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Genetic divergence analysis of yield and its component traits in safflower (*Carthamus tinctorius* L.)

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Abstract

The experiment conducted using the set of 25 genotypes of safflower in three successive year's during *rabi* 2020-21, *rabi* 2021-22 and *rabi* 2022-23 at Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.) for estimation of the extent of diversity and to estimate the contribution of each character towards genetic diversity in safflower (*Carthamus tinctorius* L.) by Mahalanobis D² distance and grouping by Tocher's method, these genotypes were grouped into five clusters. The maximum inter cluster distance was noted between cluster IV and cluster V (25.24) followed by cluster V and cluster II (16.77), cluster I and cluster V (14.50), cluster V and III (11.04), cluster II and cluster III (56.13) and cluster IV and cluster III (56.13). The contribution to the total divergence was estimated maximum for seed yield per plant (30.67%) followed by biological yield per plant (g) (20.33%), plant height (cm) (15.67%). Whereas number of seeds per capitulum (9.33%), harvest index (%) (8.33%), oil content (%) (7.33%), 100 seed weight (g) (4.34%), number of primary branches per plant (2.00%), number of effective capitulum per plant (1.00%), days to 50% flowering (0.67%) and days to maturity (0.33%) exhibited minimum contribution towards genetic divergence. According to cluster mean cluster IV recorded the first rank for the yield contributing traits viz., oil content %, number of effective capitulum per plant, number of primary branch per plant and number of seed per capitulum. It indicates that combination of these traits is very important towards the improvement of seed yield so accessions belonging to these clusters can be further used for genetic improvement.

Keywords: Genetic diversity, safflower, variations, genotypes, intra and inter cluster distance

Introduction

Oilseed plant safflower (*Carthamus tinctorius* L.) belongs to the family *Asteraceae* or *Compositae*. Safflower is a versatile crop high in calcium, iron, phosphorus and vitamin A (Khan *et al.*, 2009, Tandekar and Shrivastava, 2018) [9, 27]. It has been farmed for generations in India for its high-quality oil, which is rich in the polyunsaturated fatty acids oleic and linoleic acid (78%) and the orange-red dye (carthamin), which is collected from its brightly coloured blossoms (Hamdan *et al.*, 2009, Pillai and Shrivastava, 2023) [6, 16].

The evaluation of genetic diversity in agricultural species is crucial for the preservation of genetic resources, expansion of the genetic base, and useful application in breeding programmes (Yadav and Shrivastava, 2023) [29]. Around the world, there is a lot of variation in safflower (Knowles, 1989) [10]. Since the effectiveness of a selection programme is largely dependent on the quantity of genetic variation and heritability of a trait (Kearsey and Pooni, 1996) [8], it is necessary to know how much the phenotypic variation of a trait is heritable in order to design an optimal breeding programme (Falconer and Mackay, 1996). Both agromorphological characteristics and molecular markers have been used to examine the genetic diversity of a crop species (Patel *et al.*, 2017) [18].

Genetic diversity is of considerable practical interest in any crop improvement programme (Purkaystha *et al.*, 2017) [18]. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes (Pratibha and Shrivastava, 2018) [17]. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in 25 genotypes of safflower.

Materials and Methods

In current study, which used 25 safflower genotypes including four check varieties PBNS-12, JSI-99, DSH-185, and A-1 was conducted in *rabi* 2020–2021, *rabi* 2021–22, and *rabi* 2022–23 at IGKV, Raipur, Chhattisgarh mainly focused on assessment genetic diversity of yield and its contributing characters in safflower (*Carthamus tinctorius* L.). Three replications of the Randomised Block Design (RBD) were used to set up the experiment. The ideal growth stages of five plants from each plot were chosen at random in order to collect data on various yield and yield-contributing characters.

Results and Discussion

A set of 25 genotypes of safflower were subjected to D² analysis for eleven characters. Cluster analysis by the Tocher optimization method allowed the separation of 25 genotypes into five clusters (Table 1 and fig. 1). This will indicated that substantial diversity exists in the available gene pool of safflower. Hence, the genotypes studied are reliable enough for hybridization and selection.

