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Assessment of Genetic Variability and Association of Traits in French Marigold (*Tagetes patula* L.) Genotypes

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ABSTRACT

The experiment was conducted during *rabi* season (September, 2020–February, 2021) at Floriculture and Landscape Architecture experimental plots, University of Horticultural Sciences, Bagalkot, Karnataka, India to study the extent of genetic diversity present in the selected twenty-five genotypes for the experiment. Results obtained for heritability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance as percent of mean indicated higher values for majority of the traits studied in the experiment and their importance as basis for selection in the breeding program. Correlation studies for various parameters among the genotypes recorded positive and significant phenotypic and genotypic correlation with almost all the traits and non-significant and positive correlation was noticed for trait flower diameter. Phenotypic and genotypic path coefficients of flower yield with majority of other traits showed positive effects and their implications for further breeding was indicated. The outcome of genetic divergence gives scanty of genetic variability in the genotypes, except one all twenty-four were fallen in the same cluster. The Significance of selecting genotypes with a broader genetic base was helpful for future breeding programs. The study concludes that, yield is complex trait that is dependent on the other growth attributes, correlation and path studies gave the effect of different attributes on yield. Most of the traits were controlled by additive genes and therefore there is an opportunity to practice early selection in French marigold for breeding programs.

KEYWORDS: Breeding, genetic divergence, heritability, path coefficient, traits

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1. INTRODUCTION

Marigold (*Tagetes* spp.), a hardy commercial annual flower crop belongs to family compositae (Anuja and Jahnvi, 2012). This crop is native to South and Central America mainly Mexico. It was introduced to India by Portuguese during 16th century. The genus name gave after 'Tages' named demigod famous for his beauty. The genus *Tagetes* comprises of about 33 species, major commercial species are *Tagetes erecta* L. (African marigold) and *Tagetes patula* L. (French marigold) (Sharma and Jadagoudar, 2021). *Tagetes erecta* L. is taller in nature with colour range from lemon yellow, golden yellow, orange and *Tagetes patula* L. is shorter with yellow to mahogany-red colour flowers (Poulose et al., 2020).

Marigold is a traditional loose flower crop grown in India (Patel et al., 2020). It is choice crop for small and marginal farmers owing to its wider adaptability and ease in cultivation (Panwar et al., 2021). It is used for bedding, pot plant, rockery, edging in landscape gardening (Usha Bharathi et al., 2014 and Bhusaraddi et al., 2022) and the vibrant flower colour attracts pollinators. The carotenoids are having nutraceutical and pharmaceutical importance (Gupta et al., 2022). Carotenoids also have dietary importance in the treatment of tumor and skin diseases (Sharma et al., 2022). Compound α-tertheinyl inhibits the growth of root knot nematode without much pesticide usage and suggested as trap crop for monitoring the *Helicoverpa* incidence in vegetables and effectively checks parthenium. As marigold is a versatile crop farmer can be benefited by various ways so, identification of cultivars having wide genetic base with respect to qualitative and quantitative traits will be helpful for the breeders in further improvements.

The crop can be improved and developed for new varieties upon the immense genetic variability. Based on need, different genotypes of marigold available are evaluated for growth, flowering, yield and quality, present in the different agro- climatic zones. There are remarkable genetic variations in the growth and flowering attributes can used for commercial exploitation. Plant breeder can select and develop new varieties upon variability in population with respect to qualitative and quantitative traits will be beneficial (Pandey et al., 2022). Evaluation and selection of available genotypes is helpful for development of high yielding variety with novel colour.

The phenotypic expression of traits depends on relative influence of the heritable and non-heritable components (Latha and Dharmatti, 2018). It is difficult to tell how much of the variability is heritable and non-heritable. So overall, one cannot say variation as genetic and non-genetic components and to standardize this by obtaining the coefficients of phenotypic and genotypic variability (Kumar et al., 2014). Correlation coefficient is the significant selection parameter in breeding as it provides degree of relationship between variables and its nature (Dey et al., 2021). Correlation one can only give the relationship of independent variable with the dependent variable without specific causes and effects. Path coefficient analysis will effectively differentiate between correlations that are real (genetic effects) and inflated (environmental effects). Genetic divergence analysis estimate provides the extent of variability in the selected genotypes. These studies help to select superior combinations as parents in breeding program (Mahanta et al., 2019). The present study was aimed with the objectives: To know the genotypic and phenotypic variability of growth, yield and quality parameters in different genotypes and to study the association of characters through correlation and path coefficient analysis, further genetic divergence between the genotypes.

