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MA Patel
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

SL Chawla
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

AI Patel
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

HP Shah
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

DS Bhatt
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

Correspondence
MA Patel
ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat, India

Genetic divergence studies in marigold (*Tagetes* spp.)

MA Patel, SL Chawla, AI Patel, HP Shah and DS Bhatt

Abstract
Genetic divergence was studied among 26 marigold (*Tagetes* spp.) germplasm using Mahalanobis D^2 analysis. The study indicated that the genotypes were grouped into seven divergent clusters. Cluster I had large population containing 10 genotypes. The highest inter cluster D^2 value was recorded between cluster III and IV, indicated that cross may be attempted between genotypes of these clusters to obtain new desirable recombinants in marigold. Among all the characters, carotenoid content (62.77%) contributed maximum towards genetic divergence followed by leaf area (6.77%) and number of flowers per plant (5.54%). Cluster IV and VI and V showed higher cluster means for yield and yield components, therefore genotypes *viz.,* Local Selection 15, Sonata Orange and Local Selection 2 of these diverse clusters may be used for further hybridization.

Keywords: Marigold, genetic divergence, cluster, genotypes

Introduction
Marigold (*Tagetes* spp.) is one of the most important traditional flower crops grown in India, owing to its ornamental and industrial uses. It is grown for landscaping and occupies an ever increasing demand in medicinal and industrial sector. It is widely grown for its loose flowers used for religious and social functions for making garlands, bedding plant in landscape gardening, extraction of carotenoides for industrial uses raised the importance of this crop and increased the area under its cultivation. Marigold is suggested as trap crop for monitoring the *Helicoverpa* incidence in vegetable crops and has nematicidal properties also. Genetic diversity can be worked out with the help of D^2 analysis which was given by Mahalanobis (1936) [3]. For the first time use of this technique of assessing the genetic variability in plants was suggested by Rao (1952) [9]. It is a very potent technique for measuring genetic divergence. Now, it is reliably and extensively used in plants for measuring genetic divergence. Success of crop improvement programme depends on the extent of genetic variability, choice of parents for hybridization and selection procedure. In plant breeding, genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable recombinants (Rathi, *et al.,* 2011) [8].

Materials and Method
The present investigation was carried out during *Rabi* season (November 2014 - April 2015) at three different locations *viz.,* Floriculture Research Farm, Navsari (Dist.-Navsari), Regional Rice Research Station, Vyara (Dist.-Tapi) and Hill Millet Research Station, Waghai (Dist.-The Dangs) of Navsari Agricultural University. Twenty six (26) genotypes collected from diverse source comprising of 4 F_1 hybrids, 15 local genotypes and 7 open pollinated varieties were grown in a randomized block design (RBD) with three replications.
Seeds of all the genotypes were sown on the raised beds in the month of November to raise seedlings. Transplanting of seedlings was done when they attain three to four true leaves stage. The genotypes were planted in a single-row of 20 plants under each replication with a spacing of 60 x 40 cm with all the agronomical practices and plant protection measures. The observations were recorded on five randomly tagged plants from each genotype of each replication. For all the characters under study, the mean values of five randomly selected plants were calculated for each observation under individual location. The genetic divergence among the genotypes was quantitatively assessed through D^2 statistics (Mahalanobis, 1936) [3] and grouping of the genotypes into different clusters was done by using Ward's minimum variance method as described by Rao (1952) [3] using INDOSTAT software.

Result and Discussion

Creation of variability and selection within, leading to diverse genotypes in the common protocol that a plant breeder follows. Genetic relationship among genotypes can be measured by similarity or dissimilarity of any number of quantitative characters, assuming that the difference between characters of genotypes ultimately reflect in the divergence of the genotypes. In heterosis breeding programme, the diversity of parents is always emphasized upon. More diverse the parents within a reasonable range, better is the chance of improving economic traits under consideration in the resulting offspring. However, it is a difficult task for the breeder to select the most suitable and genetically divergent parents, unless one is provided with necessary information about genetic variability and genetic diversity present in the available germplasm.

Generally, geographical diversity is considered and taken as a measure of genetic diversity when no scientific tool is available. However, inferential criterion may not be used for discrimination among the populations occupying ecologically marginal habits. The multivariate analysis, using Mahalanobis D^2 statistics, provides a useful statistical tool for measuring the genetic diversity in a given population with respect to the characters considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters, responsible for the discrimination between populations.

