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Safflower genetic diversity based on agronomic characteristics in Mato Grosso state, Brazil, for a crop improvement program

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ABSTRACT. Safflower, *Carthamus tinctorius* (Asteraceae), is an oilseed plant with good adaptability to warm and dry climatic conditions. It is used for biodiesel production, human food, animal feed, and in the pharmaceutical industry. Recently, the crop has been highlighted, mainly for its oil quality and for biofuel production. We compared 124 safflower genotypes, which are a part of the State University of Mato Grosso germplasm collection, based on their agronomic characteristics, to provide the initial guidelines for a breeding program. Evaluations were carried out during the crop cycle and parameters were defined according to the descriptions recommended by International Board for Plant Genetic Resources and by the Ministry of Agriculture, Livestock and Supply. Multivariate analysis was used to assess the divergence among genotypes, by using Average Euclidean Distance, which ranged from 0.07 to 0.57, showing considerable genetic diversity among safflower genotypes for the agronomic characteristics that were evaluated (flowering, plant cycle, number

of branches per plant, plant height, number of chapters per plant, number of seeds per chapter, chapter diameter, stem diameter, weight of 100 seeds, seed size and plant yield. Tocher and Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering methods were partially consistent in ordering similar genotypes. The agronomic characteristics: plant yield, number of chapters per plant and plant height provided the greatest contribution to genetic divergence among the genotypes. According to the groupings established with each methodology and depending on the variation structures within each group, several genotypes stood out in terms of agronomic performance and may be indicated for future crosses aiming to obtain improved safflower cultivars for Brazil.

Key words: *Carthamus tinctorius*; Multivariate analysis; Oil; Biofuels

INTRODUCTION

Safflower (*Carthamus tinctorius*) is an oilseed herb belonging to the Asteraceae family that may be used as an alternative for oil production (Hojati et al., 2011; Pavithra et al., 2015). It is a crop with good adaptability to climatic variations and with a deep root system, which increases its capacity to extract water and nutrients that are not available for most crops subjected to hot and dry conditions (Bagheri and Sam-Dailiri, 2011; Bonfim-Silva et al., 2015). Due to the recognition of its numerous utilities in food, industrial, ornamental, and medicinal fields, safflower cultivation has expanded in the Asian, European and American continents (Sehgal et al., 2009; Hussain et al., 2016).

Cultivated for more than two millennia, safflower produces an unconventional oilseed that is used for various purposes. The raw material is mainly used for the production of bio-oil in food and feed (Hussain et al., 2016). In industry, safflower oil is used for several purposes, among them biofuel, paint manufacture, varnishes, and cosmetics (Coronado, 2010). Oil contents in the grains may reach 50%, with high levels of linoleic and oleic acids that make it of great quality for both human consumption and industry (Mundel et al., 2004).

Recently in Brazil, the cultivation of safflower has aroused the interest of producers as it is a cheaper alternative mainly for the production of oil for the pharmaceutical industry as well as an alternative for the production of biofuel. In the state of Mato Grosso, the recent increase in the production of safflower is aimed at the production of biofuel. In the country, the state of Sao Paulo stands out as the largest producer of safflower (Yesilyurt et al., 2020).

This crop has been studied mainly in research centers and its germplasm banks, distributed in distinct countries such as India, USA, Japan, and Brazil, where it was introduced by the Mato Grosso Institute of Cotton. These studies demonstrated the existence of genetic diversity among *C. tinctorius* genotypes (Pearl and Burke, 2014).

According to Shinwari et al. (2014), the genetic progress of any crop is related to the existence of genetic diversity, an important fundamental factor for programs of plants genetic breeding, because it allows identifying possible parents or even genotypes with superior characteristics, in addition to increasing the genetic base.

The diversity found in germplasm banks, work collections, origin centers or centers of diversity can be explored as the initial phase of a safflower improvement program (Lucena and Dantas, 2015). Information obtained through this characterization helps breeders to control different plants characteristics, contributing to the improvement of their characteristics and properties (Singh and Nimbkar, 2006; Golkar, 2014). Therefore, the objective of this research was to evaluate genetic divergence among safflower genotypes in the working collection of University State of Mato Grosso, through multivariate procedures based on agronomic characteristics, aiming to provide the initial guidelines for a safflower genetic breeding program.