2. MATERIALS AND METHODS

The current study was conducted with twenty-five different French marigold genotypes designed in randomized complete block design (RCBD) layout in the floriculture field at University of Horticulture Sciences, Bagalkot during September, 2020–February, 2021. The genetic variability was estimated for 18 different quantitative and qualitative traits at the time of flowering.

Genotypic, phenotypic and environmental variances were computed according to Burton and Devane (1953). PCV and GCV values calculated with method suggested by Sivasubramanian and Menon (1973). Broad-sense heritability was estimated upon formula of Johnson et al. (1955). The heritability percentage was categorized as low, moderate and high as suggested by Robinson et al. (1949). i.e., 0–30%=Low, 30–60%=Moderate and 60% and above 60%=High and the extent of genetic advance estimated according to Johnson et al. (1955).

The genotypic (rg) and phenotypic (rp) correlations were calculated using formula by AL-Jibouri et al. (1958). The calculated 'r' value was compared with table 'r' value at (n^{-2}) degrees of freedom for significance at 0.05 and 0.01 probability levels, where 'n' is number of observations.

Path coefficient analysis was carried using correlation coefficient to know direct and indirect effects of different traits on yield components as suggested by Wright (1921) and illustrated by Dewey and Lu (1959) and based on the scale given by Lenka and Misra (1973).

D^2 statistics is generally used for analysis of genetic divergence between populations given by Mahalanobis (1936). The genetic distance in any populations can be estimated as $D^2=(\lambda^{ij})$ where, (λ^{ij}) is the reciprocal matrix to the common dispersion matrix and 'i' is the difference between the mean values of the two populations for the i^{th} character. This quantity is estimated by D^2 statistic (Majumdar and Rao, 1958) as $D^2=(S^{ij})$ di dj where, S^{ij} is the sample estimate of (δ^{ij}) di and δi. As the formulae requires the inversion of the matriXof fourteenth order for calculation, simple calculation is followed to standardize correlated variable. From D^2 values obtained from analysis, the entire genotypes were classified into distinct clusters, grouping together the less divergent genotypes according to Tocher's method.

3. RESULTS AND DISCUSSION

Twenty-five genotypes were evaluated with eighteen different morphological traits. The data was recorded at grand growth stage of plants. The data was analyzed, results were tabulated and discussed.

3.1. Estimation of genetic variability parameters

The genetic variability was estimated for growth, flowering and yield attributes of different genotypes were given in Table.1. Range of variation recorded for all the traits in the study indicating sufficient amount of variability in the studied genotypes. The values of phenotypic coefficient of variance were found maximum than genotypic coefficient of variance for all the characters (Pandey et al., 2022). These GCV and PCV indicate the extent of variability due to genotypes and environment for different traits. Higher heritability estimate helps the breeder in selecting best genotypes along with the genetic advance as per cent mean which indicates the additive gene effects. Higher (>20%) genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were recorded for plant height, plant spread from east to west and north to south, leaf length, width, stem girth, flower yield plant^{-1}, plot^{-1} and hector^{-1}, individual flower weight and shelf life. Moderate (10 –20%) recorded for primary and secondary branches, days to first flowering, days to 50% flowering, number of flowers plant^{-1} and flower diameter. The lowest (0–10%) was reported for flowering duration.

Higher broad sense heritability (more than 60%) combined with maximum (20% and above) genetic advance as percent

Table 1: Genetic variability estimates for morphological parameters at grand growth stage

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
			Max	Min					
1.	Plant height (cm)	31.93	50.54	23.07	22.59	23.88	89.54	14.06	44.04
2.	Plant spread[E-W] (cm)	34.68	55.57	26.48	22.20	24.62	81.32	14.30	41.24
3.	Plant spread [N-S] (cm)	33.02	52.27	25.01	21.54	23.84	81.67	13.24	40.11
4.	Primary branches	14.75	22.4	12.3	18.19	19.02	91.47	5.28	35.83
5.	Secondary branches	28.71	44.5	21.2	19.76	20.34	94.39	11.35	39.54
6.	Leaf length (cm)	6.22	18.87	3.71	48.70	50.48	93.09	6.02	96.8
7.	Leaf width (cm)	4.67	14.1	2.43	50.77	52.49	93.55	4.73	98.15
8.	Stem girth (mm)	6.72	13.35	4.07	32.19	32.32	99.16	4.44	66.03
9.	Days to first flowering	31.66	52.40	27.50	19.32	19.45	98.71	12.52	39.54
10.	Days to 50% flowering	38.80	61.50	31.50	17.54	17.61	99.28	13.97	36.01
11.	Flowering Duration (days)	45.60	49.00	39.50	5.025	5.24	91.97	4.53	9.93
12.	Number of flowers plant^{-1}	118.87	170.70	91.30	15.18	15.45	96.48	36.52	30.72
13.	Flower yield plant^{-1} (g)	236.84	392.10	172.97	28.04	28.29	98.23	135.6	57.25
14.	Flower yield plot^{-1} (kg)	5.69	10.19	4.42	29.94	30.35	97.28	3.46	60.82
15.	Flower yield ha^{-1} (ton)	9.66	16.01	7.05	28.06	28.31	98.22	5.54	57.29
16.	Individual flower weight (g)	1.51	4.39	0.78	60.13	63.86	88.63	1.75	116.61
17.	Flower diameter (mm)	35.50	45.03	30.17	12.22	12.72	92.35	8.59	24.19
18.	Shelf life (days)	3.28	4.95	2.25	22.91	23.07	98.51	1.54	46.81