The pooled D² analysis for yield and its contributing traits were also performed and results revealed that the cluster I was the largest involving 13 genotypes with check DSH-185 followed by cluster II (5 genotypes) with checks PBNS-12 and A-1, cluster II (5 genotypes). Cluster III, IV and V involved only one genotype in each cluster. From the clustering pattern, it was found that the safflower genotypes were genetically diverse to each other. These results are in agreement with the earlier findings of Diwakar *et al.*, (2006) [3], Shivani *et al.*, (2011) [24], Harish *et al.*, (2012) [7], Pavithra *et al.*, (2015) [15], Pushpavalli and Kumar (2017) [19] and Atole *et al.*, (2018) [1] and Dhage *et al.*, (2020) [2].

Average intra and inter cluster distance values among eleven characters were calculated by Tocher's method and are presented in Table 2 and fig 2. The maximum inter cluster distance was noted in between cluster IV and cluster V (25.24) followed by between cluster V and cluster II (16.77), cluster I and cluster V (14.50), cluster V and III (11.04), cluster II and cluster III (56.13) and cluster IV and cluster III (56.13). The clusters having maximum distance were genetically divergent and hence genotypes in these clusters can be used as parents for hybridization in breeding programme to obtain maximum segregation. Present study confirm's the findings of earlier worker's Mukta *et al.*, (2008) [12], Shivani *et al.*, (2010) [23], Shivani and Sreelakshmi (2013) [25] and Dhage *et al.*, (2020) [2]. The minimum inter cluster distance was observed in between cluster I and cluster III (5.91), cluster I and cluster IV (4.80) and cluster I and cluster II (3.64) indicating a close relationship between them. Therefore, crossing to genotypes belonging to these clusters may not result into improvement in the desired direction as there might be closeness in respect of their origin. These findings are in close agreement with earlier finding of Patil *et al.*, (1984) [14], Reddy and Davasenamma (2004) [21], Mukta *et al.*, (2008) [12], Salamati *et al.*, (2011) [22], Harish *et al.*, (2012) [7] and Majidi *et al.*, (2015) [11], Pavithra *et al.*, (2015) [15] and Pushpavalli and

Sudhakar (2015) [20]. The maximum intra cluster distances were observed in cluster I (2.03) followed by cluster III (1.62) and cluster II (1.57). The selection of divergent genotype from above clusters would produce a broad spectrum of variability for morphological and quality traits studied, which enable further for selection and improvement. These results are in agreement with the earlier findings of Diwakar *et al.*, (2006) [3], Shivani *et al.*, (2011) [24], Harish *et al.*, (2012) [7], Pavithra *et al.*, (2015) [15], Pushpavalli *et al.*, (2015) [20], Tayade *et al.*, (2015) [28], Atole *et al.*, (2018) [1].

The contribution of each character towards genetic divergence has been presented in Table 3 and fig. 3. The characters contributing to most of the divergence should be given more importance for the purpose of effective selection and the choice of parents for hybridization. The contribution to the total divergence was maximum by seed yield per plant (30.67%) followed by biological yield per plant (g) (20.33%), plant height (cm) (15.67%), number of seeds per capitulum (9.33%), harvest index (%) (8.33%), oil content (%) (7.33%), 100 seed weight (g) (4.34%), number of primary branches per plant (2.00%), number of effective capitula per plant (1.00%), days to 50% flowering (0.67%) and days to maturity (0.33%) exhibited minimum contribution towards genetic divergence. These findings are similar to earlier studies of Diwakar *et al.*, (2006) [3], Sreenivasa *et al.*, (2010) [26], Shivani *et al.*, (2011) [24], Harish *et al.*, (2012) [7], Shivani and Sreelakshmi, (2013) [25], Pavithra *et al.*, (2015) [15].