MATERIAL AND METHODS

The research was carried out in an experimental area belonging to Mato Grosso State Company for Research, Assistance and Rural Extension, located at latitude 16°43'42"S and longitude 57°40'51"W with altitude of 118 meters, located in Caceres County, Mato Grosso State, Brazil.

The typical weather of this region, according to Köppen classification, is tropical, warm, humid and dry winter (Awa), with rainy season ranging from October to April and drought from May to September (Dallacort et al., 2014). The soil is classified as Chernosolic Eutrophic Yellow Red Argissoil, with a medium clay texture (Arantes et al., 2012).

One hundred and twenty-four genotypes of C. tinctorius L. from the North American Germplasm Bank Western Regional Plant Introduction Station (WRPIS) were evaluated, obtained through Germplasm Resource Information Nertword (GRIN), being imported by Mato Grosso Institute of Cotton, Mato Grosso State and assigned to the Laboratory of Genetic Resources & Biotechnology (LGR&B) of the University of the State of Mato Grosso (UNEMAT), Caceres Campus as described in Table 1.

Soil samples were collected, before experiment implementation, for chemical analysis, taken at 0-20 and 20-40 cm depths, that served as the basis for pre-sowing fertilization (Table 2), consisting of 20 g of N-P2O5-K2O compound being uniformly applied to each line of the experiment (04-14-08 formulation), totaling 80 g in each experimental plot.

Seeding was conducted manually at 0.05 m depth. The experimental unit was composed of four lines with 1 m arranged in spacing 0.50 m x 0.10 m between and within rows, respectively, analyzing only the central lines of each plot. Basic management measures were adopted, such as manual weeding, so as not to impair the crop development. Harvest was performed manually after physiological maturation according to the period of each genotype.

Agronomic characterization was performed according to the descriptors proposed by International Board for Plant Genetic Resources - IBPGR (1983) and Ministry of Agriculture, Livestock and Supply - MAPA (2013). Evaluated characteristics were:

Flowering (FLOWER): obtained by the number of days from sowing up to flowering plants (50%) with at least one open inflorescence.

Table 1. Identification and origin of the 124 genotypes of Carthamus tinctorius belonging to Laboratory of Genetic Resources and Biotechnology, University State of Mato Grosso, Cáceres Campus.

*PI	Origin	PI	Origin	PI	Origin	PI	Origin
193473	Ethiopia	306832	India	451954	India	572431	EUA
195895	Morocco	306833	India	451956	India	572439	EUA
237539	Turkey	306838	India	506426	China	572450	EUA
248385	India	306844	India	508068	EUA	572464	EUA
248620	Pakistan	306866	India	514625	China	572544	Canada
248808	India	343783	Iran	525457	EUA	576981	China
248828	India	343930	Ethiopia	537658	EUA	576985	France
248839	India	367833	Argentina	537673	EUA	613357	EUA
248852	India	369842	Armenia	537680	EUA	613361	EUA
250083	Egypt	369845	Tajikistan	537682	EUA	613366	EUA
250188	Pakistan	369849	Russia	537684	EUA	613373	EUA
250190	Pakistan	369854	Uzbekistan	537697	EUA	613380	EUA
250203	Pakistan	392029	Turkey	537712	EUA	613382	EUA
250204	Pakistan	392030	Turkey	543980	China	613384	EUA
250840	Iran	392031	Turkey	544002	China	613394	EUA
250922	Iran	393500	Iran	544013	China	613404	EUA
251978	Turkey	401474	Bangladesh	544028	China	613409	EUA
253540	Hungary	401475	Bangladesh	544030	China	613415	EUA
253899	Syria	401477	Bangladesh	544031	China	613419	EUA
259996	Pakistan	401480	Bangladesh	544036	China	613422	EUA
259997	Pakistan	401578	India	544038	China	613456	EUA
262443	Spain	401589	India	544043	China	613503	EUA
262447	Kazakhstan	405955	Iran	560178	EUA	613519	Iran
262450	India	405961	Iran	532639	India	638543	Canada
279344	Japan	405965	Iran	568787	China	653143	EUA
283757	India	405970	Iran	568792	China	653149	China
304438	Iran	405975	Iran	568795	China	653162	China
305161	India	406006	Iran	568798	China	653186	China
305198	India	406007	Iran	568836	China		
305207	India	406015	Iran	568866	China		
305209	India	407606	Turkey	568870	China		
305540	Kazakhstan	407613	Turkey	568876	China		

