

Genetic Divergence Among Safflower Genotypes (*Carthamus tinctorius* L.) by Multivariate Analyzes

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Abstract

Carthamus tinctorius L. is an oil seed, used both for human consumption and for industrial purposes. It is a crop that presents wide adaptability to various ecophysiological conditions, although it presents great productive potential and wide adaptability, it is still necessary to obtain technical information regarding its cultivation and of cultivars adapted and improved. In this sense, the estimation of genetic divergence using multivariate techniques has become a common tool among breeders. In view of the above, this research aimed to evaluate the genetic divergence of safflower genotypes originate from the Germplasm Active Bank (BAG) of the Instituto Mato-grossense do Algodão (IMA-MT) by means of multivariate analysis, aiming at the extension of information of this culture. The genetic divergence was estimated using multivariate analysis based on the Euclidean average distance, using the clustering optimization methods of Tocher and Hierarchical “UPGMA”. The results obtained allowed to identify the existence of genetic divergence among the evaluated genotypes, highlighting genotypes 5 and 38, which presented greater genetic divergence, constituting in potential sources of interest for the use in program of genetic improvement that aim at the development of superior cultivars of safflower.

Keywords: dissimilarity, oleaginous, genetic divergence

1. Introduction

Carthamus tinctorius L. is a member of the family Asteraceae, is an oilseed, used in both human and industrial purposes. It is a crop that presents a wide adaptability to several ecophysiological conditions, developing satisfactorily under low water availability in low fertility soils and in locations with temperature variations, thus being an alternative crop for Brazilian arid and semi-arid regions (Moura et al., 2015).

Although it presents great productive potential mainly due to the value of its oil and its wide adaptability, it is still scarce technical information about its cultivation and of cultivars adapted and improved in the Brazilian regions (Gerhardt, 2014). In this perspective, genetic improvement may help in this process, since one of the objectives of breeding is to increase the economic value of the species, increasing productivity, resistance to diseases and nutritional quality (Borém & Miranda, 2005).

For a breeding program to be successful there is a need for genetic divergence in populations that will be subjected to selection, that is, genetic variability in the population (Ivoglio et al., 2008). The genetic diversity is evaluated with the objective of identifying the hybrid combinations with greater heterotrophic effect, to identify the parents who, when crossed, allow the appearance of superior genotypes. In addition, the study of genetic divergence is important for the monitoring of germplasm banks, in addition to facilitating the knowledge of the genetic basis of the population (Ferrão et al., 2002; Cruz et al., 2004).

Among the predictive methods used in estimates of genetic distance is the average Euclidean distance, where it can be estimated by taking as a base data without repetitions (Carvalho et al., 2003). The estimation of genetic divergence using multivariate techniques has become common among safflower breeders (Shivani et al., 2010; Safavi et al., 2012; Zoz, 2015; Pavithra et al., 2015; Atole et al., 2018).

In this sense, the present research aimed to evaluate the genetic divergence of safflower genotypes by means of multivariate analysis, aiming at the extension of information of this culture for safflower breeding programs.

2. Materials and Methods

2.1 Site Localition and Characterization

The experiment was carried out in the experimental area belonging to the Empresa Mato-Grossense de Pesquisa, Assistência e Extensão Rural (EMPAER), in the county of Cáceres, Mato Grosso state, located at latitude 16°43'42" South and longitude 57°40'51" West with altitude of 118 meters, at BR 070, 12 km from Cáceres. The typical climate of the region, according to the classification of Köppen, is tropical, hot, humid and dry winter (Awa), with a period of rainfall ranging from October to April and from May to September (Dallacort et al., 2014). The soil is classified as Chernossolic Eutrophic Yellow Red Argissolo, with a medium clay texture (Arantes et al., 2012).

Were evaluated 50 safflower genotypes from the North American germplasm bank Western Regional Plant Introduction Station (WRPIS), obtained through the Germoplasm Resource Information Network (GRIN), imported by Instituto Mato-Grossente de Algodão (IMAT-MT) and ceded to the Laboratory of Genetic Resources and Biotechnology (LRG&B) of Universidade do Estado de Mato Grosso (UNEMAT), university campus of Cáceres (Table 1).

