Flowering capacity and botanical seed production of sweet potato genotypes

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ABSTRACT

The identification of genotypes with greater capacity for flowering and seed production is crucial for greater efficiency in the genetic improvement of the sweet potato crop. Thus, the objective of this work was to evaluate the flowering capacity and the production of botanical seeds in sweet potato genotypes. The work was carried out in the municipality of Lavras, located in the southern region of Minas Gerais, Brazil. Twenty-two sweet potato genotypes belonging to the germplasm bank of the Federal University of Lavras (UFLA) were evaluated. The characteristics evaluated were the flowering period (days), the number of viable seeds, the total weight of viable seeds, the weight of 1000 seeds and the percentage of germination. The obtained data were analyzed by means of descriptive statistics, study of correlations and analysis of main components. The sweet potato genotypes evaluated showed a high capacity for flowering and production of botanical seeds. Flowering usually starts 125 days after planting and extends on average for 72 days. Considering future recombination to promote flowering capacity, seed production and greater germination, genotypes BD-05, BD-26 and BD-44 should be prioritized.

Keywords: *Ipomoea batatas*, germination, diversity, germplasm, genetic breeding.

RESUMO

Capacidade de florescimento e produção de sementes botânicas em genótipos de batata-doce

A identificação de genótipos com maior capacidade de florescimento e produção de sementes é determinante para maior eficiência do melhoramento genético da cultura da batata-doce. Assim, o objetivo deste trabalho foi avaliar a capacidade de florescimento e a produção de sementes botânicas em genótipos de batata-doce. O trabalho foi conduzido no munícipio de Lavras, localizado na região sul de Minas Gerais, Brasil. Foram avaliados 22 genótipos de batata-doce pertencentes ao banco de germosplasma da Universidade Federal de Lavras (UFLA). Foram avaliados o período de florescimento (dias), número de sementes viáveis, peso total de sementes viáveis, peso de 1000 sementes e porcentagem de germinação. Os dados obtidos foram analisados por meio de estatística descritiva, estudo de correlações e análise de componentes principais. Os genótipos de batata-doce avaliados apresentaram elevada capacidade de florescimento e de produção de sementes botânicas. Verificou-se que a floração geralmente inicia-se 125 dias após o plantio e estende-se em média por 72 dias. Considerando futuras recombinações para promoção da capacidade de florescimento, produção de sementes e maior germinação, devem ser priorizados os genótipos BD-05, BD-26 e BD-44.

Palavras-chave: *Ipomoea batatas*, germinação, germoplasma, melhoramento genético.

Sweet potato (*Ipomoea batatas*) is widely cultivated throughout the world, standing out among the seven most consumed foods on the planet (Vargas *et al.*, 2017). Beyond its importance for human consumption, the crop also has other uses, such as animal feed, ethanol production (Torquato-Tavares *et al.*, 2017; Valadares *et al.*, 2019; Andrade Júnior *et al.*, 2020).

Considered a dicotyledonous plant, the sweet potato belongs to the Convolvulaceae family, with allogamous behavior, hexaploid (2 n = 6 x = 90) and self-incompatible, which confers high genetic and phenotypic variability of the species (Veasey *et al.*, 2007; Silva *et al.*, 2012; Alves *et al.*, 2017). Knowledge of this characteristic is essential for the genetic breeding of the crop, because of this high level of ploidy and cross-fertilization, each obtained seed can be a new clone with great agronomic potential (Torquato-Tavares *et al.*, 2017).

However, it is worth noting that the flowering of sweet potato does not occur easily in all regions, as it requires specific climatic conditions that vary according to the genotype (Gurmu *et al.*, 2013), which makes it difficult to recombine these in certain places. External factors such as photoperiod, temperature and humidity can affect flowering and seed production, restricting the installation of genetic breeding programs for this vegetable in some regions of Brazil. Another factor is related to the presence of genetic incompatibility between parents, causing limitation for the production of hybrids or carrying out random recombinations (Baafi *et al.*, 2016).