PI = Plant introduction.

Table 2. Chemical analysis, texture and samples taken at a depth of 0-20 and 20-40 cm, from the eutrophic red yellow eutrophic chernossolic medium clayey soil from the experimental area of the culture of Carthamus tinctorius.

Chemical analysis										
	pH	pH	P	K	Ca+Mg	Ca	Mg	Al	H+Al	O.M.
Profile	H_2O	$CaCl_2$	mg dm^{-3}			Cmolc dm^{-3}				g dm^{-3}
0 – 20	6.2	5.5	16.6	0.37	3.3	2.7	0.6	0.0	3.0	25
20 - 40	6.0	5.3	6.0	0.24	2.9	2.1	0.8	0.0	3.2	29

O.M. = organic matter.

Plant Cycle (CYCLE): obtained by the ratio between the number of days from sowing up to the number of days to harvest.

Number of Branches per Plant (NBP): obtained by counting the number of branches present throughout the stem, from the neck to the end of main stem.

Plant Height (PH): measure obtained in centimeters between the plant's surface and plant's apex, by using a graduated ruler.

Number of Chapters per Plant (NCP): determined by counting the total number of chapters per plant, where the chapter is the inflorescence located at the end of the branches.

Number of Seeds per Chapter (NSC): determined by counting the total number of seeds per chapter.

Chapter diameter (CD): measure obtained in millimeters with the aid of a digital caliper (Hardened model, Stainless, Fairfield, NJ, USA).

Stem diameter (SD): measure obtained in millimeters with the aid of a digital caliper (Hardened model, Stainless, Fairfield, NJ, USA).

Weight of 100 seeds (W100): mean in grams of four samples in randomized way performed with the aid of an analytical balance (model AUY220, Shimadzu, São Paulo, Brazil).

Length of seed (LS): measure obtained in centimeters with the aid of a digital caliper (Hardened model, Stainless, Fairfield, NJ, USA).

Width of seed (WD): measure obtained in centimeters with the aid of a digital caliper (Hardened model, Stainless, Fairfield, NJ, USA).

Plant Yield (PY): expressed in g plant-1, obtained by the ratio of total weight of seeds produced to the plants number.

Multivariate analysis was used to evaluate genetic divergence among 124 genotypes of C. tinctorius, based on Average Euclidean Distance for the agronomic characteristics, using the methods of cluster analysis by Toucher's optimization and hierarchical clustering between groups (UPGMA). Dendrogram consistency was verified by using cophenetic correlation coefficient. It was still possible to quantify the relative contribution of characteristics using the method proposed by Singh (1981). All analyzes were performed using Genes software (Cruz 2013).

RESULTS AND DISCUSSION

A significant level of variation was observed for the 12 agronomic characteristics among the 124 genotypes, as can be seen in Supplementary 1.

Dissimilarity measures were estimated from Average Euclidean Distance (*Dii'*) in relation to the 12 agronomic characteristics evaluated. It was possible to verify that dissimilarity magnitudes obtained through the matrix, ranged from 0.07 to 0.57, indicating the presence of genetic diversity among studied genotypes. The existence of this genetic diversity represents fundamental importance for works of this nature, as emphasized by Ambreen et al. (2018) and Costa et al. (2019). These authors also consider that genetic diversity is a primary requirement for safflower genetic

improvement and that breeding is essential to increase the acceptability and usefulness of this crop as an oleaginous of global importance.

