Journal of Spices and Aromatic Crops
Vol. 22 (1) : 01–05 (2013)
www.indianspicesociety.in/josac/index.php/josac

Indian Society for Spices

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

B T Priya, P R Devi & P Sunitha

AICRP on MAP and Betelvine, Dr. Y.S.R Horticultural University, Venkataramannagudem-534 101, Andhra Pradesh, India.
E-mail: tpriyahort@gmail.com

Received 2 January 2012; Revised 24 August 2012; Accepted 15 January 2013

Abstract

Genetic divergence was assessed in a population of 51 genotypes of betelvine (*Piper betle*) for seven characters using Mahalanobis D^2 technique. The genotypes were grouped into six clusters. The clustering pattern of the genotype was random and did not follow geographical origin, indicating that geographical isolation may not be the only factor causing genetic diversity. Leaf area contributed maximum towards genetic diversity in betelvine. Cluster analysis revealed wide genetic distance between Cluster V and Cluster VI followed by Cluster IV and Cluster VI, and Cluster III and Cluster V. Thus, selections of parents from the clusters with high inter and intra cluster distance will help to obtain substantial heterosis in respect of economic traits during hybridization programme.

Keywords: betelvine, cluster analysis, genetic diversity, hybridization

Introduction

Betelvine (*Piper betle* L.) is a leaf yielding dioecious, evergreen creeper grown in India for mastication. It is commercially propagated by vegetative means. Occurrence of flowering, fruiting and proper identification of male and female vine has opened up an avenue for the improvement of betelvine through hybridization (Maiti *et al*. 1992). A successful hybridization will help in combining desirable characters (Rao 1993). Genetic divergence of the germplasm lines plays an essential role in hybridization programme. The diversity among the parents is also important as the crosses between the parents with maximum genetic divergence would more likely yield desirable recombinants in the segregating generation. D^2 statistics developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes. An attempt was made in the present investigation to study the genetic divergence in 51 germplasm lines of betelvine.

Materials and methods

The experimental material consisted of 51 germplasm lines of betelvine collected from different parts of India during the year 2009-10 and maintained in the germplasm bank of All India Coordinated Research Project on Medicinal, Aromatic Plants and Betelvine, Bapatla, AP (India). Juvenile rooted cuttings of 15 cm length having 3-5 nodes were planted in a randomized block design with two replications. Each line was raised in two rows of three meters length with a spacing of

100 cm × 20 cm between and within the rows respectively. Observations were recorded on five randomly selected plants from each plot/lines for seven characters *viz*., vine elongation month^{-1} (cm), number of laterals, fresh weight of 100 leaves (g), leaf length (cm), leaf width (cm), leaf area (cm^2) and leaf yield (lakh leaves ha^{-1}). The analysis of genetic divergence was worked out using Mahalanobis D^2 statistics. The betelvine genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

Results and discussion

The analysis of variance for different characters showed significant differences among the genotypes studied. Based on the relative magnitude of D^2 values, all the 51 genotypes were grouped into six clusters (Table 1). Majority of the germplasm lines were grouped in Cluster I (24) followed by Cluster II (21) and Cluster III (3). Rest of the Clusters *viz*., IV, V and VI possessed only one genotype each. The pattern of distribution of genotypes into

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

Cluster No.	No. of genotype	Constituent genotype	Place of acclimatization
I	24	Swarna Kapoori (K*), Tellaku Ponnuru (K), Tellaku Chennuru (K),Tellaku Utukuru (K), Tellaku Chintalapudi (K), Kuljedu Cuddapah (K),Kapoori Chinacheppali (K), Gangeri (K)	Andhra Pradesh
		Kakair (B*), Kapoori (K)	Bihar
		Bilhari (B), Bangla Mandsore (B)	Madhya Pradesh
		Sangli Kapoori (K), Shirpurkata (K), Ramtek Bangla (B), Bangla Gunmala (B)	Maharashtra
		Godi Bangla (B)	Odisha
		Kapoori (K), SGM-1 (B)	Tamil Nadu
		Meetha Pan (B), Halisahar Sanchi (B), Ghane gate (B), Simurali Babna (B), Simurali Babna Local (B)	West Bengal
II	21	Gachipan (B), Khasi Pan (B), Awnipan (B)	Assam
		Kapoori Peda Cheppali (K), Kapoori Tuni (K), Kapoori Chittikavata (K), Kapoori Kadapa (K), Kapoori Vuyyuru (K), Black leaf (B)	Andhra Pradesh
		Maghai (B), Calcuttia Bangla (B)	Bihar
		Vasani Kapoori (K), Kalipathi, Kapoori Arvi (K), Kapoori Bangla (K)	Maharashtra
		Bangla (B), Malvi (B)	Madhya Pradesh
		Patchaikodi (K)	Tamil Nadu
		Bangla Nagaram (B), Bangla (B)	Uttar Pradesh
		Kali Bangla (B)	West Bengal
III	3	Kapoori Doddipatla (K), Kapoori Chilumuru (K)	Andhra Pradesh
		Vellaikodi (K)	Tamil Nadu
IV	1	Karapaku (B)	Andhra Pradesh
V	1	Nauva Bangla (B)	Odisha
VI	1	Yellow Leaf (K)	Andhra Pradesh

