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GENETIC DIVERSITY ANALYSIS IN MARIGOLD (*TAGETES* SPP.)

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Abstract

The present investigation was carried out to assess the extent of genetic variability, heritability, genetic advances and divergence using 16 marigold (*Tagetes* spp.) genotypes with eighteen characters. Moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for almost all the characters under study emphasizing the existence of variation in the population. All the characters showed higher heritability along with higher/moderate GCV and genetic advances indicating that most likely the heritability was due to additive gene effects and the genotypes under study were highly diverse and of great potential with regard to these characters, and therefore, these were more reliable for effective phenotypic selection. The inter-cluster average D^2 value was maximum between cluster I and IV followed by between cluster II and IV. However, minimum inter-cluster distance was obtained between cluster II and cluster V indicated that genotypes of cluster II and V are very close to each other. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical areas were grouped into same cluster as well as in different clusters indicating formal relationship between geographical diversity and genetic diversity.

Introduction

Marigold (*Tagetes* spp.) is one of the most important commercial flowers grown worldwide and is highly valued for their spectacular flowers, brilliant colours, delightful appearance, fragrance and is endowed with large spectrum of commercial potentialities in industrial sector. *Tagetes erecta* and *T. patula* are more commonly grown for loose flower production and used in landscape architecture due to their variable height and flower colours. It is also an important source of carotenoids which are used in poultry to intensify the colour of yolk (Kaul *et al.* 1997). It has gained popularity in India on account of its easy cultivation, wide adaptability and year-round production.

Marigold, being a cross-pollinated crop, provides abundant scope for exploitation through heterosis. The selection of superior variety depends upon the variations that exist in the population. Variability in a population with respect to character is an essential requirement for a successful breeding program. Estimation of heritability reveals the transmission of characters from one generation to another generation. Heritability alone is not useful for breeding programs; heritability along with genetic advance is pre-requisite for selection process. The adequate information on the extent of variability parameters maybe helpful to improve yield by selecting yield component traits because yield is a complex trait, whose manifestation depends on the component traits (Angadi and Archana 2014).The success of a breeding program depends on the amount of genetic variability in the germplasm and genetic relationships among desirable traits. The improvement of marigold has remained more or less stationary due to lack of good parents. Success in selection for new types depends on the extent of genetic variability, heritability, genetic

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advance and genetic divergence which is a pre-requisite for initiating appropriate breeding program in marigold.

Therefore, the present program was undertaken with a view to assess the extent of genetic variability, heritability, genetic advances and genetic divergence among 16 marigold genotypes.

Materials and Methods

The present experiment was conducted at Instructional Farm, Department of Floriculture and Landscape Architecture, College of Horticulture, Banda University of Agriculture and Technology, Banda, Uttar Pradesh, India which falls under Bundelkhand Agro-climatic zone of Zone 8-Central Plateau and Hills Region. The experimental material consisted of sixteen diverse genotypes, *viz.* Orange Winner, Valencia Yellow, Dainty Marrieta, Pusa Deep, Pusa Arpita, Local Banda Marigold-1, Local Banda Marigold-2, Local Banda Marigold-3, Pusa Narangi Gainda, Pusa Basanti Gainda, Pusa Bahar, Inca-II Gold, Bidhan Marigold-2, Punjab Gainda-1, Inca Orange and Arka Pari, was collected from ICAR-IARI, Pusa, New Delhi, PAU, Ludhiana, Punjab, BCKV, Kalyani, West Bengal, ICAR-IIHR Bengaluru, private firms and local growers of Banda. Marigold seeds were sown on raised beds, measuring 120×60×15 cm. The sowing was done on 9thOctober, 2020 and the seedlings were hardened by withdrawing the watering 2-3 days before lifting the seedlings. The transplanting was done with a spacing of 30 × 20 cm on 1st November, 2020. All the recommended package of practices were followed to grow a healthy crop.