GCV: Genotypic coefficient of variance; h^2: Heritability (Broad sense); PCV: Phenotypic coefficient of variance; GAM: Genetic advance as percent mean; GA: Genetic advance; GCV and PCV Low: 0–10%, Moderate: 10–20% and High: 20% and above; Heritability: Low: 0–30%, Moderate: 30–60% and High: more than 60%; GAM: Low: 0–10%, Moderate: 10–20% and High: 20% and above mean (GAM) was reported for most of the parameters excluding flowering duration, which showed higher heritability with low (0 –10%) genetic advance as percent mean. Higher PCV and GCV indicate wider genetic variability with less environmental influence. Highest heritability with higher genetic advance as percent mean implied the role of additive gene effects also reported by Latha and Dharmatti (2018), Pandey et al. (2022) and Poulose et al. (2020) in marigold.

3.2. Correlation coefficient analysis

Character associations may vary with environmental conditions. Association of economically important yield characters of quantitative nature is quite used as basis for selection. Since, breeder has to handle a very large population in achieving the objectives, it is difficult to screen the population for individual quantitative trait. Therefore, it is required to have the estimates of correlation of yield and different morphological traits for that the genotypes could be assessed visually or measured easily. The analysis correlation leads to identify the ways to improve yield associated highly correlated morphological traits. The relationship of yield and associated traits helps in selection of parents in breeding program. The proper association can only obtain with genotypic correlation as it is devoid of environmental influence. Correlation studies for various parameters in selected genotypes recorded positive and significant phenotypic and genotypic correlation with most of the morphological traits. While, positive and non-significant correlation was recorded for flower diameter. Flowering duration showed negative and significant correlation recorded in Table. 2 and 3. The proximal results were given by Karuppaiah and Senthil Kumar (2010), Anuja and Jahnvi (2012), Kumar et al. (2014), Choudhary et al. (2015), Sahu et al. (2018) and Poulose et al. (2020). The maximum positive non-significant association of flower yield per plant with flower diameter. While, positive and significant correlation with plant height and plant spread was reported by Sharma and Raghuvanshi (2011).

3.3. Path coefficient analysis

Path analysis aids in division of total correlation coefficient into direct and indirect effects, leads to understand the effect of individual traits. This was carried by taking yield as dependent variable over independent variables and nature of contribution to increase yield. Path analysis (Table. 4 and 5) for different traits among the genotypes studied showed positive and direct effect for flower yield plot^{-1} at phenotypic and genotypic levels was observed with most of the morphological traits recorded. The maximum direct positive effect was by flower yield per plant (3.7832) at genotypic level and attribute flower yield per ha showed