Dissimilarity magnitudes in a certain group of genotypes made it possible to verify their genetic divergence closely linked with heterosis degree found in the species under study (Gaur et al., 1978; Oliveira et al., 2003). In a work conducted by Zoz (2015), evaluating the genetic divergence of safflower cultivars, the author observed similar results of the present work for divergence, however, it was evaluated a smaller number of genotypes (12), favoring variations among estimated magnitudes, from 0.17 to 6.17.

The greatest distance found was between 38 and 118 genotypes (D_{ii}'= 0.57) and according to field data, these materials diverged mainly to three descriptors. Genotype 118 was superior for NBP, NCP and PY than genotype 38. It is inferred that the highest result for NBP, superior values for NCP and PY variables, according to Silva (2013) shows that there is a significant and positive correlation between number of branches, number of chapters per plant and plant yield.

The dissimilarity between these more distant genetic materials indicates the possibility that this combination may generate individual with greater variability when used in hybridizations. According to Gibori et al. (1978) and Saadia et al. (2018) crosses involving more divergent parents tend to generate populations of wide genetic variability. In the case of safflower, autogamous specie, breeding programs seek for divergent crosses to obtain greater heterosis effects and wide segregation in descending generations.

On the other hand, the combination with the smallest distance magnitude was observed between 24 and 29 genotypes with D_{ii}'= 0.07, behaving as the most similar among the materials, showing proximity in all evaluated characteristics. This lower magnitude presented by these genotypes may be related to the seven similarity centers proposed by Knowles (1969) (1: Far East, 2: India and Pakistan, 3: Middle East, 4: Egypt, 5: Sudan, 6: Ethiopia and 7: Europe) for safflower by using several plant characteristics such as standard ones, that is, 24 and 29 genotypes may belong to the same similarity center.

However, as reported by Ali et al. (2020), evaluating 94 safflower accesses from 26 different countries through morph-agronomic characteristics observed the formation of three significant groups with distribution predominance in four similarities center. But authors were emphatic in consider the need for more tests, in order to validate and consolidate genotypes distribution according to the similarity centers and geographic regions. According to Almeida (2015) genetic diversity can occur regardless of geographic origin, indicating that structuring may not occur genetics of populations in geographic space.

Tocher's clustering method based by matrix D_{ii}' classified 124 genotypes of *C. tinctorius*, into 13 distinct groups (Table 3). According to Benin et al. (2002), genotypes with less distance between them are allocated in the same group; consequently choice of parents belonging to the same group is not useful, since it does not result in descendants with wide variability in segregating generations due to genetic proximity of

the parents. Olivo et al. (2020) consider that, besides divergence degree between the parents, it is necessary to examine significant general and specific combination ability.

Table 3. Representation of the cluster generated by the Tocher´s Optimization method based on the average Euclidean distance between the 124 genotypes of *Carthamus tinctorius* evaluated, base on the 12 agronomic characteristics.

Cluster	[1]Genotypes	%
I	24, 29, 28, 4, 27, 52, 33, 13, 102, 106, 45, 66, 35, 49, 47, 25, 70, 36, 92, 46, 109, 1, 79,10, 85, 91, 14, 64, 37, 11, 88, 113, 105, 7, 57, 121, 18, 56, 21, 17, 9, 54, 65, 86, 44, 8, 104, 58, 39, 63, 3, 20, 94, 50, 40, 31, 12, 51, 41, 123, 101, 67, 124, 55, 111, 34, 107, 110, 84, 72, 30, 96, 73, 77, 90, 112, 115, 116, 68, 59, 42, 32, 26, 6, 117, 43, 89, 19, 98, 103, 2, 48	74.40
II	69, 80, 87, 60, 97, 62, 74, 61, 83, 75	8.00
III	16, 76, 53	2.40
IV	38, 81, 95	2.40
V	15, 93, 114, 119	3.20
VI	99, 108	1.60
VII	5, 71	1.60
VIII	82, 120, 22	2.40
IX	78	0.80
X	100	0.80
XI	23	0.80
XII	122	0.80
XIII	118	0.80
Total	124	100.00

