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Genetic divergence in German chamomile [*Chamomilla recutita* (L.) Rauch.]

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Abstract

Forty genotypes of chamomile (*Chamomilla recutita)* were evaluated for 12 quantitative traits at Nagla (Uttarakhand) and could be grouped into seven clusters depending upon their genetic distance on the basis of Mahalanobis D^2 analysis. Maximum number of genotypes was grouped into cluster I (13) followed by cluster VII (8). Intra-cluster distances ranged from 1.78 (cluster IV) to 2.20 (cluster I). Inter-cluster distance was maximum between cluster II and V (6.91). The results indicated the diversity among the genotypes and sufficient scope for varietal improvement through hybridization. A breeding plan can be adopted from the results of the study to enhance flower yield, flower diameter, disc floret periphery, disc floret height and number of flowers plant^{-1} through hybrid breeding programme.

Keywords: chamomile, *Chamomilla recutita,* D^2 statistic, genetic divergence.

Chamomile (*Chamomilla recutita*) (L.) Rauch. (Syn. *Matricaria chamomilla* L.), popularly known as German chamomile, a native of Europe and adjoining Asian countries, is an important aromatic as well as medicinal plant used in traditional and modern systems of medicine. The flower capitulum, bearing the oil is used in pharmaceutical and cosmetic industries. One of the major constraints in cultivation of chamomile in India is limited genetic knowledge and non availability of superior genotypes for wide adoption. Genetic improvement is mainly required for number of flowers plant^{-1}, number of flower bunches plant^{-1}, flower size, disc floret height and diameter, flower yield and oil content. Knowledge of genetic divergence among genotypes is needed for the development of superior genotypes with increased flower yield and getting potential transgressive segregants.

The experimental material for the present study comprised of 40 genotypes of chamomile drawn from a large breeding population maintained at Central Institute of Medicinal and Aromatic Plants Resource Centre, Nagla. The selection of 40 genotypes was done on the basis of morphological and yield components. The seeds of these genotypes were sown in nursery beds during the end of October 2005 and transplanted during the end of November 2005 in a randomized block design (RBD) with three replications. Each genotype was planted in two rows with a length of 4 m at a spacing of 30 cm x 40 cm following standard agronomical practices. Fully developed flowers were harvested during 15 February 2006 to 15 March 2006 at 15-day intervals. Five plants were randomly selected from each replication to record quantitative data which included plant

height, plant spread area, number of primary branches, number of secondary branches, number of flower bunches plant^{-1}, diameter of flower, disc floret diameter, disc floret height, number of flowers plant^{-1}, moisture content, fresh weight of flowers plant^{-1} and flower yield plant^{-1}.

Genetic divergence was estimated by Mahalanobis D^2 statistic (1936). The genotypes were grouped on the basis of minimum generalized distance using Toucher's method described by Rao (1952). The inter- and intra-cluster distances were worked out by using the method suggested by Murthy & Arunachalam (1967).

The analysis of variance for 12 quantitative characters showed significant differences among the 40 genotypes indicating the existence of genetic diversity. These 40 genotypes could be grouped into seven clusters (Table 1). Cluster I had maximum of 13 genotypes followed by cluster VII, which had 8 genotypes.

The clustering pattern of genotypes showed that genotypes from the same geographical area did not necessarily belong to the same cluster. These group constellations indicated that geographical diversity was not related to genetic diversity, which may be attributed to distribution of different gene constellations into a geographical region (Bergale *et al*. 2001; Goel *et al*. 2005)

The data on intra-and inter-cluster distances (Table 2) and the mean performance of the genotypes were used to select genetically diverse and agronomically superior genotypes among the 40 genotypes.