*(K)=Kapoori groups/Male clones; *(B)=Bangla groups/Female clones

different clusters was at random. Genotypes belonging to same geographic origin were included in different clusters. Differences in genetic constitution and the presence of unabated influence of environmental factors might be responsible for this type of clustering pattern (Rahaman *et al.* 1997). In addition, the clustering pattern in the present study indicated that genetic diversity was not necessarily related to geographical distribution. Further, genotypes from different geographical regions were grouped in the same clusters. This might have been due to the free exchange of propagating materials from one place to another. This was also reported by Rahaman *et al*. (1997) in contrast to Joshi & Dhawan (1966). The magnitude of inter-cluster distance measures the genetic distance between two clusters while the intra-cluster distance measures the extent of genetic diversity between the genotypes of same clusters (Krishna Veni *et al*. 2008). In general, the inter-cluster distance was relatively higher (Fig 1). The inter-cluster D^2 values ranged from 329.87 to 23194.32. Minimum inter-cluster D^2 values was observed between Cluster IV and V (329.87), indicating the close relationship among the genotypes included in these clusters. Maximum inter-cluster distance was observed between Cluster V and VI (23194.32) (Table 2), which revealed that the genotypes included in these clusters had maximum divergence. Hence, hybridization between the genotypes included in these clusters may exert high heterotic effects and consequently may generate desirable segregants. The intra-cluster distance was maximum in Cluster II (291.20) followed by Cluster I (243.30) (Table 2), indicating the existence of diverse genotypes in these cluster. Thus, these constituent genotypes could be used for increasing leaf yield through intra-varietal hybridization (Mandal & Banerjee 1991). Cluster III possessing Kapoori types, *viz*., Kapoori Chilumuru, Kapoori Doddipatla and Vellai Kodi showed minimum intra-cluster distance (129.44), revealing the genetic similarity among them (Mandal & Banerjee 1991).

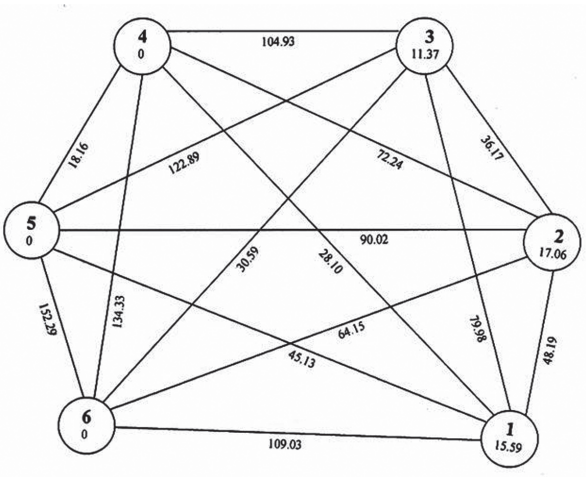

Fig.1. Distribution of clusters based on inter-cluster distances
(Figures indicate square root of average D^2 values)

Cluster mean showed appreciable differences for all the seven characters studied (Table 3). Highest mean value for number of laterals per vine (8.91), leaf yield (41.02 lakh leaves ha^{-1}) and leaf length (12.64 cm) were recorded in Cluster I while Cluster III and Cluster IV recorded high mean values for vine elongation per month (26.43 cm) and fresh weight of 100 leaves (360 g) respectively (Table 3). It is generally known that betel leaves are produced from each node of the vine hence, longer vines would be ideal for

Table 2. Average intra and inter cluster distances among six clusters of betelvine germplasm

Cluster	I	II	III	IV	V	VI
I	**243.30**	2323.01	6397.24	789.75	2037.56	11889.00
II		**291.20**	1308.83	5219.02	8104.64	4115.24
III			**129.44**	11012.35	15102.38	936.02
IV				**0.00**	329.87	18044.62
V					**0.00**	23194.32
VI						**0.00**

higher leaf production. Moreover, faster the growth of the vine, more number of leaves would be obtained within a short time (Pariari & Imam 2012). Similarly, higher the number of laterals per vine, higher would be the leaf production. Thus, the genotypes that fell under Cluster III with higher vine length and Cluster I with more number of laterals can be used in hybridization for evolving genotypes with higher leaf yield.