Table 2: Phenotypic correlation of flower yield and its contributing traits in French marigold (*Tagetes patula* L.) genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9
X1	1								
X2	0.919**	1							
X3	0.905**	0.985**	1						
X4	0.881**	0.849**	0.822**	1					
X5	0.733**	0.781**	0.767**	0.697**	1				
X6	0.723**	0.754**	0.721**	0.769**	0.589**	1			
X7	0.731**	0.783**	0.751**	0.778**	0.597**	0.970**	1		
X8	0.749**	0.815**	0.791**	0.761**	0.743**	0.880**	0.896**	1	
X9	0.421**	0.387**	0.335*	0.442**	0.276	0.685**	0.654**	0.589**	1
X10	0.089	0.077	0.003	0.116	0.089	0.278	0.227	0.258	0.546**
X11	0.434**	0.423**	0.385**	0.437**	0.407**	0.606**	0.597**	0.641**	0.769**
X12	0.555**	0.591**	0.601**	0.449**	0.803**	0.234	0.232	0.385**	-0.129
X13	0.636**	0.631**	0.591**	0.658**	0.469**	0.850**	0.881**	0.826**	0.814**
X14	0.639**	0.626**	0.587**	0.667**	0.425**	0.832**	0.851**	0.814**	0.784**
X15	-0.342*	-0.275	-0.272	-0.309*	-0.333*	-0.505**	-0.427**	-0.489**	-0.515**
X16	0.750**	0.758**	0.736**	0.734**	0.850**	0.438**	0.449**	0.631**	0.216
X17	0.694**	0.712**	0.686**	0.725**	0.813**	0.393**	0.419**	0.581**	0.207
X18	0.750**	0.758**	0.737**	0.735**	0.851**	0.438**	0.449**	0.630**	0.217

Table 2: Continue...

	X10	X11	X12	X13	X14	X15	X16	X17	X18
X10	1								
X11	0.447**	1							
X12	:0.076	0.083	1						
X13	0.372**	0.697**	0.067	1					
X14	0.361**	0.666**	0.052	0.972**	1				
X15	:0.179	:0.461**	:0.121	:0.427**	:0.425**	1			
X16	0.157	0.416**	0.734**	0.350*	0.354*	:0.232	1		
X17	0.172	0.407**	0.688**	0.339*	0.343*	:0.11	0.973**	1	
X18	0.157	0.415**	0.734**	0.350*	0.354*	:0.231	1.000**	0.973*	1

Critical rp value at 5%= 0.276; *Significant at p=0.05, rp value at 1%= 0.358; **Significant at p=0.01; X1: Plant height (cm); X2: Plant spread from east to west (cm); X3: Plant spread from north to south (cm); X4: Primary branches; X5: Secondary branches; X6: Leaf length (cm); X7: Leaf width (cm); X8: Stem girth (mm); X9: Individual flower weight (g); X10: Flower diameter (mm); X11: Shelf life (days); X12: Number of flowers plant^{-1}; X13: Days to first flowering; X14: Days to 50% flowering; X15: Flowering duration; X16: Flower yield plant^{-1} (g); X17: Flower yield plot^{-1} (kg); X18: Flower yield ha^{-1} (t)

direct positive effect (3.1874) at phenotypic level. The higher indirect effect Flower yield ha^{-1} (3.7832) at genotypic level and flower yield plant^{-1} (3.1873) at phenotypic level. This shows the association between the traits with flower yield plot^{-1}. The negative and direct effect were recorded with traits plant height, plant spread from east to west, leaf length, stem girth and days to first flowering. The higher positive direct effects from these traits explain higher association between these traits and flower yield. The significant direct effects were found with various traits on yield trait gives higher opportunity to increase yield. The proximal results were observed by Anuja and Jahnvi

Table 3: Genotypic correlation of flower yield and its contributing traits in different French marigold (*Tagetes patula* L.) genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9
X1	1								
X2	1.004**	1							
X3	0.984**	1.003**	1						
X4	0.967**	0.971**	0.931**	1					
X5	0.809**	0.878**	0.862**	0.738**	1				
X6	0.827**	0.838**	0.798**	0.838**	0.619**	1			
X7	0.802**	0.835**	0.800**	0.858**	0.627**	0.989**	1		
X8	0.801**	0.893**	0.868**	0.801**	0.761**	0.908**	0.925**	1	
X9	0.443**	0.377**	0.313*	0.470**	0.282*	0.745**	0.698**	0.617**	1
X10	0.086	0.05	0.04	0.146	0.111	0.301*	0.241	0.275	0.589**
X11	0.461**	0.453**	0.418**	0.455**	0.418**	0.635**	0.615**	0.646**	0.812**
X12	0.591**	0.648**	0.667**	0.459**	0.864**	0.246	0.254	0.395**	-0.131
X13	0.651**	0.690**	0.641**	0.679**	0.486**	0.898**	0.922**	0.836**	0.855**
X14	0.683**	0.708**	0.666**	0.698**	0.444**	0.871**	0.891**	0.824**	0.846**
X15	-0.417**	-0.360*	-0.341*	-0.329*	-0.330*	-0.553**	-0.478**	-0.512**	-0.601**
X16	0.791**	0.826**	0.802**	0.771**	0.876**	0.463**	0.468**	0.640**	0.211
X17	0.738**	0.769**	0.742**	0.766**	0.837**	0.417**	0.439**	0.591**	0.201
X18	0.792**	0.826**	0.802**	0.771**	0.876**	0.463**	0.468**	0.640**	0.211

Table 3: Continue...