Under this investigation, 18 characters related to vegetative growth, flower production and quality and seed yield were estimated. The biometrical observations were recorded on fifteen randomly taken plants from each variety in each replication. The mean values obtained for each character were used for determining phenotypic coefficient of variation (Burton and Devane 1953), heritability (Hanson *et al.* 1956) and expected genetic advances (Johnson *et al.* 1955). The genetic divergence analysis was carried out using the Mahalanobis's D^2 statistics (Mahalanobis 1936) and genotypes were grouped in clusters according to Tocher's method as described by Rao(1952). The intra and inter-cluster distances and variances were worked out as per method suggested by Gomez and Gomez (1983).

Results and Discussion

The analysis of variance revealed that all the eighteen characters were highly significant indicating considerable amount of genetic variability among the genotypes (Table 1).

The analysis of variance permits estimation of phenotypic and genotypic coefficients of variability for various polygenic traits. The genotypic coefficient of variation (GCV) measures the extent of variability among the different traits caused due to the inherent capacity of the genotype. The genotypic and phenotypic coefficients of variation (PCV) are required to understand the effect of environment on various polygenic traits. The high values of GCV (%) and PCV (%) were found for plant height (41.05, 41.16), inter-nodal length (41.75, 41.95), number of primary branches/plant (49.09, 49.24), number of secondary branches/plant (56.23, 56.39), number of leaves/plant (52.44, 52.47), stem diameter(22.81, 23.57), leaf area (66.48, 66.60), flower diameter (23.43, 23.80), fresh flower weight (70.04, 70.11), dry flower weight (74.29, 75.30), number of flowers per plant (55.66, 56.00),number of petals per flower (66.37, 66.42),flower yield per plant(51.56, 52.37) and seed yield per plant (61.14, 61.77), respectively. The moderate values of GCV (%) and PCV (%) were recorded for days taken to first flowering (20.00, 20.18),shelf life of flower (20.07, 20.07) and seed weight (20.36, 20.42), respectively. The low GCV % (10.35) and high PCV% (11.01) was exhibited in flower duration (Table 2).

Table 1. Analysis of variance (ANOVA) for eighteen traits in 16 genotypes of marigold.

Source of variation	DF	Plant height (cm)	Inter-nodal length (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of leaves/plant	Stem diameter (mm)	Leaf area (cm^2)	Days taken to first flowering	Flower duration (days)
Replication	2	0.79*	0.014	0.12	0.43	88.89*	0.38	0.15	7.29	1.58
Genotypes	15	92.40**	10.71**	81.17**	1367.15**	58388.07**	9.87**	277.36**	474.85**	84.94**
Error	30	0.17	0.03	0.16	2.57	17.41	0.22	0.32	2.87	3.59
SEm ±		0.23	0.10	0.23	0.89	2.33	0.26	0.32	0.95	1.05
CD (P = 0.05)		0.47	0.21	0.46	1.82	4.76	0.53	0.65	1.93	2.16
CD (P = 0.01)		0.68	0.31	0.68	2.67	6.96	0.78	0.95	2.83	3.16
	DF	Flower diameter (mm)	Fresh flower weight (g)	Dry flower weight (g)	No. of flowers/ plant	No. of petals/ flower	Flower yield per plant (g)	Shelf life of flower (days)	Seed weight (g)	Seed yield /plant (g)
Replication	2	0.40	0.13*	0.01	27.25	1.88	12.47	0.001	0.003	25.06
Genotypes	15	420.13**	38.81**	1.55**	2257.17**	16872.23**	35708.60**	1.44**	1.58**	1080.56**
Error	30	4.41	0.03	0.01	9.23	7.51	371.69	0.001	0.003	7.44
SEm ±		1.17	0.09	0.07	1.69	1.53	10.77	0.02	0.03	1.52
CD (P = 0.05)		2.39	0.19	0.13	3.46	3.12	22.01	0.05	0.06	3.11
CD (P = 0.01)		3.50	0.28	0.19	5.06	4.56	32.14	0.07	0.09	4.54

* indicates significant at P≤=0.05 and ** indicates significant at P≤=0.01 level of significance.