Table 1. Order, origin of the safflower genotypes belonging to the Laboratory of Genetic Resources and Biotechnology of Universidade do Estado de Mato Grosso

Order	PI ¹	Origin	Order	PI	Origin
1	193473	Ethiopia	26	283757	India
2	195895	Morocco	27	304438	Iran
3	237539	Turkey	28	305161	India
4	248385	India	29	305198	India
5	248620	Pakistan	30	305207	Índia
6	248808	India	31	305209	India
7	248828	India	32	305540	Kazakhstan
8	248839	India	33	306832	India
9	248852	India	34	306833	India
10	250083	Egypt	35	306838	India
11	250188	Pakistan	36	306844	India
12	250190	Pakistan	37	306866	India
13	250203	Pakistan	38	343783	Iran
14	250204	Pakistan	39	343930	Ethiopia
15	250840	Iran	40	367833	Argentina
16	250922	Iran	41	369842	Armenia
17	251978	Turkey	42	369845	Tajikistan
18	253540	Hungary	43	369849	Russia
19	253899	Syria	44	369854	Uzbekistan
20	259996	Paskitan	45	392029	Turkey
21	259997	Paskitan	46	392030	Turkey
22	262443	Spain	47	392031	Turkey
23	262447	Kazakhstan	48	393500	India
24	262450	India	49	401474	Bangladesh
25	279344	Japan	50	401475	Bangladesh

Note. ¹ Plant Introduction.

2.2 Morphoagronomic Characterization

The preparation of the experimental area was carried out in the conventional system, performing manual sowing on May 1st, 2018, with fertilization of 450 Kg ha⁻¹ of formulated (N P₂O₅ K₂O) 4-14-8 according to culture recommendations. The plots of each genotype consisted of four lines with 1 meter of length, with spacing of 0.50 centimeters between rows and 0.10 centimeters between plants, having a total of 10 plants per line. Basic management measures, such as manual weeding and irrigation, have been adopted by sprinkling whenever necessary.

The following agronomic characteristics were evaluated: Days for flowering (DF), Plant cycle (CYCLE), Number of ramifications per plant (NRP), Plant height (PH), Number of seeds per chapter (NSC), Number of chapter per plant (NCP), Diameter of the chapter (DC), Diameter of the stalk (DS), Width of seeds (WS), Length of seeds (LS), Weight of 100 seeds (W100) and Plant yield (PY).

2.3 Statistical Analyses

Diversity among the 25 safflower genotypes for 12 traits was assessed by estimating Euclidean average distance. Based on this matrix, we used the Tocher optimization grouping methods and Hierarchical Method of Intermediate Cluster between Groups (UPGMA) to build the genetic distance between the genotypes in clusters. The criterion of Singh (1981) was also used to quantify the relative contribution of the characteristics to genetic divergence. All analyzes were performed using the computational resources of the Genes software (Cruz, 2013).

3. Results and Discussion

Table 2 shows the descriptive analysis of the twelve quantitative traits evaluated in the 50 safflower genotypes, where it is possible to observe that the genotypes showed an average flowering time of 84.5 days, with the genotypes PI248852 and PI250083 showing a shorter flowering time 75 days and the later flowering genotype PI248620 at 104 days. These results are superior to those obtained by Shinwari et al. (2014), in Islamabad-Pakistan, evaluating 122 genotypes collected from several geographic ecosystems in the world, where the average for this parameter was 175.2 days, with minimum and maximum values of 160 and 188 days, respectively.

In relation to the crop cycle, safflower genotypes presented values ranging from 118 to 156 days, and genotypes PI343783, PI193473, PI250083 and PI369849 showed to be early, while genotypes PI248620 and PI305209 were found to be late (Table 2). These values are similar to those of Pavithra et al. (2015), in which they obtained values from 128 to 148 days, evaluating 150 safflower accesses in the Karnataka region of India during the years 2011/12. According to Galant et al. (2015), the safflower cycle tends to vary from 130 to 150 days, and may be an option for growing in the dry season, or for the dry period in some Brazilian agricultural regions.

