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Genetic divergence in betelvine (*Piper betle* L.)

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INTRODUCTION

Betelvine is vegetatively propagated for cultivation. Occurrence of flowering, fruiting and proper identification of male and female vines have opened up a new avenue for the improvement of betelvine through hybridization (Raghavendra Rao and Maiti, 6; Maiti and Biswas, 3). A successful hybridization helps in this regard to combine desirable characters (Raghavendra Rao, 7). There has been a need for launching a massive breeding programme based on genetic divergence and to develop hybrids with high heterosis followed by desirable segregants for effective selection. Keeping all these facts in view, the present study was initiated to estimate the genetic divergence present in a set of 16 genotypes of betelvine.

MATERIAL AND METHODS

The investigations were carried out in 16 genotypes of betelvine collected from different parts of India and maintained in the germplasm bank of the All India Co-ordinated Research Project on betelvine at Bhubaneswar. Juvenile rooted cuttings of 15 cm length were planted at a planting distance of 100 cm × 10 cm in the betelvine conservatory (bareja) in a completely randomized block design with 3 replications. A composite mixture of mustard oil cake and river bank soils was applied to the beds and irrigation as per schedule was provided. The vines were lowered for rejuvenation at an interval of 3 months. Observations on 12 quantitative traits were recorded from 6 randomly selected vines from each treatment. This was done for 2 successive years (1996-97 and 1997-98). The data collected was statistically analyse. Spectrophotometric determination of chlorophyll a and b was carried out following the procedure of Arnon(1). The genetic diversity among the genotypes was worked out using Mahalanobis' D^2-statistics as described by Rao (9). On the basis of the magnitude of D^2 values, Tocher's method was employed to group the genotypes into different clusters.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for number of laterals/vine and length of leaf indicating wide range of variability among them. Depending on the average D^2 values, all the 16 genotypes were grouped into 5 clusters (Table 1). The genotypes collected from the same source were found to be distributed in different clusters. Differences in genetic constitution and the presence of unabated influence of environmental factors might be responsbile for this type of clustering pattern as suggested by Murthy and Arunachalam (5) and Rahaman *et al.* (8). In spite of emphasis laid by Joshi and Dhawan (2), the clustering pattern in the present study indicated that the genetic diversity was not necessarily related to geographical distribution. Further, genotypes from different geographical regions were

Table 1. Clustering pattern of genotypes in different clusters and their places of acclimatization.

Cluster No.	No.	Constituent genotypes	Place of acclimatization
I	10	Nauwa Bangla, Godi Bangla, Utkal Sudam	Orissa
		Kapoori Telaku, Karapaku	Andhra Pradesh
		Halishahar, Simurali Bhavana	West Bengal
		Mahaba Bangla	Uttar Pradesh
		Maghai	Bihar
		SGM-I	Tamil Nadu
II	2	Desi Meetha Pan	West Bengal
		Ramtek Bangla	Maharashtra
III	2	Gandhi Pan	Assam
		Kali Bangla	West Bengal
IV	1	Awani	Assam
V	1	Kapoori	Maharashtra

grouped in the same cluster. This might have been due to the free exchange of propagating materials from one place to another.

The maximum intra-cluster distance was observed in cluster I, followed by III and II in the descending order (Table 2), which is the indicative of wide genetic divergence between the constituent genotypes. These constituent genotypes could be used in yield improvement through intervarietal hybridization as postulated by Mandal and Banerjee (4). The minimum intra-cluster distance was recorded by cluster II, comprising only 2 genotypes indicating gross genetic similarity between them. In this cluster, Desi Meetha Pan and Ramtek Bangla (Bangla types) had been placed together which might be due to their pedigree similarity (Mandal and Banerjee, 4).

In general, the inter-cluster distance was relatively higher (Fig. 1). The cluster V was found to be a quite distinct genetic group. The highest inter-cluster value between cluster II and V can be expected to exert high heterotic effect in the hybrids when crossed and consequently may generate desirable segregants.