Despite the importance of knowledge about flourishing capacity and seed

production in the genetic breeding of sweet potato, studies that are specifically dedicated to the evaluation of these characteristics in the crop are rare.

Due to the commercial multiplication of sweet potato being carried out vegetatively, professionals involved in the genetic breeding of this crop often do not prioritize the selection of genotypes with high flowering capacity and seed production. However, Mwanja *et al.* (2015) highlight that the selection of sweet potato genotypes with higher flowering capacity is important, because even clones able to flourish in tropical regions, have low pollen viability, short flowering, slow pollen tube growth rate and seed malformation, in addition to the presence of dormancy. Thus, the production of larger amounts of seeds can favor the obtainment of more promising genotypes.

Therefore, selecting genotypes with these characteristics, associated with good agronomic characters, can allow the expansion of sweet potato breeding programs to different regions in Brazil. Thus, the objective of this work was to evaluate the flowering capacity and the production of botanical seeds of sweet potato genotypes.

MATERIAL AND METHODS

The work was carried out at the Horticulture Sector of the Federal University of Lavras (UFLA), MG, Brazil (21º14'43"S, 44º59'59"W, 919 m altitude). The region's climate is humid temperate with hot summer and dry winter, being, therefore, the Cwa type in the Köppen classification, with an average annual temperature of 20.4°C and an average annual precipitation of 1460 mm.

As treatments, 22 sweet potato genotypes belonging to the UFLA germplasm bank, from different regions of Brazil and described in Table 1, were evaluated.

Soil preparation was carried out by means of plowing and harrowing, with the subsequent lifting of beds and lifting of windrows manually from these beds, 1 m spaced. Planting was carried out on March 30, 2017, using vine segments 0.30 m long and spaced 0.30 m apart in 4.5 m windrows, no previous rooting and need for replanting. Fertilization and other cultural managements were carried out as recommended for the culture (Ribeiro *et al.*, 1999; Embrapa, 2021).

Thus, 15 plants were obtained from each treatment, representing the evaluated parcel in the study. Subsequently, all plants in the plot were evaluated in relation to flowering capacity and seed production, providing the average value for each treatment. Five characters were evaluated, such as flowering duration, number of seeds, seed weight, 1000-seed weight and germination percentage.

The flowering period had its beginning considered when at least 50% of the plants in the plot flowered, from the planting date. The plots were periodically monitored every 2 days, ending as the flower issue ended. Seed collections happened from August to November 2017, with two weekly harvests. At the end of the collection period, the seeds were counted and the total number per genotype was obtained. The weight of harvested seeds (g) was obtained by weighing the seeds of each genotype on an analytical balance. So, considering the total number of seeds, it was possible to estimate the weight of 1000 seeds.

Seeds at physiological maturity, characterized by being dry and with brown capsules, were placed in paper packagings and identified according to each genotype. After quantifying the number of seeds, they were dried in a forced air circulation oven at 30°C temperature, for 24 hours, to reduce humidity. Subsequently, they were cleaned by manual threshing, in addition to removing the pericarp and other residues present. Then, the seeds were placed in plastic tubes with lids identified by genotype and stored in a BOD (Biosystem Organized Development) oven at 10°C.

To determine the percentage of germination, the seeds were submitted to chemical scarification, immerging the same in concentrated sulfuric acid (98%) for 40 minutes and subsequent washing in running water for 10 minutes, according to the methodology proposed by Rossel *et al.* (2008). After breaking the dormancy, the seeds were submitted to the germination test. For this purpose, the seeds were evenly distributed in gerbox boxes lined with germitest paper, constantly moistened with distilled water. Subsequently, the boxes were identified and kept for seven days in BOD-type oven for germination at 25ºC and a 12-hour photoperiod. The germination percentage of each genotype was calculated from the relationship between the number of initial scarified seeds and the number of effectively germinated seeds of each genotype.