For the number of ramifications per plant, the average of the evaluated genotypes was 13.58, and the genotypes PI248385, PI253899 and PI305198 presented values higher than 20 ramifications per plant (Table 2). Although this quantitative factor is important in the question of productivity, since the trend would be that the larger the number of branches the greater the number of inflorescences and consequently the greater the number of chapters, these characteristics should be carefully analyzed, since for the safflower crop, there is no interest in obtaining stalks with many ramifications due to differences in flowering rates within the chapter. Bellé et al. (2012), considers that many ramifications result in lack of uniformity in the anthesis, which reduces the quality of the stems.

Table 2. Descriptive analysis of fifty safflower genotypes evaluated in the city of Cáceres, state of MatoGrosso

Genotypes	Characteristics evaluated											
	DF	CYCLE	NRP	PH	NSC	NCP	DC	DS	WS	LS	W100	PY
PI193473	79.00	121.00	12.00	86.00	23.00	33.00	2.50	10.45	0.75	0.45	5.17	46.35
PI195895	88.00	150.00	20.00	111.00	33.00	55.00	2.48	12.05	0.71	0.41	4.94	26.13
PI237539	83.00	139.00	15.00	97.00	42.00	37.00	2.60	10.94	0.84	0.42	5.40	42.35
PI248385	83.00	123.00	21.00	82.00	19.00	43.00	2.07	8.11	0.72	0.40	3.88	19.98
PI248620	104.00	156.00	18.00	108.00	19.00	32.00	2.22	13.23	0.76	0.45	4.34	16.43
PI248808	81.00	130.00	19.00	72.00	10.00	48.00	2.39	9.71	0.71	0.40	6.04	39.33
PI248828	80.00	125.00	12.00	77.00	22.00	33.00	2.62	8.75	0.80	0.43	6.16	19.33
PI248839	83.00	143.00	9.00	95.00	28.00	41.00	2.68	10.78	0.85	0.47	6.04	19.41
PI248852	75.00	130.00	14.00	72.00	28.00	25.00	2.27	9.57	0.85	0.42	5.99	26.33
PI250083	75.00	121.00	14.00	90.00	17.00	48.00	2.18	10.15	0.75	0.47	4.45	21.00
PI250188	83.00	125.00	11.00	89.00	29.00	21.00	2.74	8.97	0.80	0.38	5.14	12.68
PI250190	75.00	125.00	11.00	82.00	24.00	36.00	2.55	9.30	0.93	0.47	5.50	33.66
PI250203	89.00	139.00	13.00	86.00	33.00	54.00	2.43	10.68	0.77	0.41	4.20	33.66
PI250204	79.00	123.00	9.00	66.00	22.00	32.00	2.44	8.82	0.73	0.45	5.11	17.21
PI250840	86.00	127.00	14.00	101.00	42.00	55.00	3.16	11.39	0.80	0.47	5.00	69.97
PI250922	77.00	123.00	15.00	73.00	31.00	31.00	2.67	10.50	0.89	0.51	7.10	39.67
PI251978	95.00	140.00	20.00	87.00	23.00	32.00	2.36	10.60	0.77	0.42	5.99	9.68
PI253540	88.00	139.00	12.00	93.00	14.00	22.00	2.67	10.93	0.80	0.48	5.95	12.53
PI253899	84.00	134.00	22.00	80.00	19.00	59.00	2.24	13.44	0.80	0.47	5.29	68.41
PI259996	81.00	150.00	12.00	77.50	24.00	32.00	2.89	10.38	0.81	0.50	4.57	38.26
PI259997	90.00	130.00	15.00	92.00	21.00	27.00	2.75	11.73	0.82	0.38	5.70	31.54
