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Genetic divergence study for growth characters among the accessions of Safed Musli

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Abstract

The present investigation was carried out in College of Forestry, Navsari Agricultural University, Navsari, Gujarat to study the genetic divergence for growth traits among 10 accessions of safed musli (*Chlorophytum borivilianum* Sant. & Fernand) collected from different parts of India. The genetic divergence in safed musli was estimated based on the growth traits of accessions grown. Accordingly, a field experiment was performed using a randomized block design and three replications to compare divergences in different growth traits. Tocher's clustering method was performed using the Mahalanobis distance. D₂ analysis grouped the 10 accessions into 3 clusters. In view of genetic divergence, tuber yield contributed the highest divergence over other growth attributes. Cluster II contained maximum number of accessions. Maximum inter cluster distance was found between Cluster -II and Cluster-III. Therefore, accession C₁ and C₇, C₈, C₆, C₅, C₂ are to be selected for further breeding purpose as these accession are with maximum genetic divergence. So, these accessions may be selected for improvement programme.

Keywords: Safed musli, genetic divergence, growth characters

Introduction

Safed musli (*Chlorophytum borivilianum*) is a known medicinal plant for its use from ancient age. The Indian Pharmacopoeia (1966) has recognized safed musli as one of the 85 drug plants, whose ingredients are used in various pharmaceutical preparations. The National Medicinal Plants Board (NMPB), set up by the Government of India has ranked safed musli as the 6th among the 28 selected priority medicinal plants, for cultivation and export (Purohit and Prajapathi, 2003; Gayathri and Uma, 2009) ^[20, 5]. The Board encourages mainstream cultivation of safed musli by farmers by extending a subsidy of 20% through National Horticultural board on project cost (Desale, 2013) ^[4]. Dried roots of *C. borivilianum*, popularly known as safed musli in trade in India, is considered as wonder drug in Indian system of medicine (Ayurveda, Unani and Siddha) due to its aphrodisiac and sex tonic properties. Because of great therapeutic importance, safed musli roots are the major constituents of more than 100 Ayurvedic formulations (Oudhia, 2000) ^[17].

Genetic variation is the basis for adaptation and survival of living organisms under changing environmental conditions. Knowledge of genetic diversity is important for any breeding strategy and provides a scientific basis for the better management of the genetic heritage of forest species (Poltri *et al.*, 2003) ^[19]. On the other hand, clustering progeny according to similarity has become essential for selecting the crossing cultivars based on quantitative traits of economic interest (Manfio *et al.*, 2012; Silva *et al.*, 2012) ^[15, 24]. For years, the use of multivariate analysis has been an important tool for genetic diversity studies, helping to organize germplasm banks and determine breeding strategies for different species: Yam (*Dioscoria* spp.) (Rivera-Jiménez, 2011) ^[23]; Aerial yam (*Dioscorea bulbifera*) (Beyene, 2013) ^[11]; *Asparagus adscendens* Roxb (Thakur, 2016) ^[26]; Velvet Bean (*Mucuna pruriens* (*L.*) *DC.*) (Chinapolaiah, 2016) ^[3] and others. In this study a successful attempt was made to find out the genetic divergence among ten accessions of safed musli for growth traits in South Gujarat conditions.

Material and Methods

The present experiment was carried at instructional farm of College of Forestry, Navsari Agricultural University, Navsari. For the genetic divergence study, 10 accessions collected from different parts of India were evaluated. 10 accessions of Safed musli (*Chlorophytum*

borivilianum) are C₁- Kalamkhet (Dang, Gujarat), C₂-Melghat (Maharashtra), C₃- JNKVV (Jabalpur, Madhya Pradesh), C₄- Satpuda (Maharastra), C₅-Sahyadri (Maharashtra), C₆- Bhuvadi (Dang, Gujarat), C₇- Rambhas chikar (Dang, Gujarat), C8- Pratapgarh (Rajasthan), C9- SFRI (Madhya Pradesh) and C10- Dhar (Madhya Pradesh) were selected for the present study. Before the receipt of monsoon showers, raised beds of 15 cm height and 2 m length and 2 m width were prepared. Different accessions of safed musli fingers (tubers) were planted on raised beds at the spacing of 30cm X 15 cm. Field experiment of safed musli was replicated three times in a randomized block design. For measuring the genetic divergence, data of field experiment of safed musli was utilized. Genetic divergence of safed musli for growth characters and yield characters were studied using Mahalanobis D²- statistics (1936) ^[14]. Grouping of genotypes into various clusters was made by Tocher's method as described by Rao (1952)^[21].

