Genetic Divergence of Kapoori Betelvine Accessions based on Morphological Traits

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ABSTRACT: Betelvine is a heritage crop of India and is cultivated for its fresh leaves which are masticatory. As it is a dioecious, Kapoori accessions belongs to male plants which are useful for hybridization programmes in betelvine. Genetic diversity is major tool for crop improvement, so there is a need to analyse the diversity in the accessions. Genetic divergence was assessed using mahalanobis D^{2}analysis for 17 betelvine accessions for 18 characters. Based on morphological characters the accessions were grouped into five clusters, the highest inter cluster distance was observed between cluster V and IV, which indicates that there was much diversity and the highest intra cluster distance was observed in cluster II which indicates that it has most divergent accessions within the cluster. Based on cluster means, cluster IV has highest mean values for plant, leaf and yield characters. Hence these divergent and the genotypes with desirable character can be used as male parent for further crop improvement programme in betelvine.

Keywords: Kapoori, Mahalanobis D^2 analysis, Genetic Divergence, Cluster analysis.

INTRODUCTION

Betelvine (*Piper betle* L.), a dioecious, aromatic, perennial, evergreen, shade loving climber, is an important small holders plantation crop of India. It belongs to the family Piperaceae, which is native to Malaysia. It is well known for its economical, medicinal, cultural and religious importance. Extracts of betelvine are used for the treatment of various aliments since ages due to its essential antioxidant, antiallergic, anticancer, anti-inflammatory, antidiabetic, antifertility, antidermatophytic, antimicrobial, antihypercglycemic and radioprotective properties. It is widely cultivated in Andhra Pradesh, Bihar, Karnataka, Madhya Pradesh, Maharashtra, Odisha, Tamil Nadu, Uttar Pradesh and West Bengal. In Andhra Pradesh it is largely grown in Guntur, Kadapa, Nellore, Ananthapur, East and West Godavari Districts. It is generally found in hot and moist climatic conditions. As it is a creeper, it needs a compatible tree or a long pole for support.

On the basis of chemical constituents of leaf essential oils, five prominent groups of betelvine landraces, namely Bangla, Kapoori, Meetha, Sanchii and Desawari have been recognized (Suryanasta *et al.,* 2006). Apoori types are male plants, which has smooth and non pungent leaves with pale green colour. These male plants are used in hybridization programme of betelvine for desirable character. Characterization of germplasm is essential to provide information on the traits of accessions assuring the maximum utilization of the germplasm collection to the final users. Medda *et al.* (2011) analysed the genetic diversity among 12 betelvine cultivars which exhibited significant variations with respect to their growth, yield and yield attributing characters. Preethy *et al.* (2018) carried out research on genetic diversity through morphological characterization in five betelvine cultivars of Malappuram district in Kerala.

Genetic diversity is of fundamental importance within the continuity of a species, provides the required adaptation to the prevailing biotic and abiotic environmental conditions, and enables change within the genetic composition to deal with changes within the environment. In present study, 17 Kapoori accessions subjected to the diversity analysis with the objective to assess the divergence among these accessions

MATERIAL AND METHODS

The experiment was carried out during 2021-22 at Horticultural Research Station, Venkataramannagudem. The experiment was laid out in randomized complete block design with three replications. Seventeen Kapoori accessions were selected from the existing germplasm and subjected for genetic divergence analysis. The rooted cuttings of 20 cm length having 3-5 nodes were planted in a randomized block design with three replications.

Observations were recorded on five randomly selected plants from each replication for18 characters *viz.,* vine length (cm), internodal length (cm), number of branches, leaf length (cm), leaf width (cm), orthotropic vine length (cm), orthotropic leaf length (cm), orthotropic leaf width (cm), orthotropic leaf petiole length (cm), orthotopic shoot internodal length (cm), plagiotropic vine length (cm), plagiotropic leaf length (cm), plagiotropic leaf width (cm), plagiotropic leaf petiole length (cm), leaf yield per vine, leaf yield of laterals and 100 leaves weight (g)

Statistical analysis: The analysis of genetic divergence was carried out using Mahalanobis D^2 statistics. The betelvine accessions were grouped into various cluster following Tocher's method (Rao, 1952)

RESULTS AND DISCUSSION

Improvement of betelvine is based on recombination breeding programme which utilizes superior accessions, possessing desirable traits like high yield, resistance to biotic and abiotic stress as male parents. Since success of the improvement programme is dependent on the selection of genetically diverse parents.