PI262443	78.00	150.00	20.00	62.00	22.00	48.00	1.98	12.00	0.78	0.35	3.86	24.35
PI262447	96.00	140.00	36.00	107.00	43.00	52.00	2.30	10.48	0.77	0.44	4.61	52.31
PI262450	85.00	132.00	23.00	82.00	30.00	33.00	2.26	9.49	0.75	0.43	4.33	27.23
PI279344	86.00	136.00	9.00	97.00	22.00	25.00	2.42	12.78	0.73	0.42	4.09	23.14
PI283757	84.00	156.00	16.00	70.00	24.00	20.00	2.10	11.86	0.80	0.44	3.76	14.00
PI304438	91.00	136.00	15.00	90.00	28.00	40.00	2.30	9.87	0.83	0.39	3.95	16.23
PI305161	88.00	136.00	18.00	89.00	26.00	27.00	2.31	9.92	0.79	0.44	4.34	19.98
PI305198	86.00	132.00	24.00	80.00	20.00	31.00	2.20	8.80	0.76	0.41	4.08	26.82
PI305207	83.00	132.00	16.00	94.00	29.00	39.00	2.98	12.05	0.80	0.42	5.60	70.28
PI305209	94.00	156.00	10.00	86.00	25.00	36.00	2.39	9.19	0.85	0.42	4.48	20.31
PI305540	94.00	139.00	22.00	104.00	37.00	49.00	2.29	11.29	0.87	0.45	5.12	15.69
PI306832	98.00	136.00	15.00	88.00	25.00	19.00	2.46	10.15	0.84	0.44	4.52	20.30
PI306833	77.00	123.00	11.00	85.00	38.00	23.00	2.94	9.44	0.73	0.40	5.39	31.30
PI306838	86.00	130.00	9.00	76.00	31.00	17.00	2.37	8.77	0.74	0.43	5.15	15.40
PI306844	84.00	134.00	11.00	80.00	23.00	25.00	2.29	9.52	0.73	0.46	5.87	21.90
PI306866	84.00	133.00	7.00	75.00	23.00	12.00	2.45	7.39	0.74	0.39	4.99	5.67
PI343783	79.00	118.00	7.00	56.00	42.00	6.00	2.59	7.00	0.60	0.44	4.04	15.89
PI343930	88.00	134.00	14.00	100.00	30.00	19.00	2.47	10.84	0.74	0.46	6.53	32.31
PI367833	81.00	132.00	10.00	80.00	37.00	25.00	2.72	9.67	0.91	0.45	4.31	14.20
PI369842	80.00	127.00	9.00	78.00	29.00	25.00	2.65	11.75	0.90	0.52	5.40	29.24
PI369845	79.00	125.00	6.00	62.00	47.00	23.00	2.80	9.46	0.82	0.44	4.68	45.91
PI369849	75.00	121.00	7.00	68.00	30.00	16.00	2.61	7.10	0.82	0.44	6.68	17.14
PI369854	82.00	143.00	7.00	70.00	22.00	19.00	2.39	9.15	0.89	0.42	4.85	15.43
PI392029	84.00	130.00	9.00	89.00	22.00	12.00	2.33	10.02	0.75	0.47	4.45	21.85
PI392030	95.00	139.00	9.00	100.00	18.00	16.00	2.60	10.89	0.80	0.46	4.30	14.03
PI392031	82.00	136.00	8.00	98.00	30.00	17.00	2.63	9.73	0.76	0.46	4.81	15.17
PI393500	82.00	143.00	9.00	88.00	10.00	21.00	2.19	9.12	0.89	0.52	6.20	8.79
PI401474	85.00	127.00	8.00	85.00	21.00	24.00	2.22	8.45	0.83	0.47	4.30	14.06
PI401475	81.00	125.00	6.00	71.00	33.00	16.00	2.54	9.50	0.89	0.47	5.09	18.68
Mean	84.50	133.88	13.58	84.53	26.80	30.62	2.47	10.12	0.43	0.79	5.03	26.23

Note. ¹DF = Days for flowering; CYCLE = Plant cycle, NRP = Number of ramifications per plant; PH = Plant height; NSC = Number of seeds per chapter; NCP = Number of chapter per plant; DC = Diameter of the chapter (cm); DS = Diameter of the stalk (cm); WS = Width of seeds (cm); LS = Length of seeds (cm); W100 = Weight of 100 seeds and PY = Plant yield.