Results and Discussion

The genetically diverse parents are preferred for hybridization programme because crosses involving diverse parents may offer greater possibility of obtaining hybrid vigour through new recombinants. The importance of genetic divergence in plant breeding has well been emphasized by several researchers (Murty and Qadri, 1966; Singh et al., 1987 and Rauf et al., 2010)^[16, 25, 22]. Result of the present study shows that, among various growth and yield attributes, tuber yield contributed to highest genetic divergence with 40.00 per cent, followed by leaf area (37.78 %) and number of tuber (8.89 %). Moreover parameters like plant height, collar diameter, number of leaves, total fresh weight of leaves, dry weight of leaves and fresh weight of tuber showed no contribution towards genetic divergence (Table 1). As per D^2 analysis, total ten accessions of safed musli were grouped into 3 clusters on the basis of growth attributes (Table 2). Cluster - I was formed with 4 accession viz. C3, C4, C9 and C10. Cluster -II contained five accessions namely C7, C8, C6, C5 and C2 where as cluster III had only one accession *i.e.* C₁. It was revealed that intra-cluster distance for Cluster - I and Cluster -II was 3.76 and 5.42, respectively (Table 3). However, maximum inter cluster distance was found between Cluster -II and Cluster - III (19.94), followed by Cluster - I and Cluster - II (15.26). Inter-cluster distance between Cluster - I and Cluster - III was the least (5.88). Result also showed that accession such as C1 and accessions like C7, C8, C6, C5 and C2 resulted in better divergence having maximum distances over following accessions like C3, C4, C9 and C10.Considering cluster mean values for different growth and yield attributes, tuber length, leaf area and plant height contributed more for all the clusters, whereas dry weight of single tuber/ finger contributed the least to all the clusters (Table 4). Plant height (34.21), collar diameter (15.10), number of leaves (18.87), fresh weight of leaves (22.92), dry weight of leaves (5.26), leaf area (49.82), tuber length (85.05), tuber width (6.53), number of tubers(13.04), steroidal Saponin (0.83) and tuber yield (10.75) were found maximum in Cluster - II whereas fresh weight of tuber (1.77) and dry weight of tuber (0.44)were found maximum in Cluster - I and III.

In the present study, *safed musli* accessions were grouped into three distinct clusters which indicate presence of high degree of diversity among the accessions. On the basis of clustering pattern, maximum number of accessions appeared in cluster II (5) followed cluster I (4) and remaining cluster III consisting single accession source. The results of present study are in accordance with studies carried out by Kumar et al. (2008)^[12] in C. borivilianum. Significant genetic variability through estimates of heritability and genetic correlations were reported by many workers for C. borivilianum (Yadav et al., 2007; Singh, 2008, Kumar et al., 2007, 2008) [27, 11, 12] and in germplasm of Asparagus officinalis from France and Denmark (Lopez Anido, 1997)^[13]. In C. borivilianum, greater variability for leaf size and fleshy root number was recorded by various workers in germplasm collection (Jat, 1993; Bordia et al., 1995; Jat and Sharma, 1996; Kothari and Singh, 2001; Geetha and Maiti, 2002) ^[8, 2, 9, 10, 6]. Genetic divergence study among different species were studied by many researchers viz. Parveen (2012) ^[18] in *A. recamosus* and Haghighi et al. (2012)^[7] in Amaranthus hypochondriacus. It is apparent that considerable diversity existed for all the characters among various accessions. The genotypes exhibited random pattern of distribution of various clusters revealing that genetic diversity and geographical diversity were not related.

 Table 1: Contribution of growth attributes towards total divergence among different accessions of *safed musli*

Trait	Per cent contribution (%)		
Plant height	0.00		
Collar diameter	0.00		
Number of leaves	0.00		
Fresh weight of Leaves	0.00		
Dry weight of Leaves	0.00		
Leaf area	37.78		
Tuber length	2.22		
Tuber width	2.22		
Number of tubers	8.89		
Fresh weight of single tuber	4.44		
Dry weight of single tuber	2.22		
Steroidal saponin	2.22		
Tuber yield	40.00		

 Table 2: Composition of Euclidean clusters for growth attributes in safed musli accessions

Cluster	Number of accessions	Accessions	
Ι	4	C3, C4, C9, C10	
II	5	C7, C8, C6, C5, C2	
III	1	C1	

 Table 3: Average intra and inter distances (D²) among different clusters for growth attributes

	Ι	II	III
Ι	3.76		
II	15.26	5.42	
III	5.88	19.94	0.00

 Table 4: Cluster mean values for growth attributes among different accessions

Trait	Ι	II	III
Plant height	29.68	34.21	25.98
Collar diameter	13.11	15.10	11.33
Number of leaves	17.23	18.87	15.62
Fresh weight of Leaves	17.02	22.92	14.17
Dry weight of Leaves	4.42	5.26	2.91
Leaf area	32.83	49.82	29.80
Tuber length	73.42	85.05	67.20
Tuber width	6.52	6.53	5.94
Number of tubers	9.05	13.04	7.10
Fresh weight of single tuber	1.77	1.56	1.77
Dry weight of single tuber	0.44	0.39	0.44
Steroidal saponin	0.83	0.83	0.82
Tuber yield	8.37	10.75	7.57

Conclusion

Based on genetic divergence studies, it can be concluded that tuber yield contributed the highest divergence over other growth attributes. D^2 analysis grouped the 10 accessions into 3 clusters. Cluster II contained maximum number of accessions. Maximum inter cluster distance was found between Cluster-II and Cluster-III. Therefore, accession C_1 and C_7 , C_8 , C_6 , C_5 , C_2 are to be selected for further breeding purpose as these accession are with maximum genetic divergence. Therefore, these accessions may be used in future for further breeding programme to exploit heterosis and improve the growth and yield parameters among the accessions of safed musli.

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