An overall study of cluster means for all eleven characters is presented in Table 4. Analysis revealed that the cluster V exhibited maximum mean for character viz., seed yield per plant (21.93g) and minimum mean value for days to 50% flowering (100.22) indicating that these genotypes can be utilized for breeding for early duration. Maximum cluster mean value for oil content % (41.93%), number of effective capitulum per plant (28.40), number of primary branch per plant (6.44) and number of seed per capitulum (44.34) were exhibited in cluster IV. The cluster I exhibited lowest cluster mean for days to maturity (144.65 days) indicating that these genotypes can be utilized for breeding for early duration to escape drought conditions and maximum mean for 100 seed weight (4.98g) was also exhibited in cluster I. Maximum cluster mean recorded for biological yield per plant (73.64g) was exhibited in cluster II. The cluster III exhibited highest cluster mean for harvest index (%) (49.36%) and plant height (92.96 cm). According to cluster mean cluster IV recorded the first rank for the yield contributing trait contributing traits viz., oil content %, number of effective capitulum per plant, number of primary branch per plant and number of seed per capitulum. It indicates that combination of these traits is very important for the improvement of seed yield so accessions belonging to these clusters can be further used in genetic improvement. These results are in agreement with the earlier findings of Diwakar *et al.*, (2006) [3], Shivani *et al.*, (2011) [24], Harish *et al.*, (2012) [7], Pavithra *et al.*, (2015) [15] and Tayade *et al.*, (2015) [28].

Table 1: Pooled distribution of 25 genotypes of safflower in V clusters in *rabi* 2020-21, 2021-22 and 2022-23:

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	13	AKS-351, SSF-18-37, ISF-867, RVS-118, TSF-89, ISH-413, DSH-185, SSF-18-02, PBNS-200, PBNS-202, ISF-300, PBNS-194, SSF-16-30
2 Cluster	5	PBNS-198, PBNS-12, ISH-419, RVS-119, A-1
3 Cluster	5	ISF-351, ISH-417, PBNS-201, TSF-91, SSF-18-72
4 Cluster	1	RVS-120
5 Cluster	1	JSI-99

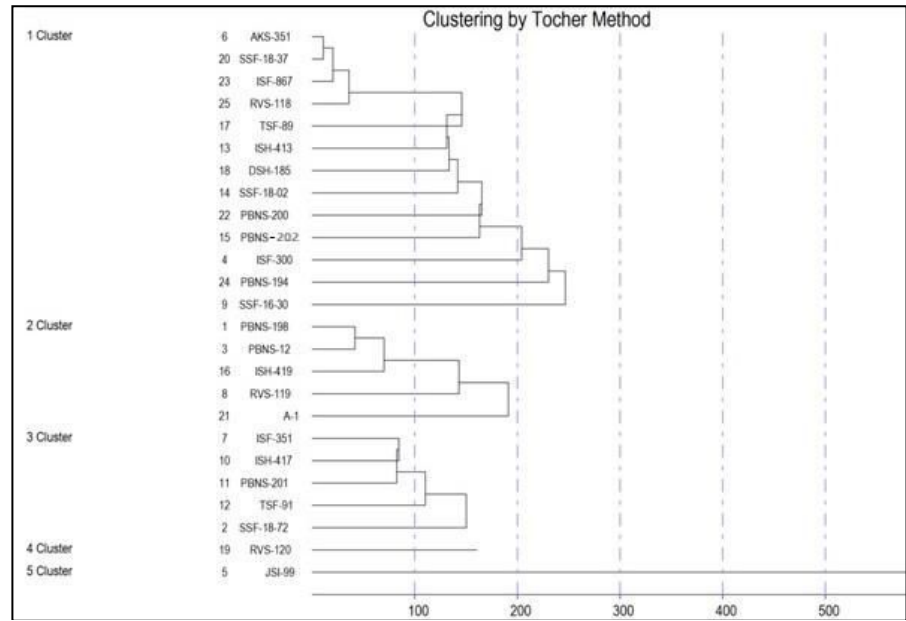


Fig 1: Clustering by tocher method

Table 2: Pooled Inter and intra cluster difference of genotypes in safflower in *rabi* 2020-21, 2021-22 and 2022-23:

Cluster Distances					
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	2.03	3.64	5.91	4.80	14.50
Cluster 2		1.57	10.96	6.89	16.77
Cluster 3			1.62	9.80	11.04
Cluster 4				0.00	25.24
Cluster 5					0.00