The obtained data from each treatment were subjected to descriptive statistical analysis, and the means for each studied characteristic and the coefficient of variation were determined. The observed frequencies were also determined, whose number of classes were determined by the empirical method, applying the rule of Sturges (1926), where $k=1+3,322 * log_{10} (N)$, k is the number of classes, N is the total number of observations in the sample, and log_{10} is the common logarithm of base 10.

The amplitude of classes (α) was determined by $α=(LS-LI)/k$, being *LS* the upper limit and *LI* the lower limit. Descriptive analyzes and frequency distributions were determined using the SISVAR software version 5.7 (Ferreira, 2019).

The correlations between characteristics was studied using the Pearson correlation coefficient, whose significance was obtained by the t test at 5% significance. The genetic divergence of genotypes was estimated via principal component analysis, using the *prcomp* function from the *Stats* package, while the graph significance was obtained using the *fviz_pca_biplot* function from the *factoextra* package. These analyzes were performed using the R software (R Core Team, 2019).

RESULTS AND DISCUSSION

All studied genotypes showed flowering and seed production under

the studied edaphoclimatic conditions (Figure 1). However, the longest flowering period was observed for non-commercial accessions BD-43, Cambraia, Arruba, BD-05, BD-22 and BD 44, with values between 84 and 101 days. Therefore, these non-commercial genotypes may present greater segregation and the possibility of obtaining new superior clones to the pre-existing ones, considering their high flowering capacity and the possibility of recombination. We noted that commercial cultivars were not among the genotypes with the longest flowering period.

The flowering began in the first ten days of August 2017 for all genotypes, that is, approximately 125 days after planting the vines and reaching up to 206 days after planting, depending on the genotype. In a similar study to evaluate flowering and seed production in sweet potato clones in Nigeria, Mwanja *et al.* (2015) found that the studied clones started flowering between
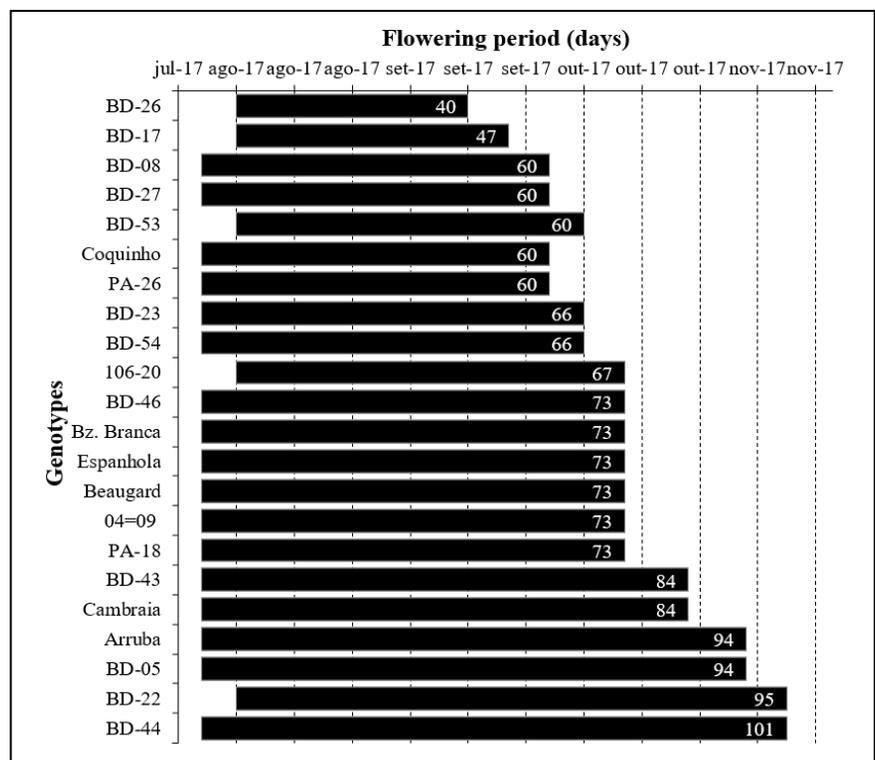
Figure 1. Flowering period, in days, of 22 sweet potato genotypes evaluated in southern Minas Gerais. Lavras, UFLA, 2020.