	X10	X11	X12	X13	X14	X15	X16	X17	X18
X10	1								
X11	0.476**	1							
X12	-0.094	0.087	1						
X13	0.385**	0.704**	0.066	1					
X14	0.379**	0.673**	0.047	0.982**	1				
X15	-0.187	-0.492**	-0.14	-0.447**	-0.447**	1			
X16	0.151	0.420**	0.754**	0.352*	0.358*	-0.247	1		
X17	0.167	0.410**	0.712**	0.343*	0.348*	-0.119	0.975**	1	
X18	0.15	0.419**	0.754**	0.352*	0.357*	-0.247	1.000**	0.975**	1

Critical rp value at 5%= 0.276; *Significant at p=0.05, rp value at 1%= 0.358; **Significant at p=0.01; X1: Plant height (cm); X2: Plant spread from east to west (cm); X3: Plant spread from north to south (cm); X4: Primary branches; X5: Secondary branches; X6: Leaf length (cm); X7: Leaf width (cm); X8: Stem girth (mm); X9: Individual flower weight (g); X10: Flower diameter (mm); X11: Shelf life (days); X12: Number of flowers plant^{-1}; X13: Days to first flowering; X14: Days to 50% flowering; X15: Flowering duration; X16: Flower yield plant^{-1} (g) X17: Flower yield plot^{-1} (kg); X18: Flower yield ha^{-1} (ton)

(2012), Choudhary et al. (2015), Patel et al. (2018), Sahu et al. (2018) and Poulose et al. (2020).

3.4. Divergence analysis

Diversity can ensure sustainability and improvement of crops. However, it is most difficult task for the breeder to select suitable and genetically variable parents. Mahalanobis D^2 statistics was used to analyze the genetic diversity which provides clustering of varieties into different groups exhibiting genetic distance between and within groups, hence facilitates selection of varieties from distant groups as parents in breeding programme. The resultant hybrids are expected to show higher heterosis for yield and other economical traits Mahanta et al. (2019).

The cluster I was biggest with 24 genotypes while the

Table 4: Phenotypic path coefficient of flower yield and its contributing traits in different French marigold (*Tagetes patula* L.) genotype

	X1	X2	X3	X4	X5	X6	X7	X8	X9
X1	-0.1692	-0.0513	0.0446	0.1668	0.0931	-0.0975	0.0694	-0.0870	0.0025
X2	-0.1555	-0.0558	0.0486	0.1607	0.0991	-0.1016	0.0744	-0.0947	0.0023
X3	-0.1532	-0.055	0.0493	0.1555	0.0974	-0.0971	0.0713	-0.0919	0.0020
X4	-0.1491	-0.0474	0.0405	0.1893	0.0885	-0.1037	0.0739	-0.0883	0.0027
X5	-0.1241	-0.0436	0.0378	0.1319	0.1269	-0.0793	0.0567	-0.0863	0.0017
X6	-0.1224	-0.0421	0.0355	0.1457	0.0747	-0.1348	0.0922	-0.1022	0.0041
X7	-0.1236	-0.0437	0.0370	0.1473	0.0758	-0.1308	0.0950	-0.1040	0.0039
X8	-0.1268	-0.0455	0.0390	0.1440	0.0943	-0.1187	0.0851	-0.1161	0.0035
X9	-0.0712	-0.0216	0.0165	0.0837	0.0350	-0.0923	0.0622	-0.0683	0.0060
X10	-0.0150	-0.0043	0.0014	0.0219	0.0113	-0.0374	0.0216	-0.0299	0.0033
X11	-0.0734	-0.0236	0.019	0.0827	0.0517	-0.0817	0.0567	-0.0744	0.0046
X12	-0.0939	-0.033	0.0296	0.0850	0.1020	-0.0315	0.0221	-0.0447	-0.0008
X13	-0.1077	-0.0352	0.0291	0.1245	0.0596	-0.1146	0.0837	-0.0959	0.0049
X14	-0.1081	-0.0349	0.0290	0.1262	0.0540	-0.1122	0.0809	-0.0945	0.0047
X15	0.0579	0.0153	-0.0134	-0.0585	-0.0422	0.0681	-0.0406	0.0568	-0.0031
X16	-0.1269	-0.0423	0.0363	0.1390	0.1080	-0.0590	0.0427	-0.0733	0.0013
X17	-0.1270	-0.0423	0.0363	0.1391	0.108	-0.0590	0.0427	-0.0732	0.0013

Table 4: Continue...