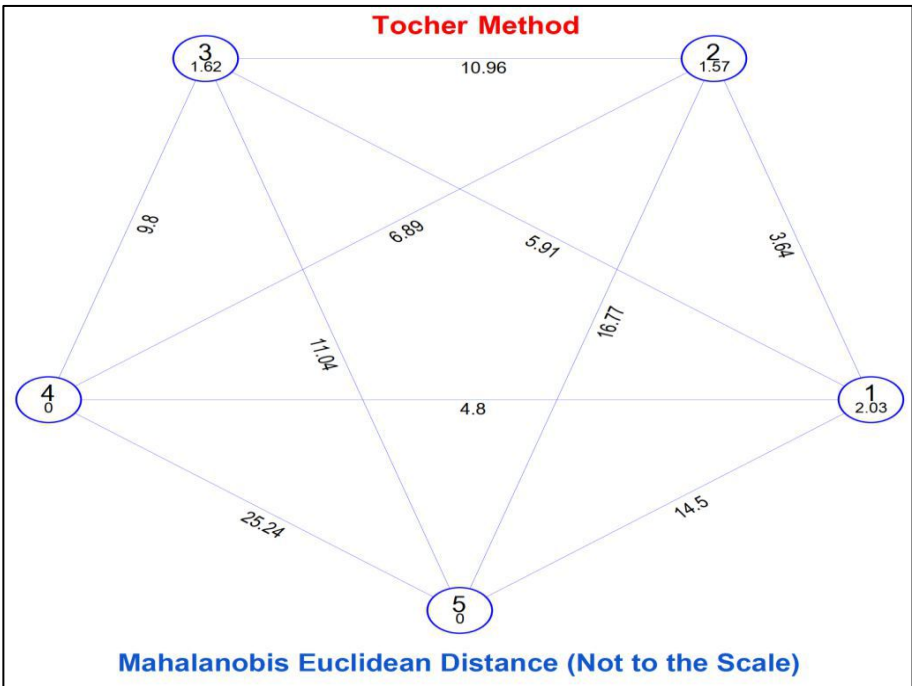
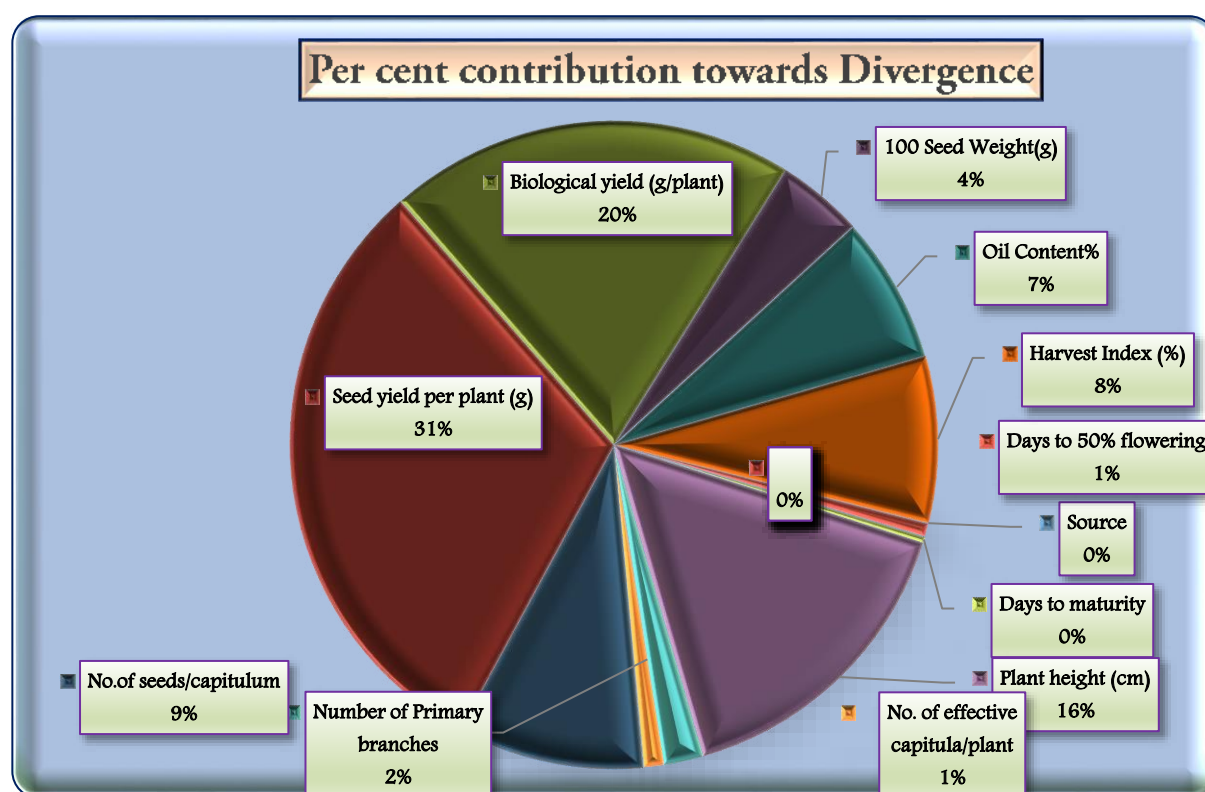


