**, Recife, v. 3, n. 1, p. 85-89, 2008.

MELO, M. M. et al. Estudo fitoquímico da *Calotropis procera* Ait. sua utilização na alimentação de caprinos: efeitos clínicos e bioquímicos séricos. **Revista Brasileira de Saúde e Produção Animal**, Salvador, v. 2, n. 1, p. 15-20, 2001.

MOREIRA FILHO, E. C. et al. Estimação da área foliar da flor de seda (*Calotropis procera*). **Archivos de Zootecnia**, Cordoba, v. 56, n. 214, p. 245-248, 2007.

MULAMBA, N. N.; MOCK, J. J. Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. **Egyptian Journal of Genetics and Cytology**, Alexandria, v. 7, n. 1, p. 40-51, 1978.

OLIVEIRA, S. H. F. de et al. Seedling growth of the invader *Calotropis procera* in ironstone rupestrian field and seasonally dry forest soils. **Neotropical Biology and Conservation**, São Leopoldo, v. 4, n. 2, p. 69-76, 2009.

OLIVEIRA, V. M.; SOUTO, J. S. Estimativa da produção de biomassa de *Calotropis procera* (Ait) R. BR. e avaliação de sua composição química no estado da Paraíba. **Revista Verde**, Mossoró, v. 4, n. 1, p. 141-161, 2009.

OLIVEIRA-BENTO, S. R. S. et al. Biometria de frutos e sementes e germinação de *Calotropis procera* AITON (Apocynaceae). **Bioscience journal**, Uberlândia, v. 29, n. 5, p. 1194-1205, 2013.

OLIVEIRA-BENTO, S. R. S. et al. Armazenamento de sementes de flor-de-seda [*Calotropis procera* (AITON) W.T. AITON]. **Revista Caatinga**, Mossoró, v. 28, n. 1, p. 39-47, 2015.

RAMADAN, A. et al. Metabolomic response of Calotropis procera growing in the desert to changes in water availability. **Plos One**, Cambridge, v. 9, n. 2, e87895, 2014.

RAMALHO, M. A. P.; FERREIRA, D. F.; OLIVEIRA, A. C. **Experimentação em genética e melhoramento de plantas**. 1. ed. Lavras, MG: UFLA, 2000. 326 p.

RAHMAN, M. A.; WILCOCK, C. C. A taxonomic revision of Calotropis (Asclepiadaceae). **Nordic Journal of Botany**, Lund, v. 11, n. 3, p. 301-308, 1991.

RESENDE, M. D. V. **Genética biométrica e estatística no melhoramento de plantas perenes**. 1. ed. Brasília, DF: EMBRAPA Informação Tecnológica, 2002. 975 p.

SILVA, J. R. et al. Temperatura e substrato na germinação de sementes de flor-de-seda. **Revista Caatinga**, Mossoró, v. 22, n. 1, p. 175-179, 2009.

SILVA, J. G. M. et al. Cactáceas nativas associadas a fenos de flor de seda e sabiá na alimentação de borregos. **Revista Caatinga**, Mossoró, v. 23, n. 3, p. 123-129, 2010.

SOBRINHO, M. S. et al. Reproductive phenological pattern of *Calotropis procera* (Apocynaceae), an invasive species in Brazil: annual in native areas; continuous in invaded areas of caatinga. **Acta Botanica Brasilica**, Belo Horizonte, v. 27, n. 2, p. 456-459, 2013.

TEAM, R. C. **R: A language and environment for statistical computing**. Vienna, Austria: R Foundation for Statistical Computing; 2013. Disponivel em:<https://www.r-project.org/>. Acesso em: 20 jan. 2015.

TEKRONY, M. D.; EGLI, D. B. Relationship of seed vigour to crop yield: a review. **Crop Science**, Madison, v. 31, n. 3, p. 816-822, 1991.

VENCOVSKY, R. Herança quantitativa. In: PATERNIANI, E.; VIEGAS, G. P. (Ed.). **Melhoramento e produção de milho no Brasil**. Campinas, SP: Fundação Gargill, 1987. v. 1, cap. 5, p. 137-214.

YAO, D. A. R. A. et al. AFLP assessment of the genetic diversity of *Calotropis procera* (Apocynaceae) in the West Africa region (Benin). **Genetic Resources and Crop Evolution**, Heidelberg, v. 62, n. 6, p. 863-878, 2015.