Table 2. Genotypic and phenotypic co-efficient of variation, heritability and genetic advance for 18 traits in 16 genotypes of marigold.

Characters	Range	GCV (%)	PCV (%)	Broad sense heritability (%)	Genetic advance as percentage of mean
Plant height (cm) at 50 DAT	5.40-21.62	41.05	41.16	99.46	84.33
Inter-nodal length (cm) at 50 DAT	2.20-6.97	41.75	41.95	99.05	85.59
No. of primary branches/ plant at 60 DAT	3.96-19.54	49.09	49.24	99.39	100.82
No. of secondary branches/ plant at 60 DAT	11.37-78.50	56.23	56.39	99.44	115.51
No. of leaves / plant at 60 DAT	9.12-555.62	52.44	52.47	99.91	107.98
Stem diameter (mm) at 60 DAT	5.01-11.62	22.81	23.57	93.62	45.46
Leaf area (cm^2)	4.43-38.68	66.48	66.60	96.65	136.71
Days taken to first flowering	43.21-86.33	20.00	20.18	98.21	40.83
Flower duration (days)	42.46-59.08	10.35	11.01	88.30	20.03
Flower diameter (mm)	35.58-74.83	23.43	23.80	96.91	47.51
Fresh flower weight (g)	1.19-11.55	70.04	70.11	99.79	144.13
Dry flower weight (g)	0.24-2.36	74.29	75.30	97.33	150.99
No. of flowers per plant	16.71-113.75	55.66	56.00	98.78	113.96
No. of petals per flowers	6.46-240.20	66.37	66.42	99.87	136.63
Flower yield per plant (g)	22.06-367.30	51.56	52.37	96.94	104.58
Shelf life of flower (days)	2.23-4.17	20.07	20.07	99.96	41.34
Seed weight (g)	2.02-4.17	20.36	20.42	99.42	41.81
Seed yield per plant (g)	10.60- 69.10	61.14	61.77	97.96	124.65

DAT- Days after transplanting.

These results suggested that characters with high GCV have high amount of genetic variability and effective for selection because the response to selection is directly proportional to the genetic variability and effective for improvement of these traits. The results of the present experiment are in conformity with the previous results as reported by Namita *et al.* (2009), Pratap *et al.* (2009), Kumar *et al.* (2014) and Kumar *et al.* (2019), in marigold. Narrow differences between GCV and PCV were observed for all the characters except stem diameter, flower duration, dry flower weight, number of flowers per plant and flower yield per plant revealed that variability existing among different genotypes of marigold was mainly due to genetic makeup and there was less environmental influence on the expression of these traits. Heritability in broad sense and genetic advances as per cent mean was calculated for 18 characters. Heritability and genetic advances are important selection parameters. Heritability estimates along with genetic advances are more useful in predicting the gain under selection than heritability estimates alone (Robinson *et al.* 1949).

In the present study, the magnitude of heritability ranged from 88.30 to 99.96 and genetic advances was ranged from 20.03 to 150.99 (Table 2). The higher magnitude of heritability was exhibited in all the characters, *viz.* plant height (99.46%), inter-nodal length (99.05%), number of primary branches/plant (99.39%), number of secondary branches/plant (99.44%), number of leaves/plant (99.91%), stem diameter (93.62%), leaf area (96.65%), days taken to first flowering (98.21%), flower duration (88.30%), flower diameter (96.91%), fresh flower weight (99.79%), dry flower weight (97.33%), number of flowers per plant (98.78%), number of petals per flower (99.87%), flower yield per plant (96.94%), shelf life of flowers (99.96%), seed weight (99.42%) and seed yield per plant (97.96%). This indicates good correspondence between genotypic and phenotypic values and thereby low environmental effect on the expression of these characters. These results are in agreement with the findings of Mathew *et al.* (2005), Namita *et al.* (2009), Yuvraj and Dhatt (2014) andTamut and Singh (2019) in marigold.