[1]1-PI193473, 2-PI195895, 3-PI237539, 4-PI248385, 5-PI248620, 6-PI248808, 7-PI248828, 8-PI248839, 9-PI248852, 10-PI250083, 11-PI250188, 12-PI250190, 13-PI250203, 14-PI250204, 15-PI250840, 16-PI250922, 17-PI251978, 18-PI253540, 19-PI253899, 20-PI259996, 21-PI259997, 22-PI262443, 23-PI262447, 24-PI262450, 25-PI279344, 26-PI283757, 27-PI304438, 28-PI305161, 29-PI305198, 30-PI305207, 31-PI305209, 32-PI305540, 33-PI306832, 34-PI306833, 35-PI306838, 36-PI306844, 37-PI306866, 38-PI343783, 39-PI343930, 40-PI367833, 41-PI369842, 42-PI369845, 43-PI369849, 44-PI369854, 45-PI392029, 46-PI392030, 47-PI392031, 48-PI393500, 49-PI401474, 50-PI401475, 51-PI401477, 52-PI401480, 53-PI401578, 54-PI401589, 55-PI405955, 56-PI405961, 57-PI405965, 58-PI405970, 59-PI405975, 60-PI406006, 61-PI406007, 62-PI406015, 63-PI407606, 64-PI407613, 65-PI451954, 66-PI451956, 67-PI506426, 68-PI508068, 69-PI514625, 70-PI525457, 71-PI537658, 72-PI537673, 73-PI537680, 74-PI537682, 75-PI537684, 76-PI537697, 77-PI537712, 78-PI543980, 79-PI544002, 80-PI544013, 81-PI544028, 82-PI544030, 83-PI544031, 84-PI544036, 85-PI544038, 86-PI544043, 87-PI560178, 88-PI532639, 89-PI568787, 90-PI568792, 91-PI568795, 92-PI568798, 93-PI568836, 94-PI568866, 95-PI568870, 96-PI568876, 97-PI572431, 98-PI572439, 99-PI572450, 100-PI572464, 101-PI572544, 102-PI576981, 103-PI576985, 104-PI613357, 105-PI613361, 106-PI613366, 107-PI613373, 108-PI613380, 109-PI613382, 110-PI613384, 111-PI613394, 112-PI613404, 113-PI613409, 114-PI613415, 115-PI613419, 116-PI613422, 117-PI613456, 118-PI613503, 119-PI613519, 120-PI638543, 121-PI653143, 122-PI653149, 123-PI653162, 124-PI653186.

Group I was composed of 92 genotypes with 57% of them of Asian origin; Group II presented 10 genotypes with most coming from the USA; Groups III, IV and VIII allocated only three genotypes each, with genetic materials from different origins, except for Group IV presenting two genotypes from the same origin center (China) and one from Iran; Group V consisted of four genotypes, presenting materials from Iran, the USA and China.

Groups VI and VII were formed by two genotypes each and Group VI clustered materials from the same origin (USA), while Group VII was characterized for genotypes from different origin (USA and Pakistan); Groups IX, X, XI, XII and XIII allocated only one genotype each. According to Benitez et al. (2011) groups formed by only one individual indicated that the direction of this unique genotype is more divergent in relation to other, since genotypes in unit groups are more dissimilar in relation to the set.

In other studies, also using the Tocher grouping method for the safflower crop, similar results to ours were found (Silva, 2013; Pavithra et al., 2015). Silva (2013) using the Tocher method for grouping 100 safflower accessions evaluated in his research, found that the genotypes were grouped into 16 distinct groups. This author considers that the use of the information generated by these techniques allowed the researcher to group many genotypes according to their degree of similarity or to plan crosses between contrasting individuals

aiming at the heterosis between possible hybrid combinations or increasing the variability between descendants.