	X10	X11	X12	X13	X14	X15	X16	X17	Rg
X1	0.0020	0.0261	-0.0203	-0.0353	0.0786	-0.0425	-1.6777	2.3917	0.694**
X2	0.0017	0.0254	-0.0216	-0.0350	0.0770	-0.034	-1.6954	2.4165	0.712**
X3	0.0001	0.0231	-0.0220	-0.0328	0.0723	-0.0338	-1.6469	2.3476	0.686**
X4	0.0026	0.0262	-0.0164	-0.0365	0.0821	-0.0384	-1.6430	2.3417	0.725**
X5	0.0020	0.0245	-0.0294	-0.0261	0.0524	-0.0414	-1.9023	2.7115	0.813**
X6	0.0062	0.0364	-0.0085	-0.0472	0.1024	-0.063	-0.9798	1.3958	0.393**
X7	0.0051	0.0359	-0.0085	-0.0489	0.1048	-0.0531	-1.0043	1.4313	0.419**
X8	0.0058	0.0385	-0.0141	-0.0459	0.1002	-0.0608	-1.4113	2.0094	0.581**
X9	0.0122	0.0462	0.0047	-0.0452	0.0965	-0.0640	-0.4841	0.6903	0.207
X10	0.0224	0.0267	0.0028	-0.0206	0.0445	-0.0222	-0.3515	0.4989	0.172
X11	0.01	0.0601	-0.0030	-0.0387	0.0820	-0.0574	-0.9312	1.3238	0.407**
X12	-0.002	0.0049	-0.0366	-0.0037	0.0064	-0.0151	-1.6415	2.3410	0.688**
X13	0.0083	0.0419	-0.0024	-0.0555	0.1196	-0.0531	-0.7823	1.1145	0.339*
X14	0.0081	0.0400	-0.0019	-0.0540	0.1231	-0.0529	-0.7921	1.1275	0.343*
X15	-0.004	-0.0277	0.0045	0.0237	-0.0523	0.1244	0.5180	-0.7366	-0.11
X16	0.0035	0.0250	-0.0268	-0.0194	0.0436	-0.0288	-2.2368	3.1873	0.973**
X17	0.0035	0.0250	-0.0268	-0.0194	0.0435	-0.0287	-2.2368	3.1874	0.973**

Diagonal values indicate direct effect; Residual effect=0.0238; X1: Plant height (cm); X2: Plant spread from east to west (cm); X3: Plant spread from north to south (cm); X4: Primary branches; X5: Secondary branches; X6: Leaf length (cm); X7: Leaf width (cm); X8: Stem girth (mm); X9: Individual flower weight (g); X10: Flower diameter (mm); X11: Shelf life (days); X12: Number of flowers plant^{-1}; X13: Days to first flowering; X14: Days to 50% flowering; X15: Flowering duration; X16: Flower yield plant^{-1} (g) X17: Flower yield plot^{-1} (kg

Table 5: Genotypic path coefficient of flower yield and its contributing traits in different French marigold (*Tagetes patula* L.) genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9
X1	-0.1217	-0.070	-0.0645	0.3051	0.1951	-0.6435	0.6101	-0.0177	0.1378
X2	-0.1222	-0.07	-0.0657	0.3064	0.2118	-0.6517	0.6351	-0.0197	0.1173
X3	-0.1198	-0.070	-0.0656	0.2938	0.2078	-0.6205	0.6085	-0.0191	0.0973
X4	-0.1177	-0.0680	-0.0611	0.3156	0.1780	-0.6519	0.6526	-0.0177	0.1464
X5	-0.0985	-0.0615	-0.0565	0.2329	0.2412	-0.4813	0.4768	-0.0168	0.0878
X6	-0.1007	-0.0586	-0.0523	0.2645	0.14925	-0.7779	0.7520	-0.0200	0.2319
X7	-0.0976	-0.0584	-0.0525	0.2708	0.1512	-0.7691	0.7606	-0.0204	0.2173
X8	-0.0976	-0.0625	-0.0569	0.2529	0.1836	-0.7062	0.7038	-0.0221	0.1919
X9	-0.0539	-0.0264	-0.0205	0.1484	0.0680	-0.5794	0.5308	-0.0136	0.3113
X10	-0.0105	-0.0035	0.0026	0.0460	0.0267	-0.2344	0.1834	-0.0061	0.1834
X11	-0.0561	-0.032	-0.0274	0.1436	0.1008	-0.4943	0.4680	-0.0143	0.2529
X12	-0.0720	-0.0453	-0.0438	0.1447	0.2085	-0.1916	0.1935	-0.0087	-0.0409
X13	-0.0792	-0.0483	-0.0420	0.2144	0.1171	-0.6984	0.7012	-0.0185	0.2661
X14	-0.0831	-0.0496	-0.0437	0.2203	0.1071	-0.6776	0.6775	-0.0182	0.2633
X15	0.0507	0.0252	0.0224	-0.1039	-0.0797	0.4299	-0.3632	0.0113	-0.1871
X16	-0.0963	-0.0578	-0.0526	0.2434	0.2114	-0.3599	0.3560	-0.0141	0.0667
X17	-0.0964	-0.0578	-0.0526	0.2434	0.2114	-0.3599	0.3561	-0.0141	0.0657