In the present study, based on D^2 values, all the twenty six genotypes were grouped into seven clusters (Table 1) indicating the presence of appreciable amount of genetic diversity among the genotypes under the study. The maximum number of genotypes (10) were grouped into cluster I, followed by cluster II and cluster III possessed 6 genotypes each, whereas cluster IV, cluster V, cluster VI as well as cluster VII possessed 1 genotype each. Grouping of genotypes into seven clusters suggested the presence of considerable diversity in the material under investigation. Singh *et al.* (2002) [11] studied genetic divergence in marigold and grouped 30 accessions into two clusters and cluster I include 29 genotypes showed tight and complete linkage. Kavitha and Anburani (2009) [2] formed eight clusters in 30 genotypes of marigold on the basis of 9 characters revealed the genetic diversity was independent of the geographical diversity. Swaroop (2010) [12] grouped 28 gladiolus genotypes into 8 clusters. Nimbalkar *et al.* (2006) [5] grouped 101 genotypes of gladiolus into 18 clusters on the basis of 13 characters.

The intra-cluster and inter-cluster distance (Table 2) revealed that inter-cluster distance values were greater than the intra-cluster values. Intra-cluster distance was maximum in cluster III followed by the cluster II, while minimum intra-cluster distance was observed in cluster I which included maximum genotypes (10), indicating that genotypes of cluster III varied in genetic architecture and might have originated from different genetic pool. In cluster- I, the trend was exactly reverse of the cluster-III. The maximum inter- cluster distance was observed between cluster III and IV suggesting about possibility of genetic makeup of these genotypes. The minimum inter-cluster distance was observed between cluster I and cluster IV, indicating the resemblance among the genotypes of this group for all characters studied. Low magnitude of inter- cluster distance values suggested that very little domestication has occurred. Similar results had also been suggested by Bihari *et al.* (2009) [1], Sheikh and Khanday (2008) [10], Nimbalkar *et al.* (2006) [5] and Raj and Misra (2000) [7] in gladiolus and Punitha *et al.* (2010) [6] and Manivannan *et al.* (2003) [4] in sunflower; Kavitha and Anburani (2009) [2] in marigold.

The contribution of individual characters to the divergence was worked out in terms of number of times it appeared first (Table 3). Carotenoid content (mg/100g) contributed maximum towards genetic divergence followed by leaf area (cm^2). Genotypes included in cluster IV showed maximum cluster means for number of primary branches per plant, stem diameter (mm), duration of flowering (days), flower diameter (mm), flower weight (g), number of flowers per plant, flower yield per plant(g), flower longevity (days), 1000-seed weight (g), seed yield per plant (g) and harvest index (%). Whereas, cluster VII showed maximum mean value for plant height, leaf area (cm^2) and leaf biomass; cluster I showed maximum mean value for shelf life of flower (days); cluster V showed maximum mean value for number of secondary branches per plant and photosynthetic rate (μ $Mol/m^2/sec$), while cluster VI recorded maximum mean value for plant spread. Moreover, cluster III had minimum values for days taken to first flowering. It can further be concluded from the present study that hybridization among genotypes of these clusters combination is expected to enhanced variability in marigold for the targeted traits.

In fact, the genotypes forming single clusters were extraordinary for one or more characters, which made them so divergent from others. This fact also reflected in cluster means. Analysis of clusters means indicated substantial variations among clusters grouped according to D^2 analysis. Based on the range means, it was possible to know the characters influencing divergence. The cluster having single or less genotypes revealed highest or lowest mean values for different characters as evident from mean data (Table 4). Although, the distance between various clusters was reflected in cluster means but it was not proportional for few characters. It seems that there were some other factors responsible for divergence. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean for almost all the component characters.

Table 1: The distribution of 26 genotypes of marigold to different clusters on the basis of D^2 statistics

Clusters	No. of genotypes	Genotypes
I	10	Indus Orange Bunch, Local Selection 10, Local Selection 9, Suvarna Orange, Local Selection 1, Local Selection 13, Local Selection 5, Local Selection 3, Local Selection 4, Local Selection 6
II	06	Swati Orange, F_1 White Dwarf, Pusa Narangi Gainda, Namdhari African Orange, Inca Yellow, Local Selection 8
III	06	Hawaii Orange, Local Selection 14, Summer Sugat, Inca Gold, Local Selection 12, Local Selection 7
IV	01	Local Selection 15
V	01	Sonata Orange
VI	01	Local Selection 2
VII	01	Local Selection 11