Regarding plant height, the safflower genotypes evaluated obtained an average of 84.53 cm, ranging from 62 to 111 cm (Table 2). These results are similar to Silva (2013), where plant height varied between 57 and 136 cm. According to Gracia et al. (2010), the observed values, for the most part, are within the limits commonly observed in the improved safflower cultivars, whose averages normally ranging between 90 and 150 cm.

As for the number of seeds per chapter, the average obtained by the genotypes evaluated in the present study was 26.8 (Table 2). Shinwari et al. (2014) found similar results, in a work conducted in Islamabad-Pakistan, where this variable presented an average of 28.2.

Considering the number of chapters per plant, the genotypes evaluated presented values ranging from 6 to 59 (Table 2). In a study carried out by Silva (2013), in Botucatu-SP, evaluating 170 accessions of safflower, there was a variation from 9 to 78. This parameter of production is relevant, since the larger the number of chapters per plant, the greater the number of seeds produced, which can promote productivity increases. Hajghami et al. (2009), emphasizes that to obtain promising cultivars in breeding programs, should select the materials with the highest number of chapters per plant to obtain highly productive plants. Therefore, the genotypes PI195895, PI250203, PI250840, PI253899 and PI262447 are distinguished for this characteristic producing more than 50 chapters per plant.

For the characteristic diameter of the chapter the safflower breeding programs search genotypes that present larger diameter, since the greater the chapter the greater the capacity of flower formation and, consequently, the greater the number of seeds, thus favoring productivity (Silva, 2013). Among the genotypes evaluated in the present study, PI250840 presented the highest result with a diameter of 3.16 cm (Table 2). This value is higher than those obtained by Atole et al. (2018), evaluating 155 safflower genotypes evaluated in Maharashtra-India, whose maximum value was 2.78 cm and by Silva et al. (2015), evaluating 20 genotypes evaluated in Botucatu-São Paulo, the highest value was 2.4 cm.

The diameter of the stalk is a very important feature in a plant of the same safflower family, as the sunflower (Asteraceae). Considering that it allows less bedding of the crop, facilitating its management, treatments and harvesting (Biscaro et al., 2008). As previously reported by Anicésio (2014), the study of this variable also applies to safflower, because this crop presents bedding problems that hamper, among other steps, mechanized harvesting. Thus, in the present research the genotypes PI 195895, PI248620, PI253899, PI262443, PI279344 and PI305207 are outstanding, since they have a diameter with values equal to or greater than 12 cm.

For the weight of 100 seeds, the genotypes varied from 3.76 to 7.10 g and average of 5.05 g (Table 2). These results are higher than those obtained by Pushpavalliet et al. (2017) evaluating 47 safflower genotypes in the 2015/16 crop in Telangana State, India, where the values obtained were 3.67 g maximum.

Regarding the variable plant yield, the average of the 50 safflower genotypes evaluated in the present study was 26.23 g, with a maximum value for genotypes PI305207 with a value of 70.28 g (Table 2). This result is similar to that obtained by the hybrid combination between the genotypes PI537697 and PI653152 in Olivo (2017), in which the grain yield per plant was 73.80 g.

The genetic divergence of the evaluated genotypes was based on the average Euclidean distance, in which the most dissimilar pair was composed of genotypes PI248620 and PI343783, this dissimilarity between these genotypes may be linked to their geographical origin, considering that genotype PI248620 is from Pakistan and genotype PI343783 is of Iranian origin (Table 1). These results seem to be a trend, as they were previously reported in studies conducted by Derakhsan et al. (2014), in which the genetic divergence of 42 genotypes of six species of *Carthamus tinctorius* L. was evaluated, via microsatellite markers, where the results indicated that, in most cases, safflower genotypes are divided into subgroups consistent with the country of origin, that is, genotypes of different geographical origin are expected to be divergent.

From the point of view of genetic improvement, the divergence between these genotypes is of great importance, since as pointed out by Cruz et al. (2004), it is recommended to cross between divergent materials, for maximum heterosis in the progenies increasing the possibility of genetic gains in the segregating populations.

In relation to similarity, genotypes PI262450 and PI305198 are the closest, this fact, can be considered, because of their origins, since both are from India, because they present this similarity, the crossing of this combination is not recommended, having since for genetic breeding programs variability is indispensable (Santos et al., 2014).