Heritability estimates alone do not provide reliable information about the gene action governing the expression of a particular character and also it does not provide the information of the amount of genetic progress that would result from the selection of best individuals. Burton (1952) pointed out that heritability in combination with intensity of selection and amount of variability present in the population influences the genes to be obtained from the selection. Thus, a genetic advance is another important selection parameter. Highest genetic advances over mean were recorded for all the characters, except flower duration. The high magnitude of heritability was coupled with high to moderate expected genetic advances, indicated that the predominance of additive gene action for these traits and early generation selection could be practical to improve these characters due to reliability of additive gene action for selection. Similar results were reported by Namita *et al.* (2009), Kumar *et al.* (2014) and Singh *et al.* (2014) in marigold.

On basis of D^2 analysis (Mahalanobis 1936), the sixteen genotypes were grouped into five clusters. The cluster III was very large and comprised of six genotypes, cluster II consisted of four genotypes, cluster IV comprised of three genotypes, cluster I comprised two genotypes and cluster V was solitary (Table 3). The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity. It revealed that genetic diversity has nothing to do with geographical diversity as the genotypes from different parts of the country were accommodated in the same clusters. There are forces other than geographical separation, such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation, which are responsible for diversity. The magnitude of diversity among parents

determines the inherent potential of a cross. Therefore, the selection of a parent based on the genetic divergence would be desirable for creating the maximum variability. Similar results were also reported by Kavitha and Anburani (2009), Giri *et al.* (2019) and Mahanta *et al.* (2019) in marigold.

Table 3. Distribution of 16 genotypes of marigold into five different clusters.

Cluster	No.of genotypes	Genotypes
I	2	Inca-Gold and Inca Orange
II	4	Dainty Marrieta, Arka Pari, Valencia Yellow and Orange Winner
III	6	Pusa Bahar, Punjab Gainda-1, Pusa Basanti Gainda, Pusa Narangi Gainda, Bidhan Marigold-2 and Local Banda Marigold-3
IV	3	Local Banda Marigold-1, Local Banda Marigold-2 and Pusa Arpita
V	1	Pusa Deep

Table 4. Average intra and inter-cluster (D^2) value for 16 genotypes of marigold.

Cluster	I	II	III	IV	V
I	95.54	8246.08	3917.57	12786.63	6984.64
II		571.78	6096.19	10529.18	2307.83
III			1085.75	5315.62	2394.57
IV				1056.22	4626.56
V					0.0

Table 5. Cluster means for eighteen characters in sixteen genotypes of marigold.

Cluster number	Plant height (cm)	Inter-nodal length (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of leaves/ plant	Stem diameter (mm)	Leaf area (cm^2)	Days taken to first flowering	Flower duration (days)
I	10.57	2.91	6.08	19.81	176.44	7.77	4.91	55.35	53.29
II	6.14	2.36	6.37	25.30	122.53	5.83	6.86	51.62	43.06
III	15.92	5.62	10.46	32.57	275.01	8.14	213.41	62.84	55.04
IV	21.05	6.29	18.60	68.94	512.00	10.22	18.18	84.12	49.11
V	11.77	4.50	13.11	63.83	226.71	7.44	10.98	56.66	48.66
	Flower diameter (mm)	Fresh flower weight (g)	Dry flower weight (g)	No. of flowers/ plant	No. of petals/ flower	Flower yield/ plant (g)	Shelf life of flower (days)	Seed weight (g)	Seed yield/plant (g)
I	74.55	11.52	2.33	29.85	231.07	352.47	2.02	2.02	10.93
II	38.09	1.54	0.31	40.62	24.51	64.23	3.78	3.78	18.27
III	51.11	7.09	1.29	35.38	161.68	254.76	3.99	4.07	30.80
IV	47.37	2.46	0.43	98.37	75.58	235.19	3.26	3.09	64.00
V	53.66	3.04	0.45	57.29	50.46	171.79	2.97	4.11	23.23