Table 2: Average intra and inter- cluster (D^2) values for 26 genotypes of marigold

Clusters	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7
I	14.57	21.54	26.79	18.90	24.30	21.14	23.73
II		16.22	35.61	21.31	36.87	27.45	23.33
III			18.39	36.99	24.32	29.35	36.03
IV				0.00	32.31	20.88	23.43
V					0.00	25.60	35.34
VI						0.00	25.53
VII							0.00

Table 3: Contribution of twenty-one characters under study to total divergence

Sr. No.	Source	Times Ranked 1st	Contribution %
1	Plant height (cm)	0	0.00%
2	Plant spread (cm)	1	0.31%
3	Number of primary branches per plant	0	0.00%
4	Number of secondary branches per plant	6	1.85%
5	Stem diameter (mm)	0	0.00%
6	Leaf area (cm^2)	22	6.77%
7	Leaf biomass (g)	8	2.46%
8	Photosynthetic rate (µmol/m2/sec)	16	4.92%
9	Days to first flowering	0	0.00%
10	Duration of flowering (days)	3	0.92%
11	Flower diameter (mm)	0	0.00%
12	Flower weight (g)	16	4.92%
13	Number of flowers / plant	18	5.54%
14	Flower yield / plant (g)	6	1.85%
15	Flower longevity (days)	9	2.77%
16	Shelf life of flower (days)	0	0.00%
17	1000 seed weight (g)	11	3.38%
18	Seed yield /plant (g)	5	1.54%
19	Harvest index (%)	0	0.00%
20	Carotenoid content (mg/100g)	204	62.77%

Table 4: Cluster means of 26 genotypes of marigold for various growth and flowering related traits

Clusters	Plant height (cm)	Plant spread (cm)	Number of primary branches per plant	Number of secondary branches per plant	Stem diameter (mm)	Leaf area (cm^2)	Leaf biomass (g)	Photosynthetic rate (µmol/m2/sec)	Days to first flowering	Duration of flowering (days)
I	69.3	46.29	10.58	32.07	11.14	19.83	80.79	24.59	58.82	79.93
II	60.8	39.3	9.84	30.67	10.48	21.86	97.9	20.06	57.71	75.76
III	41.34	29.48	9.67	18.8	8.87	18.59	60.63	16.92	48.74	63.69
IV	70.29	46.12	13.15	35.33	12.09	28.6	97.1	24.03	52.25	110.51
V	67.14	45.1	10.13	36.96	10.91	22.65	86.32	24.86	59.31	84.75
VI	64.38	50.23	11.73	32.96	10.45	27.74	72.78	7.91	56.49	110.24
VII	76.58	40.39	9.35	31.6	10.07	47.74	150.16	14.3	75.47	47.69
Clusters	**Flower diameter (mm)**	**Flower weight (g)**	**Number of flowers / plant**	**Flower yield/plant (g)**	**Flower longevity (days)**	**Shelf life of flower (days)**	**1000 seed weight (g)**	**Seed yield /plant (g)**	**Harvest index (%)**	**Carotenoid content (mg/100g)**
I	68.46	10.33	36.77	386.52	48.64	4.46	3.47	127.85	52.09	311.79
II	55.1	7.3	36.28	259.49	44.73	4.15	2.9	106.84	49.06	408.7
III	59.77	8.39	24.97	210.96	46.9	4.02	2.82	53.87	48.63	139.58
IV	81.63	12.82	47.27	575.41	50.09	4.07	3.5	171.55	62.45	403.08
V	65.8	9.1	37.69	410.81	43.18	4.15	3.32	166.2	49.63	133.04
VI	64.82	9.84	44.33	414.36	47.8	4.11	3.18	150.43	50.86	271.75
VII	75.72	11.51	27.07	306.02	39.05	4.29	3.43	94.42	48.48	357.48

Conclusion

In the present investigation, seven divergent clusters were formed as per Mahalanobis D^2 analysis indicated a presence of wide range of diversity in marigold genotypes. On the basis of inter- cluster distance, cluster III and IV were identified as more divergent clusters and genotypes. Among all the twenty characters under study, carotenoid content (62.77%) contributed maximum towards genetic divergence followed by leaf area (6.77%) and number of flowers per plant (5.54%). Genotypes included in cluster IV showed maximum cluster means for more number of yield contributing traits under study. Among the 26 genotypes, Local Selection 15, Sonata Orange and Local Selection 2 should be used for further hybridization in heterosis in yield targeted traits with creation of wider variability.

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