In the cluster analysis by the Tocher optimization method, based on the dissimilarity matrix using the average Euclidean distance, the formation of 13 groups was obtained (Table 3). Group I had the highest number of genotypes, comprising 58% of the genotypes evaluated; group II, V and VII were composed of two genotypes,

constituting 4% of genotypes, group III, IV and VI were composed of three genotypes, 6% of the evaluated materials, respectively.

Table 3. Group of safflower genotypes with similar patterns, established by the Tocher method, using the average Euclidean distance as a measure of dissimilarity evaluated in the city of Cáceres, state of Mato Grosso

Groups	Genotypes ¹	Frequency (%)
I	24, 29, 28, 27, 4, 13, 33, 49, 35, 45, 36, 47, 14, 11, 7, 1, 9, 44, 37, 40, 50, 12, 17, 25, 18, 46, 21, 8, 39	58%
II	16, 41	4%
III	15, 30, 3	6%
IV	2, 32, 23	6%
V	34, 42	4%
VI	26, 31, 20	6%
VII	6, 10	4%
VIII	19	2%
IX	22	2%
X	48	2%
XI	43	2%
XII	38	2%
XIII	5	2%

Note. ¹1-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.

Groups VIII, IX, X, XI, XII and XIII presented a single genotype (Table 3), this formation of groups with only one individual confirms the existence of genetic divergence, which is a positive aspect from the point of view of the use of these genotypes in artificial hybridizations with the purpose of increasing the genetic variability. In this sense, it is indicated the choice of parents of different groups because they present greater genetic distances.

According to the dendrogram obtained by the UPGMA hierarchical method, the genotypes were collected in seven groups. Group I was subdivided into subgroup GI-A composed of genotypes PI262450, PI305198, PI283757, PI248385, PI250203, PI304438, PI305209, PI306832, PI392030, PI392029, PI401474, PI392031 and PI279344, the GI-B subgroup consisting of genotypes PI248839, PI253540, PI343930, PI251978 and PI259997.

The GI-C subgroup allocated to genotypes PI193473, PI250083 and PI248808, and the GI-D subgroup composed of the largest number of individuals, formed by genotypes PI250188, PI306833, PI306838, PI306844, PI248828, PI250204, PI306866, PI369854, PI369849, PI248852, PI250190, PI367833, PI401475, PI369842, PI250922 and PI369845 and genotype PI259996 belongs to the GI-E subgroup (Figure 1).