In the analysis of genetic divergence among 150 safflower genotypes performed by Pavithra et al. (2015) materials were grouped by Tocher's method into 24 distinct groups, indicating that through the groups it is possible to identify possible combinations for breeding programs in order to obtain hybrid combinations to generate segregant populations. According to results from plant yield, harvest index, plant height, volume weight, number of seeds per chapter and chapter per plant, authors cited that these important characteristics should be considered to select genotypes for hybridization.

Dendrogram obtained by UPGMA´s method, with a significant cutoff at 62% genetic distance, made it possible to divide 124 safflower genotypes into 11 distinct groups (Figure 1). Analyzing this dendrogram and according to dissimilarity measures, genotypes 38 and 118 were the most divergent, allocated in different groups, (V and I respectively) and the most similar, 24 and 29 genotypes, were located in Group XI.

The value for cophenetic correlation coefficient (CCC) obtained from the dendrogram was 0.70 and it is considered satisfactory, since this one adequately represents the information contained in the matrix. According to Rohlf (1970) for fit CCC classification, it is necessary to reach values ≥0.70.

Tocher's and UPGMA methodologies presented similarity in group formation, both with 13 groups, with differences only in relation to genotype allocation. According to Buttow et al. (2010), the differences between Tocher and UPGMA methods are due to the way in that each method calculates genetic variability since the same matrix data is used.

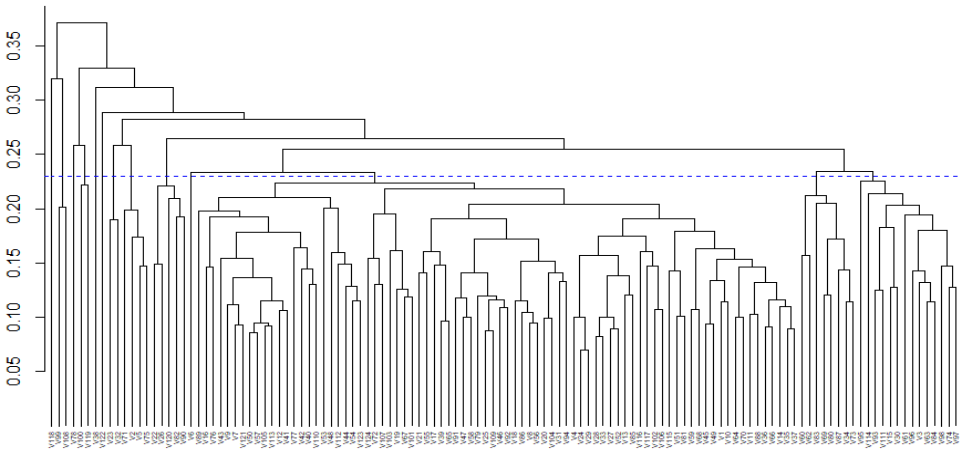

Figure 1. Dendrogram of genetic dissimilarity among 124 genotypes of Carthamus tinctorius obtained by UPGMA method based on 12 agronomic characteristics. Cophenetic correlation coefficient = 0.70.

Groups I, III, V, VI and X were composed of only one genotype according to the UPGMA method: genotypes 118, 78, 38, 122 and 6 respectively. Genotypes 78, 118 and 122 were grouped by Tocher's method, suggesting that these materials are more dissimilarity in relation to each other. Groups II, IV and VII contain two genotypes each, and the composition of Group II by UPGMA´s methodology was similar to Group VI based the Tocher's method, showing as the main characteristics for cluster: CYCLE, PH and NSC.

Genotypes 100 and 119 belonging to Group IV and 23 and 32 to Group VII were clustered in other groups according to Tocher's procedure.

Results obtained by UPGMA´s method about Group VIII was not similar to any Tocher´s Group presenting as main characteristics responsible for group formation group: FLOWER, CYCLE and PH. Group IX was composed by five genotypes, being possible to verify that, similarity to Tocher's procedure, Group VIII showed genotypes grouped in the same group (82, 120 and 22), and Group I (also by Tocher), showed genotypes 26 and 90 located into the same group, presenting as main characteristics for clustering: FLOWER, NSC and PY characteristics.