Table 1. Description of 22 sweet potato genotypes from the UFLA germplasm bank. Lavras, UFLA, 2020.

Genotype Identification	Peel color	Flesh color	Origin
04=09	Cream	Cream	Palmas-TO
106-20	Pink	White	Palmas-TO
BD-05	Cream	White	São Tiago-MG
BD-08	Brownish orange	White	São Tiago-MG
BD-17	Pink	Cream	Diamantina-MG
BD-22	Cream	Dark Cream	Felício dos Santos-MG
BD-23	Pink	Cream	Felício dos Santos-MG
BD-26	Brownish orange	White	Felício dos Santos-MG
BD-27	Pink	Cream	Felício dos Santos-MG
BD-43	Pink	Cream	Governador Valadares-MG
BD-44	Pink	Cream	Conselheiro Mata-MG
BD-46	Pink	Cream	Diamantina-MG (Batatal)
BD-53	Brownish orange	White	Diamantina-MG (Sopa)
BD-54	Pink	Cream	Felício dos Santos-MG
PA-18*	Purple red	Purple/White(Pigmented)	Palmas-TO
PA-26*	Cream	Cream	Palmas-TO
Arruba	Brownish Orange	White	Araçuaí-MG
Beauregard*	Pink	Orange	EUA
Bz. Branca*	Cream	White	Embrapa/CNPH, DF
Cambraia	Cream	White	Felício dos Santos-MG
Coquinho*	Brownish Orange	Cream	Embrapa/CNPH-DF
Espanhola	Cream	White	Diamantina-MG

*Commercial cultivars: Palmas PA-18; Palmas PA-26; Beauregard; Brazlândia Branca; Coquinho.

56 and 102 days, which reinforces the wide variation of this characteristic in relation to different environments and genotypes. The knowledge of this behavior in the sweet potato crop is of great relevance, as it allows planning the recombination schedule and obtaining genotypes. When analyzing the climatic conditions of the period, it is observed that the beginning of flowering coincided with low temperatures and the absence of precipitation. This may indicate that milder temperatures are more conducive to sweet potato flowering. According to Rossel *et al.* (2008), flowering and fruiting are higher at temperatures between 20°C and 25°C and relative humidity above 75%.

Despite few studies on the characterization of sweet potato flowering, the results available in literature demonstrate great variability for this characteristic, with expressive variations in relation to genotypes, locations and also periods of the year. In a study conducted by Veasey *et al.* (2007), the authors observed that in 53 genotypes studied in the São Paulo region of Vale do Ribeira, Brazil, only 13.2% did not flower, with flowering occurring from January to September, with flowering peaks in April, May and June. Similar values (13.9%) of no flowering were reported by Rajendran & Amma (1996) who evaluated flowering in 764 sweet potato genotypes in India. On the other hand, Mok & Schmiediche (1999), in studies carried out in Indonesia, found the absence of flowering in 40% of the sweet potato genotypes. The highest frequency of flowering period occurred between 63 and 78 days, where 40.91% of the studied genotypes were concentrated (Figure 2A). However, 54.50% of the studied genotypes had a flowering period longer than the general average, which was 72 days.

The genotypes with a long flowering period, possibly show better adaptation to the climatic conditions of the studied region, mainly in relation to the flowering capacity. Furthermore, the fact that flowering occurred in 100% of the genotypes, suggests that the southern region of Minas Gerais has great potential for the installation of genetic breeding programs, especially for the recombination of accessions.