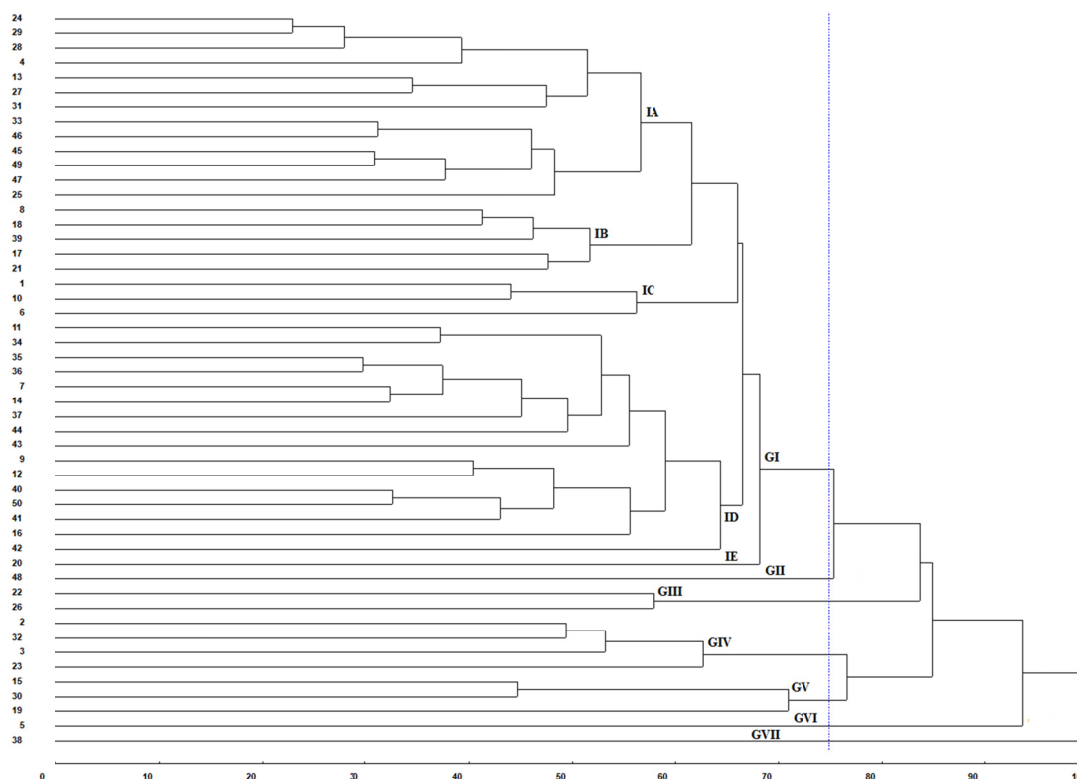


Figure 1. Dendrogram illustrating the genetic divergence among fifty genotypes of safflower, obtained by the method of average bonds (UPGMA), using the average Euclidean distance

Note. ¹1-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.

The GII group allocated only one genotype: PI393500, GIII was composed of genotypes PI262443 and PI283757, genotypes PI195895, PI305540, PI237539 and PI262447 belong to the GIV group, genotypes PI250840, PI305207 and PI253899 were designated to GV, genotype PI248620 and PI343783 were determined in the GVI and GVII groups, respectively (Figure 1).

The agglomerative optimization methods Tocher and Hierarchical UPGMA were partially similar, in which group 1 of both clustering methods the largest number of genotypes, another fact of this similarity between clustering methods can be observed by the allocation of genotypes PI248620 and PI343783 in which these were allocated only in different groups.

In relation to the relative importance of the traits, the characteristics with the greatest contributions to the evaluation of the genetic diversity among the genotypes evaluated in the present study were according to the method of Singh (1981) yield per plants, chapter number per plant and plant height with 28, 82, 20.86 and 19.73% respectively (Table 4).

Table 4. Relative contribution of the eleven agronomic characters to the genetic divergence among fifty safflower genotypes evaluated in the city of Cáceres, state of Mato Grosso

Character ¹	Relative importance (%)
DF	5.0904
CYCLE	11.6188
NRP	4.2973
PH	19.7399
NSC	8.4615
NCP	20.8689
DC	0.7603
DS	0.2588
W100	0.0829
WS	0.0002
LS	0.0005
PY	28.8205

Note. ¹DF = Days for flowering; CYCLE = Plant cycle, NRP = Number of ramifications per plant; PH = Plant height; NSC = Number of seeds per chapter; NCP = Number of chapter per plant; DC = Diameter of the chapter; DS = Diameter of the stalk; WS = Width of seeds; LS = Length of seeds; W100 = Weight of 100 seeds and PY = Plant yield.

In a study conducted in the state of Maharashtra, India, evaluating 155 genotypes by Atole et al. (2018), plant height and number of seeds per chapters also stood out for discrimination of genetic diversity with 22.75 and 20.68%, respectively. In the research carried out by Tayade et al. (2015), in Akola, India, evaluating 155 genotypes and five safflower varieties, the number of chapters per plant characteristics was also an important trait with 26.98% relative importance.

The trait that contributed less to diversity, were seed size per width and seed size per length. Tayade et al. (2015) obtained divergent results, where the characteristics that contributed least were hull content and weight of 100 seeds, with 0.00 and 0.05, respectively.

4. Conclusion

The safflower genotypes analyzed presented genetic divergence regarding the agronomic traits and the highest dissimilarity were PI248620 and PI343783, on the other hand, the less divergent genotypes were PI262450 and PI305198. The Tocher clustering and UPGMA hierarchical methods were partially concordant in ordering the similar accessions. The characteristics yield per plant and chapter number per plant are the ones that contributed the most for genetic dissimilarity in the safflower genotypes evaluated in the present research.

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