Intra and inter-cluster distance (D^2) were computed for five clusters and presented in Table 4. The inter-cluster average D^2 value was maximum 12786.63 between cluster I and IV followed by 10529.18 between cluster II and IV. The minimum inter-cluster distance was obtained between cluster II and V (2307.83) which indicates that genotypes of cluster II and V were very close to each other. The maximum intra-cluster distance was observed in cluster III (1085.75) indicating differences in genotypes within the cluster. Similar results were portrayed by Kavitha and Anburani (2009) and Patel *et al.* (2018) in marigold.

A considerable range of variation was found in cluster mean value with respect to all eighteen characters embodied in Table 5. A close perusal of cluster means for different characters indicated that cluster IV had highest cluster mean for plant height (21.05 cm), inter-nodal length (6.29 cm), number of primary branches per plant (18.60), number of secondary branches per plant (68.94), number of leaves per plant (512.00), stem diameter (10.22 mm), days taken to first flowering (84.12), number of flowers per plant (98.37) and seed yield per plant (64.00). However, the cultivars included in cluster III showed highest cluster mean for leaf area (213.41cm^2), flower duration (55.04 days), shelf life of flower (3.99 days) and seed weight (4.07 g). Cluster I exhibited maximum mean value for flower diameter (74.55 mm), fresh flower weight (11.52 g), dry flower weight (2.33 g), number of petals per flower (231.07 g) and flower yield per plant (352.47 g). These results indicated that different clusters were superior for different characters under study.

Table 6. Per cent contribution of eighteen characters towards genetic divergence in marigold.

Character	Contribution (%)
Plant height (cm)	0.0
Inter-nodal length (cm)	0.0
No. of primary branches/plant	0.83
No. of secondary branches/plant	2.50
No. of leaves/plant	24.17
Stem diameter (mm)	0.0
Leaf area (cm^2)	8.33
Days taken to first flowering	0.0
Flower duration (days)	0.0
Flower diameter (mm)	0.0
Fresh flower weight (g)	34.17
Dry flower weight (g)	0.0
No. of flowers/plant	0.0
No. of petals/flowers	7.50
Flower yield/plant (g)	6.67
Shelf life of flower (days)	10.83
Seed yield/plant (g)	2.50
Seed weight (g)	2.50

The relative contribution of different quantitative characters under evaluation towards the expression of genetic divergence is given in Table 6. The trait fresh flower weight contributed maximum (34.17%) towards genetic divergence followed by number of leaves per plant

(24.17 %), shelf life of flower (10.83 %), leaf area (8.33 %), number of petals per flower (7.50 %) and flower yield per plant (6.67 %). Based on inter-cluster distant crosses and selection from more diverse parents expected to get better genotype, these clusters constituent genotype could be used in yield improvement. The highest inter-cluster distance between cluster I and IV could be expected to exert high heterosis effect in the hybrids when crossed and consequently might generate desirable segregates. The characters which contributed maximum in genetic divergence *viz.* fresh flower weight, number of leaves per plant, shelf life of flower, leaf area, number of petals per flower and flower yield per plant can be used in selecting diverse parent for hybridization programs.

Thus, apparently contribution of additive gene effect in the expression of these traits was indicated. Consequently, improvement in these characters through direct selection to develop better cultivars of marigold can easily be done.

Finally, it could be concluded that characters having high heritability with high genetic advance *i.e.* dry flower weight, fresh flower weight, leaf area, number of petals per flowers, seed yield per plant, number of secondary branches per plant, number of flowers per plant and number of leaves per plant must be considered during selection for effective breeding program. In addition, the genotypes from cluster I and IV deserve to be considered as potent parents for flower and seed yield in hybridization program to obtain high-yielding segregants in marigold. Therefore, progeny derived from such diverse crosses are expected to show greater genetic variability and wider scope for isolating transgressive segregants in advanced generations.

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