Fig 2: Mahalanobis Euclidean distance of 5 clusters in safflower

Table 3: Pooled percent contribution of yield and its contributing traits towards genetic divergence in *rabi* 2020-21, 2021-22 and 2022-23:

Sl. No.	Source	Contribution %	Times ranked 1 st
1	Days to 50% flowering	0.67	2
2	Days to maturity	0.33	1
3	Plant height (cm)	15.67	47
4	Number of Primary branches	2	6
5	No. of effective capitula/plant	1	3
6	No. of seeds/capitulum	9.33	28
7	Seed yield per plant (g)	30.67	92
8	Biological yield (g/plant)	20.33	61
9	100 Seed Weight(g)	4.34	13
10	Oil Content%	7.33	22
11	Harvest Index (%)	8.33	25

**Fig 3:** Pooled percent contribution of yield and its contributing traits towards genetic divergence in *rabi* 2020-21, 2021-22 and 2022-23**Table 4:** Pooled cluster mean of different yield and yield contributing traits in safflower in *rabi* 2020-21, 2021-22 and 2022-23:

Clusters	Cluster Means :Tocher Method					
	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	No. of capitula/plant	No. of seeds/capitulum
Cluster 1	101.03	144.65	91.24	6.26	24.10	35.71
Cluster 2	101.91	144.82	91.84	5.84	24.88	30.11
Cluster 3	102.53	145.56	92.26	5.77	23.91	34.98
Cluster 4	100.44	144.67	89.68	6.44	28.40	44.34
Cluster 5	100.22	147.22	54.06	4.69	18.17	20.44

Clusters	Cluster Means : Tocher Method				
	Seed yield per plant (g)	Biological yield /plant (g)	100 Seed weight(g)	Oil content%	Harvest Index (%)
Cluster 1	18.37	57.29	4.98	35.45	32.32
Cluster 2	20.40	73.64	5.38	34.88	27.92
Cluster 3	19.96	40.84	4.84	34.49	49.36
Cluster 4	20.54	61.82	3.96	41.93	33.50
Cluster 5	21.93	45.72	5.33	26.79	48.41

Conclusion

The maximum inter cluster distance was noted in between cluster IV and cluster V followed by between cluster V and cluster II. The clusters having maximum distance were

genetically divergent and hence genotypes in these clusters can be used as parents for hybridization in breeding programme to obtain maximum segregation. The minimum inter cluster distance was observed in between cluster I and

cluster III, cluster I and cluster IV and cluster I and cluster II indicating a close relationship between them. Therefore, crossing to genotypes belonging to these clusters may not result into improvement in the desired direction as there might be closeness in respect of their origin. The characters contributing to most of the divergence should be given more importance for the purpose of effective selection and the choice of parents for hybridization. The contribution to the total divergence was maximum by seed yield per plant followed by biological yield per plant (g), plant height (cm) number of seeds per capitulum, harvest index (%), oil content (%), 100 seed weight (g), number of primary branches per plant, number of effective capitulum per plant, days to 50% flowering and days to maturity exhibited minimum contribution towards genetic divergence.

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