According to UPGMA´s methodology, in relation to Group XII it was possible to observe similarity with Tocher's procedure; Group II for genotypes 60, 62, 69, 80, 83 and 89 and also for Group I by Tocher´s that allocated genotypes 34 and 73, presenting as main characteristics NBP, NSC and PH. UPGMA clustered Group XIII allocating genotypes present in Groups I, II, IV and V from Tocher's procedure, showing as main characteristic responsible for grouping, the following characteristics: NSC, CD and CYCLE. Grouping methods aim to separate an original group of observations into several groups, so that there is homogeneity within the group and heterogeneity between them (Bertan et al., 2006).

The use of multivariate techniques is an important tool in the aid of genetic diversity, since it is based on the behavior of each individual in relation to the others through the simultaneous study of several characteristics, which is simplified by means of indexes that can facilitate making conclusions (Gerhardt, 2014). In this way, one can plan crosses based on the results of the different groups formed by the two methodologies, in order to obtain genetic gains.

The analysis of relative contribution from 12 characteristics evaluated for 124 safflower genotypes (Table 4) allowed the identification of the most important characteristics for genetic divergence. According to Correa and Gonçalves (2012), identifying these characteristics that contribute the most is really important to help discarding those that contribute less to genotypes differentiation, reducing manpower, time and costs related to experimental evaluation.

Table 4. Relative contribution of 12 agronomic characteristics evaluated for genetic divergence among the 124 genotypes of *Carthamus tinctorius* L.

Evaluated Characteristics[1]	S .j²	Relative Contribution (%)
FLOWER	1008174.00	5.26
CYCLE	1576206.00	8.23
NBP	416466.00	2.17
PH	2667912.50	13.93
NCP	4680506.00	24.44
NSC	1619664.00	8.45
CD	111543.93	0.58
SD	57966.90	0.30
W100	14880.65	0.0777
LS	147.66	0.0008
WS	54.25	0.0003
PY	6992190.47	36.52

[1/] FLOWER: Days for flowering; CYCLE: Cycle; NBP: Number of branches per plant; PH: Plant height; NCP: Number of chapters per plant; NSC: Number of seeds per chapter; CD: Chapter diameter; SD: Stem diameter; W100: Weight of 100 seeds; LS: Length of seed; WS: Width of seed; PY: Plant yield. [2/]Sj: contribution of variable x to the value of the average Euclidean distance between genotypes *i* e *i*'.

In studies conducted by Singh (1981) and using its methodology, it was identified that three characteristics contributed with 74.90% of genetic divergence. The variable that most contributed to the divergence was PY with 36.52%, followed by NCP with 24.44% and PH with 13.93%.

Characteristics that least contributed were WS (0.0003%), LS (0.0008%) and W100 (0.0777%). According to Rêgo et al. (2003), the characteristics with less contribution be disregarded. This allows a better choice of characteristics to be considered in an evaluation study of genetic divergence among populations or genotypes (Cruz and Regazzi, 2001).

Similar results were observed by Shivani et al. (2010), who also used Singh´s methodology (1981) to quantify the relative contribution of characters to estimate genetic divergence in safflower genotypes, with the PY characteristic contributing most to divergence, followed by NCP and NSC. In a study conducted in Maharashtra in India by Atole et al. (2018) evaluating the genetic divergence of 155 *C. tinctorius* L. genotypes, it was found that the maximum contribution was obtained by the PY trait, followed by PH and NCP, while W100, LS and WS did not contribute to the genetic divergence. Therefore, using the results of the relative contribution of the characters it is possible to infer that, to select genetically diverse genotypes for hybridization, the characteristics PY, PH and NCP should be mainly considered.

CONCLUSIONS

We found considerable genetic variability among 124 safflower genotypes based on their agronomic characteristics under Brazilian conditions. Clusters of the genotypes based on Tocher's and UPGMA methodologies were partially concordant in ordering the genotypes. The characteristics PY, NCP, and PH contributed most to the genetic diversity among these safflower genotypes.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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