Considering all studied genotypes, we observed that seed production varied between 4 and 68 seeds plant^{-1}, which indicates a large variation among genotypes. This average production per plant helps in the recombination program, better defining the number of plants needed as a function of the average number of seeds desired for each genotype. Genotypes BD-44, BD-
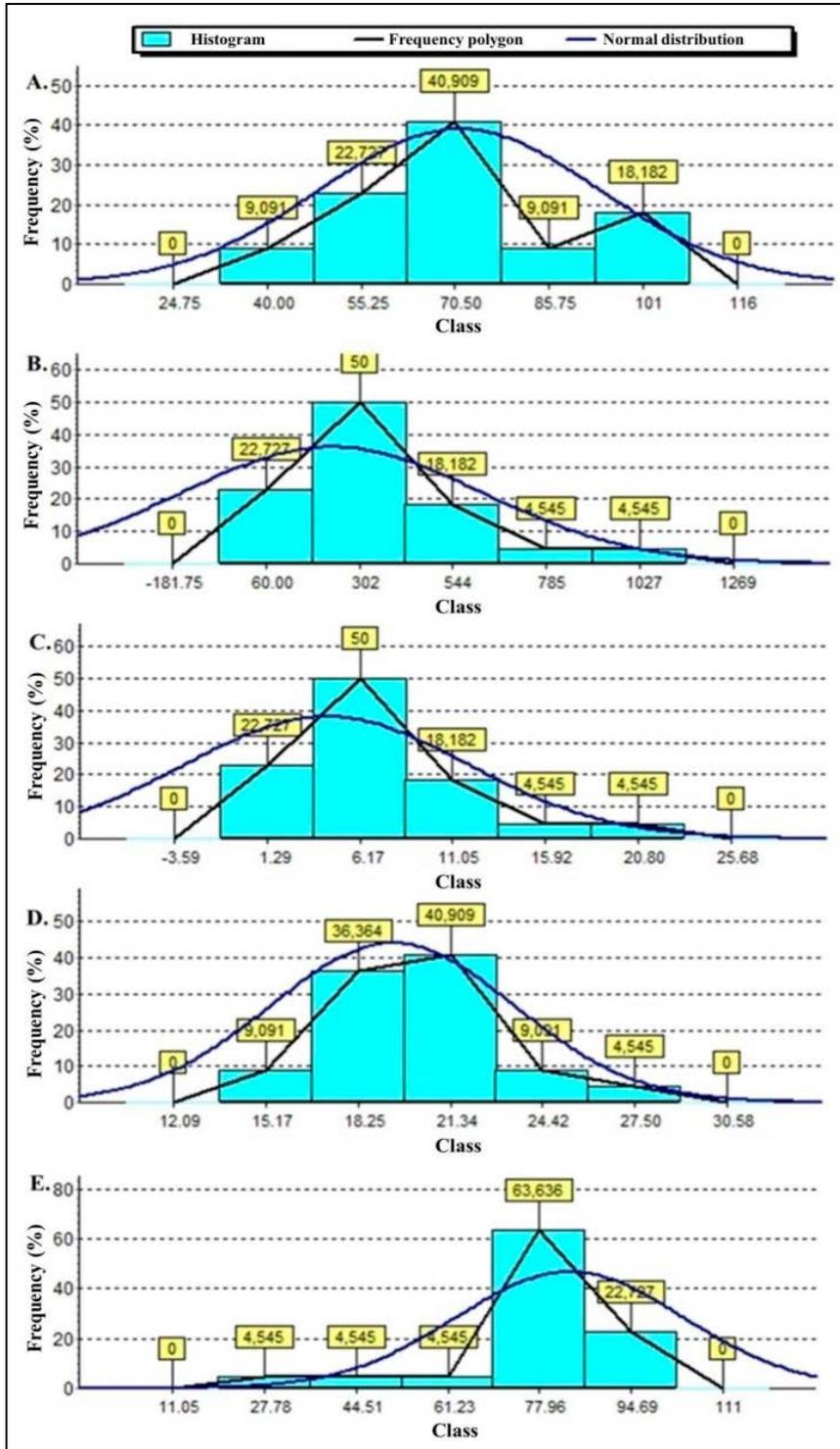
Figure 2. Frequency distribution for flowering period (A), number of harvested seeds (B), weight of harvested seeds (C), 1000 seed weight (D) and germination percentage (E) of 22 sweet potato genotypes, evaluated in southern Minas Gerais, Brazil. Lavras, UFLA, 2020.