Table 5: Continue...

	X10	X11	X12	X13	X14	X15	X16	X17	Rg
X1	-0.0009	0.0123	0.0052	-0.4160	0.2382	-0.0663	2.9943	-2.3595	0.738**
X2	-0.0005	0.0120	0.0057	-0.4411	0.2471	-0.0572	3.1245	-2.4621	0.769**
X3	0.0004	0.0111	0.0059	-0.4097	0.2325	-0.0542	3.0347	-2.3908	0.742**
X4	-0.0016	0.0121	0.0040	-0.4343	0.2436	-0.0524	2.9173	-2.2991	0.766**
X5	-0.0012	0.0111	0.0076	-0.3105	0.1549	-0.0525	3.3158	-2.6122	0.837**
X6	-0.0033	0.0169	0.0022	-0.5740	0.3034	-0.0879	1.7503	-1.3790	0.417**
X7	-0.0026	0.0164	0.0022	-0.5895	0.3108	-0.0759	1.7710	-1.3953	0.439**
X8	-0.0030	0.0172	0.0035	-0.5348	0.2874	-0.0814	2.4221	-1.9068	0.591**
X9	-0.0065	0.0216	-0.0012	-0.5464	0.2950	-0.0956	0.7983	-0.6287	0.201
X10	-0.0110	0.0127	-0.0008	-0.2462	0.1321	-0.0297	0.5696	-0.4477	0.167
X11	-0.0052	0.0266	0.0008	-0.4503	0.2349	-0.0782	1.5884	-1.2485	0.410**
X12	0.0010	0.0023	0.0088	-0.0425	0.0162	-0.0223	2.8507	-2.2468	0.712**
X13	-0.0042	0.0187	0.0006	-0.6394	0.3427	-0.0711	1.3327	-1.0492	0.343*
X14	-0.0042	0.0179	0.0004	-0.6280	0.3489	-0.0712	1.3532	-1.0651	0.348*
X15	0.0021	-0.013	-0.0012	0.2859	-0.156	0.1591	-0.9363	0.7355	-0.119
X16	-0.0017	0.0112	0.0066	-0.2252	0.1248	-0.0394	3.7832	-2.9806	0.975**
X17	-0.0016	0.0111	0.0066	-0.2251	0.1247	-0.0392	3.7832	-2.9806	0.975**

Diagonal values indicate direct effect; Residual effect=0.00939

cluster II was solitary by Tocher's method results were given in Table. 6 and Figure 1. This indicated the presence of appreciable genetic diversity between genotypes of the two clusters Mahanta et al. (2019). The cluster I showed tight and complete linkage. The study also revealed that the varieties in cluster I are started flowering at a same time with average of 30–40 days after planting whereas, cluster II variety Pusa Arpita started flowering after 54 Days after planting also showed marked difference with other genotypes.

The intra cluster distance between the cluster's ranges from

Table 6: Clustering pattern of twenty-five french marigold (*Tagetes patula* L.) genotypes

Clusters	No. of genotypes	Genotypes
I	24	Pusa Deep, Fine grow dwarf mix, IC-250323, IC-250325, IC-250303, IC-250321, UHSFm-1, UHSFm-2, UHSFm-3, UHSFm-4, UHSFm-5, UHSFm-6, UHSFm-7, UHSFm-8, UHSFm-10, UHSFm-9, IC-250310, IIHRFm-184, Bonanza mix, IIHRFm-13, IC-250322, IC-250316, IC-250322-01, IIHRFm-411
II	1	Pusa Arpita