The intra cluster distance varied from 1.78 (cluster IV) to 2.20 (cluster I). This suggested that genotypes occupying the same cluster have little diversity and selection of parents from within the cluster may not be considered

Table 1. Clustering pattern of 40 genotypes on the basis of genetic divergence in German chamomile

Cluster	No. of genotypes	Genotypes
I	13	CH-3, CH-5, CH-6, CH-7, CH-8, CH-9, CH-10, CH-14, CH-16, CH-25, CH-26, CH-27, CH-28
II	2	CH-31, CH-39
III	6	C-12, CH-13, CH-15, CH-19, CH-29, CH-30
IV	4	CH-18, CH-35, CH-36, CH-38
V	2	CH-1, CH-4
VI	5	CH-32, CH-33, CH-34, CH-37, CH-40
VII	8	CH-2, CH-11, CH-17, CH-20, CH-21, CH-22, CH-23, CH-24

Table 2. Average inter-and intra-cluster D^2 values among seven clusters in German chamomile

Cluster	I	II	III	IV	V	VI	VII
I	**2.201**	6.146	2.830	4.81	4.850	4.200	2.657
II		**1.905**	5.683	4.033	6.911	4.130	6.886
III			**1.903**	2.897	5.101	4.208	2.733
IV				**1.781**	5.995	2.886	4.983
V					**1.863**	5.253	4.511
VI						**1.849**	5.453
VII							**2.148**

Values in bold are intra-cluster distances

promising for the development of good segregants through hybridization programme (Goel *et a*l. 2005). The inter cluster distances were greater than the intra cluster distances, further indicating the considerable amount of diversity among the genotypes studied. Inter-cluster distance is the main criterion for selection of genotypes on the basis of D^2 analysis. The inter-cluster distance was maximum between cluster II and cluster V (6.91) followed by cluster II and cluster IV (6.88). Genetic diversity is the most important tool to select prospective parents for improvement programmes. The genotypes belonging to the clusters separated by high estimated distance could be utilized in hybridization programmes for obtaining wide variation among the segregants (Shukla & Singh 2002).

The mean values of different characters of seven clusters indicated the superior expression of some characters in different clusters (Table 3). Among these, cluster II had genotypes having the highest mean values for flower yield, fresh weight, flowers plant^{-1}, number of flower bunches plant^{-1} and number of secondary branches while low mean values for moisture content, plant height, disc floret height, diameter of flower and number of primary branches. This is followed by clusters VI, I, II, III and VII. It is interesting to note that flower yield in different clusters were greatly influenced by the different component traits, mainly plant height, number of flower bunches plant^{-1}, disc floret height and diameter of flower. This indicates the utility of genetic diversity analysis in identifying useful parents with highest flower yield and other desirable traits. In breeding programmes aimed at crop improvement, the choice of the parent is quite important and only component characters of flower yield should be taken into account for selecting genetically divergent parents. Hybridization among genetically diverse parental genotypes for specific traits may be helpful in bringing the new gene pool in a population with wider adoption.

Table 3. Cluster mean of 12 characters studied in German chamomile

Cluster	Plant height (cm)	Spread area (cm)	No. of primary branches	No. of sec. branches	No. of flower bunches plant^{-1}	Diameter of flower (cm)	Disc floret diam. (cm)	Disc floret height (cm)	No.of flowers plant^{-1}	Moisture content (%)	Fresh flower wt. (g) plant^{-1}	Flower yield plant^{-1} (g)
I	36.64	155.15	7.79	7.41	170.95	2.33	2.41	0.68	331.20	36.19	33.82	12.24
II	35.67	141.76	8.33	11.17	614.33	2.38	2.48	0.66	251.67	24.97	111.73	27.35
III	39.61	125.41	8.55	7.05	255.11	2.56	2.57	0.85	509.16	29.50	46.88	13.83
IV	33.75	128.85	9.91	8.41	385.75	2.54	2.56	0.73	769.16	25.51	81.72	20.85
V	67.00	208.60	9.00	8.85	204.83	2.26	3.05	0.70	407.00	30.54	42.00	12.83
VI	44.60	161.40	9.40	10.06	370.33	2.24	2.28	0.57	736.27	26.82	71.20	19.10
VII	40.37	161.95	10.20	7.16	145.25	2.56	2.68	0.83	276.46	36.38	29.13	10.57

The genotypes CH-3, CH-10, CH-11, CH-21 and CH-25 could be considered for hybridization and population improvement. These genotypes had performed better and their *per se* performance was at par for flower yield.

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