05, BD-43, BD-23, 04=09, BD-08 and BD-27 had the highest number of seeds harvested per plant, with production higher than the general average of the genotypes (340.05 seeds), representing 32% of the evaluated genotypes (Table 2). In percentage terms, those genotypes with higher seed production produced between 1.75 and 208.08% more than the overall average observed. This great difference between genotypes may be related to different environmental and genetic factors, as the effect of crossings is not only dependent on the presence of flowering, but mainly on the compatibility between parents, presence of pollinators and favorable climatic conditions.

As highlighted by Vimala & Hariprakash (2011), self-incompatibility and cross-incompatibility are still the greatest limitations for sexual recombinations, seed production and genetic breeding of sweet potato. However, the high number of seeds obtained can be explained by the fact that the pollinations were carried out in an open (random) manner. Under these conditions, crossings are more effective, as there is greater diversity of pollen, which reduces the chances of incompatibility. Furthermore, these random pollinations allow obtaining half-sib progenies in a less expensive way, which facilitates the use of recurrent selection in the culture. When these pollinations are carried out in a controlled manner, for the production of hybrids, for example, the efficiency of seed production is low, as in addition to presenting characters of interest, the parents must present flowering period and genetic compatibility to establish crosses (Baafi et al., 2016).

According to the frequency distribution, we found that the highest concentration of seed production occurred between 181 and 423 seeds per plot, encompassing in this range 50% of the evaluated genotypes (Figure 2B), which points to a high range of variation for this feature, just as it occurred for the flowering period. This is important from the point of view of plant breeding, as it indicates the existence of genetic variability among genotypes, which enables the selection

Table 2. Mean values of the number of seeds harvested (NHS), weight of harvested seeds (WHS), weight of 1000 seeds (W1000) and germination percentage (GERM) in 22 sweet potato genotypes evaluated in southern Minas Gerais, Brazil. Lavras, UFLA, 2020.

Genotypes	NHS[/1]	WHS[/1] (g)	W1000 (g)	GERM (%)
Arruba	316.00	7.64	24.18	92.00
04=09	483.00	9.58	19.83	71.33
106-20	74.00	1.37	18.51	86.00
BD-05	994.00	16.92	17.02	83.00
BD-08	472.00	10.09	21.38	73.00
BD-17	60.00	1.29	21.50	90.91
BD-22	82.00	1.39	16.95	70.00
BD-23	545.00	11.57	21.23	85.83
BD-26	88.00	2.42	27.50	91.43
BD-27	346.00	7.09	20.49	76.67
BD-43	660.00	12.96	19.64	62.00
BD-44	1027.00	20.80	20.25	78.75
BD-46	313.00	6.00	19.17	87.00
BD-53	187.00	3.98	21.28	75.00
BD-54	258.00	5.44	21.09	81.00
Cambraia	259.00	3.93	15.17	65.88
Espanhola	244.00	3.82	15.66	70.00
Beauregard*	242.00	4.54	18.76	27.78
Brazlândia Branca*	278.00	5.32	19.14	81.72
Coquinho*	191.00	4.53	23.72	82.35
Palmas PA-18*	223.00	4.37	19.60	94.69
Palmas PA-26*	139.00	2.95	21.22	70.49
Overall average	340.04	6.76	20.15	77.13
Coef. of variation (%)	78.55	75.89	13.83	18.48

[1]Average values of the plot (15 plants).