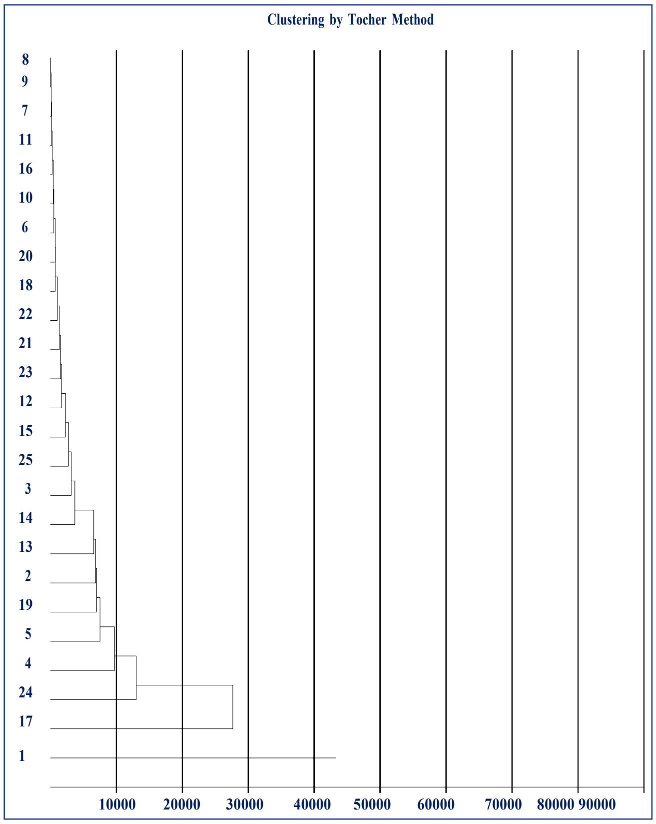

Figure 1: Dendrogram of twenty-five french marigold (*Tagetes patula* L.) genotype

0.00 to 85.20 and inter-cluster distance is maximum 352.39 (Table 7) also reported by Kavitha and Anuburani (2009) and Usha Bharathi et al. (2014). The maximum cluster mean was seen for trait flower yield plant^{-1} followed by number of flowers plant^{-1}, minimum was recorded in traits such as individual flower weight and shelf life (Table 8). Flowering duration trait showed maximum contribution towards divergence (Table 9). When a crop continuously flowers for longer duration means yield will be increased and it will be economically helpful. Yield traits contributed maximum towards divergence reported by Mahanta et al. (2019) and Poulose et al. (2021) in African marigold.

Table 7: Intra (bold) and inter cluster distance among the clusters

Clusters	I	II
I	85.20	
II	352.39	0.00

Table 8: Cluster means for various characters

Sl. No	Characters	Clusters	
		Cluster I	Cluster II
1.	Plant height (cm)	31.16	50.54
2.	Plant Spread (E-W) in cm	33.85	54.64
3.	Plant Spread (N-S) in cm	32.30	50.28
4.	Primary branches	14.43	22.40
5.	Secondary branches	28.50	33.90
6.	Leaf length(cm)	5.69	18.87
7.	Leaf width (cm)	4.28	14.10
8.	Stem girth (mm)	6.44	13.35
9.	Individual flower weight (g)	1.38	4.40
10.	Flower diameter (mm)	35.29	40.49
11.	Shelf life (days)	3.21	4.95
12.	No. of flowers plant^{-1}	119.52	103.40
13.	Days to first flowering	30.69	54.00
14.	Days to 50% flowering	37.85	61.50
15.	Duration of flowering (days)	45.85	39.50
16.	Flower yield plant^{-1} (g)	235.66	265.14
17.	Flower yield plot^{-1} (kg)	5.68	5.86
18.	Flower yield ha^{-1} (t)	9.62	10.82

Table 9: Contribution of various characters towards divergence

Sl. No.	Characters	Contribution
1.	Individual flower weight (g)	0.33%
2.	Flower diameter (mm)	2.00%
3.	Shelf life (days)	3.33%
4.	Number of flowers plant^{-1}	2.00%
5.	Days to first flowering	0.33%
6.	Days to 50% flowering	9.33%
7.	Flowering duration (days)	51.00%
8.	Flower yield plant^{-1} (g)	10.33%
9.	Flower yield plot^{-1} (kg)	6.33%
10.	Flower yield ha^{-1} (t)	15.00%

4. CONCLUSION

Genetic variability estimated for the traits found maximum heritability and genetic advance as percent mean indicated to choose for further improvement. Correlation estimate given significant positive effect for most of the traits at genotypic and phenotypic levels and path analysis showed the direction of influence on yield by different attributes. The divergence study gave cluster I contains higher number of genotypes.

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