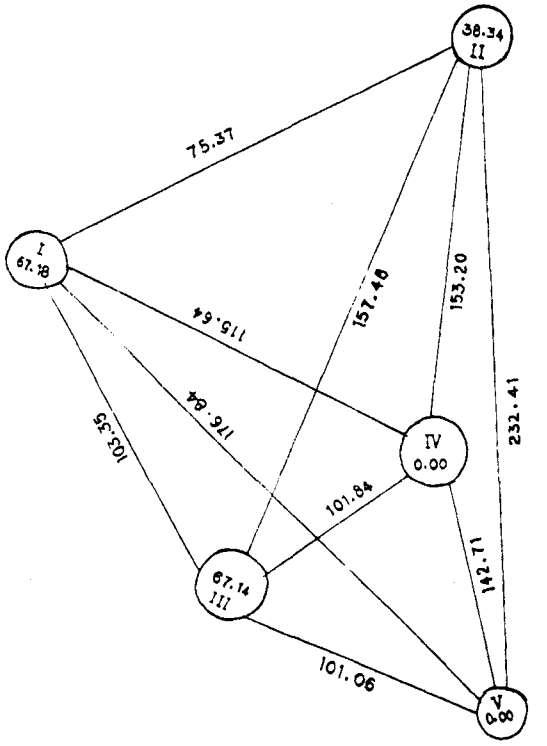

Fig. 1. Relative disposition clusters showing average genetic distances (Ds) between and within them in betelvine.

The cluster IV was made up of a single genotype Awani which had larger main vine length and internode length, rapid growth with least number of diseases but with short shelf-life (Table 3). On the other hand, the cluster V, a widely divergent cluster from IV was constituted by a single genotype, Kapoori which was characterized by smaller main vine and internode length, with slow growth habit but having longer shelf-life. Therefore, these 2 genotypes coming from distantly related clusters may be selected as parents for hybridization. This type of assumption has already been made by Rawat and Balasubrahmanyam (10) for evolving betelvine cultivars.

Present study has revealed that Awani of cluster IV and Kapoori of cluster V are most genetically divergent genotypes and selection involving these 2 parents would generate meaningful results. The ideal pair of clusters expected to give good combining parents for successful recombination were identified to be clusters II and V, I and V, II and III, II and IV, IV and V, and I and IV in the descending order for

Table 2. Inter- and intra-cluster average distance among different clusters D^2 value.

Cluster No.	I	II	III	IV	V
I	4513.02	5680.67	10722.54	13371.60	31273.36
II		1469.74	24799.17	23469.14	54012.34
III			4507.66	10371.54	10213.13
IV				0.00	20364.77
V					0.00

Table 3. Cluster mean for quantitative characters in betelvine.

Character	I	II	III	IV	V
Leaf area (cm^2)	119.62	124.70	121.35	45.37	29.00
Petiole length (cm)	6.61	6.28	5.39	8.43	3.47
Leaf length (cm)	14.42	14.47	8.85	7.40	9.10
Leaf breadth (cm)	11.64	12.12	8.74	7.37	4.67
Internodal length (cm)	5.14	5.33	6.45	6.30	3.13
No. of laterals/vine	3.47	3.50	1.17	1.67	2.67
Vine length (cm)	160.34	164.33	148.00	278.33	77.33
Diameter of internode (cm)	4.55	4.57	4.00	3.33	2.37
Chlorophyll a (mg/g)	0.60	0.60	0.45	0.23	0.44
Chlorophyll b (mg/g)	0.22	0.33	0.18	0.22	0.22
No. of leaves/vine	53.70	56.67	30.67	54.33	26.00
100-leaf weight (g)	289.82	372.22	157.27	152.77	77.20

Table 4. Relative contribution of different characters to genetic divergence among betelvine genotypes.

Characters	Average D^2	% contribution of divergence D^2	Rank (total)	Percentage
Leaf area (cm^2)	201.11	2.03	865	9.24
Petiole length (cm)	105.93	1.07	959	10.24
Leaf length (cm)	217.68	2.20	871	9.30
Leaf breadth (cm)	108.19	1.10	962	10.28
Internodal length (cm)	121.99	1.23	891	9.52
No. of laterals/vine	37.12	0.37	1142	12.20
Main vine length (cm)	999.15	10.08	556	5.94
Diameter of internode (cm)	445.75	4.50	701	7.49
Chlorophyll a (mg/g)	502.49	5.07	728	7.79
Chlorophyll b (mg/g)	196.62	1.98	816	8.72
No. of leaves/vine	702.96	7.10	635	6.78
100-leaf weight (g)	6269.64	63.27	234	2.50

hybridization programme in view of their superior performance in respect of 100-leaf weight, main vine length and number of leaves/vine which are the most important yield-attributing characters for betelvine production.

SUMMARY

Genetic divergence in a set of 16 genotypes of betelvine measured using Mahalanobis' D^2-technique, indicated the existence of substantial genetic diversity. The genotypes were grouped into 5 different clusters. The clustering pattern of genotypes was random and did not follow the geographical origin. A wide range of variation was found in the cluster mean values in respect of number of leaves/vine, leaf area, petiole length, internode length, leaf length, leaf breadth, number of laterals/vine, vine length, diameter of internode, chlorophyll a and b and 100-leaf weight of which number of laterals/vine as well as leaf length were the potent variables These may be used in selecting diverse parents in hybridization programme.

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