Table 3. Pearson correlation coefficients among flowering duration (FD), number of harvested seeds (NHS), weight of harvested seeds (WHS), 1000-seed weight (W1000) and germination percentage (GERM) in 22 genotypes of sweet potato, evaluated in the south of Minas Gerais, Brazil. Lavras, UFLA, 2020.

Variable	FD	NHS	WHS	W1000	GERM
FD	1	0.58**	0.54*	-0.53*	-0.18[ns]
NHS	-	1	0.99***	-0.18[ns]	-0.38[ns]
WHS	-	-	1	-0.06[ns]	-0.01[ns]
W1000	-	-	-	1	-0.38[ns]
GERM	-	-	-	-	1

*,**,***significant at 5%; 1% and 0.1% by t test at 5% significance, respectively. [ns]Not significant.

of those with greater seed production capacity, a characteristic that is possibly passed onto offspring.

In general, the highest total seed weight (WHS) occurred for the genotypes that produced the highest amount of seeds (Table 2). From the observed frequencies, we found that 50% of the genotypes concentrated their seed production between 3.73 and 8.61 g (Figure 2C). However, only the BD-44, BD-05, BD-43, BD-23, BD-08, 04=09, Arruba and BD-27 genotypes presented seed weights higher than the general average of the genotypes (6.73) (Table 2). These genotypes represent

36% of the studied genotypes and presented seed production from 5.4 to 209% higher than the general average of the study. As expected, the total seed weights showed a high and significant positive correlation with the number of seeds (Table 3).

It is noteworthy that the BD-44, BD-05 and BD-43 genotypes stood out, simultaneously in relation to the flowering period, number of harvested seeds and total seed weight. This reinforces what was observed in the study of established phenotypic correlations (Table 3), as the flowering period correlated significantly and positively with the number of harvested seeds (NHS) and with the weight of harvested seeds (WHS), presenting correlation coefficients of 0.58 and 0.54, respectively. In this sense, the longer flowering period allowed a greater quantity of seeds, making it interesting in recurrent selection programs.

The highest weights of 1000 seeds (W1000) were observed for genotypes BD-44, BD-27, BD-54, PA-26, BD-23, BD-53, BD-08, BD-17, Coquinho, Arruba and BD-26, with weights varying between 20.25 and 27.50 g (Table 2). These genotypes had W1000 higher than the general average (20.1 g) and represent 50% of the total evaluated. In the evaluation of the frequency distribution for this character, the highest frequency (40.9%) was observed in the range of 19.79 and 22.89 (Figure 2D). However, in absolute terms, there was little variation in the data observed for this characteristic, whose values ranged between 15 and 28 g. As for the correlations, it was observed that there was a significant negative correlation between the flowering duration and the W1000, that is, the longer the flowering duration, the smaller the mass of 1000 seeds. Possibly this is related to physiological restrictions in translocation of photoassimilates for seed production, so that, despite producing more seeds by extending flowering, the last seeds tend to be smaller and lighter.

The highest germination percentages were observed for the PA-18, Aruba, BD-26 and BD-17 genotypes, with values considered very good (>90%)

(Table 2). However, 57% of the studied genotypes had higher germination than the general average, which was 77.13%. This average, although low, represents a satisfactory value for sweet potato, as each germinated seed can give rise to a new cultivar. Considering the observed frequencies for seed germination, 63.64% of the genotypes had a germination percentage between 69.60% and 86.32% (Figure 2E). The germination percentage did not correlate with any of the evaluated characteristics.

The two-dimensional dispersion of genotypes via principal component analysis (PCA) (Figure 3) indicated the formation of four isolated groups. The first was composed of the BD-44 and BD-05 genotypes, the second by the commercial cultivar Beauregard and the Espanhola, Cambraia and BD-22 genotypes, the third formed exclusively by the BD-26 genotype, and the last by the other genotypes.