Correspondingly, Cluster IV constituting single genotype Karapaku (Bangla type) recorded high means for leaf width (10.00 cm) and leaf area (90 cm^2). On the other hand, the Cluster VI constituted by a single genotype Yellow Leaf (Kapoori type), recorded high number of laterals (8.00), leaf yields (40.81 lakh leaves ha^{-1}) and less fresh weight of 100 leaves (110 g) (Table 3). Similar variations in leaf quality *viz*., length, width, area and fresh weight of 100 leaves and yield were observed among the 27 genotypes under the study conducted by Rahman *et al*. (1997). Therefore, the constituent genotype of Cluster IV and VI can be utilized as a parent for increasing leaf quality and yield, respectively. Similar trend was followed by the genotype of Cluster V and VI. Thus, the genotypes coming from distantly related clusters may be selected as parents for hybridization. This type of assumption has already been made by Rawat & Balasubrahmanyam (1988) for evolving betelvine cultivars. Among the characters studied, leaf area contributed maximum to genetic divergence (85.57%) followed by leaf length (5.88%) and leaf yield (4.08%). This is in conformity with Das *et al.* (2000), who reported that the leaf quality contributed maximum to genetic divergence followed by leaf yield in betelvine.

Thus, the present study revealed that the ideal pair of Clusters that produce best combining parents for successful recombination were Cluster V & VI, IV & VI, III & V, I & VI and III & IV in the descending order for hybridization programme to accumulate favourable genes in single variety, because of their superior performance in respect of vine elongation per month, number of laterals per vine, leaf yield per hectare, fresh weight of 100 leaves, leaf length, leaf width and leaf area.

Acknowledgments

The authors are grateful to the Director, Directorate of Medicinal and Aromatic Plants Research, Boriavi, Anand, Gujarat for the financial support. The authors are also thankful to the Director of Research, Dr. Y.S.R Horticultural University, Andhra Pradesh for providing the facilities to carry out the study.

References

Das R C, Das J N & Misra P K 2000 Genetic divergence in betelvine (*Piper betle* L.). Ind. J. Hort. 57: 259–263.

Joshi A B & Dhawan N L 1966 Genetic improvement of yield with special reference to self fertilizing crops. Ind. J. Genet. 26: 101–113.

Table 3. Mean value and contribution of different characters of six clusters for 51 betelvine germplasm

Cluster	Vine elongation/ month (cm)	No. of laterals	Leaf yield (lakh leaves ha^{-1})	Fresh weight of 100 leaves (g)	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)
I	24.63	8.91	41.02	283.13	12.64	8.41	74.78
II	25.89	6.25	38.00	210.05	12.24	8.81	74.15
III	26.43	3.40	35.21	157.80	11.76	8.20	65.80
IV	22.85	3.00	32.30	330.67	12.60	10.00	90.00
V	24.28	3.00	38.20	360.00	12.00	8.50	77.00
VI	17.67	8.00	40.81	110.00	10.20	7.10	52.00
Contribution %	0.08	1.73	4.08	2.67	5.88	0.00	85.57

Krishna Veni B, Pramila Rani B & Raman M V 2008 Genetic divergence studies in soyabean (*Glycine max* L.). Soyab. Res. 6: 77–80.

Mahalanobis P C 1936 On the generalized distance in statistics. In: Proceedings of National Academy of Sciences (India), 2: 49–55.

Maiti S, Biswas S R & Raghavendra Rao N N 1992 Divergence in sexual dimorphism among betelvine (*Piper betle*) clones. Ind. J. Agric. Sci. 62: 780–782.

Mandal A B & Banerjee S P 1991 Genetic divergence in Safflower (*Carthamus tinctorius* L.). Phytobreedon 7: 29–36.

Pariari A & Imam M N 2012 Evaluation of betelvine (*Piper betle* L.) cultivars in the gangetic alluvial plains of W. Bengal, India. J. Spices Arom. Crops 21: 1-8.

Rahaman M, Hossain M & Das N D 1997 Genetic divergence in Betelvine (*Piper betle* L.). J. Plantn. Crops 25: 57–61.

Rao C R 1952 Advanced Statistical Methods in Biometric Research. John, Willey & Sons, New York, p.390.

Rao N N R 1993 Scope for the genetic improvement in betelvine (*Piper betle* L.) through hybridization with special reference to disease resistance, In: Abstracts, Golden Jubilee Symposium, Horticultural Society of Indian, Bangalore, India.

Rawat A K S & Balasubrahmanyam V R 1988 Betelvine cultivars need to be classified. Ind. Hort. 32: 4–6.