The correlations between the principal components and the studied characteristics (Figure 3) indicated

that the BD-44 and BD-05 genotypes diverged from the others mainly because they presented a high number and weight of seeds, which is relevant for sweet potato breeding programs. The BD-26 genotype also diverged due to its characteristics of interest, such as a high weight of 1000 seeds and a high percentage of germination. The genotypes Beauregard, Espanhola, Cambraia and BD-22 were especially grouped for presenting, in general, lower weights of 1000 seeds and lower germination percentages, undesirable characteristics for selection in order to increase flowering capacity and seed production. The other genotypes, from a multivariate point of view, showed little variation sufficiently explained by the first two principal components.

It is important to note that, although flowering is strongly related to genetic predispositions and environmental conditions, for genotypes with difficulty in flowering, and consequent recombination, this flowering can be stimulated through techniques such as
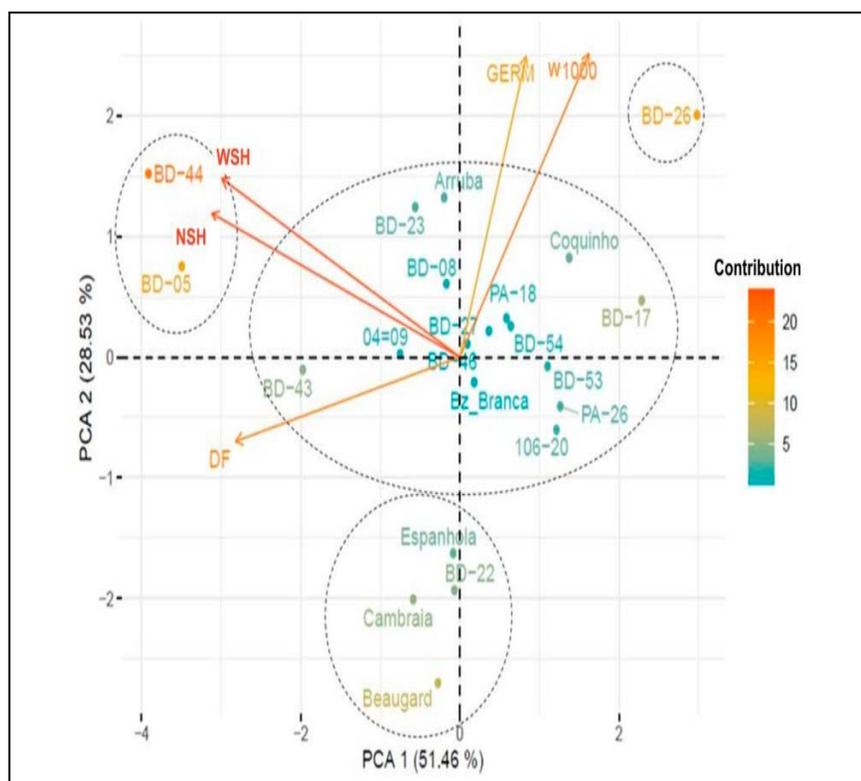
Figure 3. Biplot graphic dispersion of 22 sweet potato genotypes and correlations of the characteristics number of harvested seeds (NHS), weight of harvested seeds (WSH), weight of 1000 seeds (W1000) and germination percentage (GERM) with both first Principal Components – PCA1 and PCA2. Lavras, UFLA, 2020.

physiological stresses, grafting, girdling and chemical treatments (Edmond & Martin Junior, 1946), but the effects of these techniques are not always effective. Therefore, the search for genotypes with characteristics of interest and high seed production is the best strategy within sweet potato breeding program, as it is more practical and less costly.

We can conclude that the genotypes evaluated in this study have high flowering and seed production capacity in the southern region of Minas Gerais. For the evaluated genotypes, flowering usually begins 125 days after planting and extends for an average of 72 days. Considering future recombinations to promote flowering capacity and seed production, genotypes BD-05, BD-26 and BD-44 should be prioritized in the formation of recombinant populations.

ACKNOWLEDGMENTS

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