The accessions were grouped into five clusters on the basis of relative magnitude of D^2 values (Table 1). The Mahalanobis D^2 analysis grouped the accessions into five clusters. Cluster I consists of seven accessions, cluster II consists of eight accessions, cluster III and cluster V, each consists one accession and cluster V consists of two accessions (Fig. 1). Cluster mean values of 18 characters were presented in Table 2.

Table 1: Distribution of genotypes into different clusters.

Sr. No.	Clusters	No. of genotypes	Genotypes of cluster
1.	Cluster I	7	Kapoori Doddipatla, Kapoori Vuyyuru, Kapoori Chinthalapudi, Kuljedu Kadapa, Kapoori Kadapa and Yellow Leaf
2.	Cluster II	8	Kapoori Tuni, Kapoori Bhambla, Gangeri, Tellaku Chennuru, Kapoori Chittikavata, Tellaku Uthukuru and Kapoori Peddacheppali
3.	Cluster III	1	Kapoori Chilumuru
4.	Cluster IV	2	Swarna Kapoori and Tellaku Ponnuru
5.	Cluster V	1	Kapoori Chinnacheppali

Cluster means. Cluster IV had the maximum cluster mean for vine length (163.07 cm), number of branches (5.88), stem girth (1.49 cm), leaf length (15.41 cm), leaf width (8.97 cm), orthotropic vine length (56.97 cm), orthotropic leaf length (11.72 cm), orthotropic leaf width (9.40 cm), orthotropic leaf petiole length (5.63 cm), plagiotropic vine length (35.67 cm), plagiotropic leaf length (11.29 cm), plagiotropic leaf width (7.43 cm), leaf yield of laterals (45.36), leaf yield per vine (64.60) and 100 leaves weight (310.35 g) whereas it had minimum values for orthotropic shoot internodal length (6.69 cm) and internodal length (5.31 cm).

Cluster III had the minimum cluster mean for vine length (123 cm), number of branches (4.47), stem girth (1.15 cm), leaf length (11.97 cm), leaf length (7.23 cm), orthotropic vine length (33.09 cm), orthotropic leaf length (9.10 cm), plagiotropic vine length (20.61 cm), plagiotropic leaf length (8.05 cm), plagiotropic leaf petiole length (4.80 cm), leaf yield of laterals (28.16) and leaf yield per vine (44.69). Cluster V had the highest cluster mean values for orthotropic shoot internodal length (8.14 cm) and internodal length (6.46 cm), and the lowest values for number of branches (4.73), leaf width (7.00 cm), orthotropic leaf width (8.04 cm), plagiotropic leaf width (6.25 cm) and 100 leaves weight (110.89 g). Cluster 1 had the minimum orthotropic leaf petiole length (5.30 cm) and plagiotropic leaf petiole length (3.70 cm). Cluster IV recorded highest means for most of morphological parameters, so we can utilize the genotypes from these clusters as a high yielding male parent in hybridization programme. The accessions of cluster III (Kapoori Chilumuru) and cluster V (Kapoori Chinnacheppali) are diverse genotypes based on cluster analysis, hence these genotypes can be used for further crop improvement studies to find any desirable characters.

Table 2: Mean values of clusters.

Sr. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1.	Vine length	139.23	140.62	123.00	163.07	130.05
2.	Internodal length	6.31	6.23	6.12	5.31	6.46
3.	Number of branches	5.07	5.20	4.47	5.88	4.73
4.	Stem girth	1.21	1.21	1.15	1.49	1.19
5.	Leaf length	14.05	13.09	11.97	15.41	11.99
6.	Leaf width	7.97	7.56	7.23	8.97	7.00
7.	Orthotropic vine length	42.92	44.86	33.09	56.97	36.99
8.	Orthotropic leaf length	10.66	10.04	9.10	11.72	9.12
9.	Orthotropic leaf width	9.03	8.70	8.31	9.40	8.04
10.	Orthotropic leaf petiole length	4.67	4.84	5.60	5.63	5.30
11.	Orthotropic shoot internodal length	7.95	7.85	7.72	6.69	8.14
12.	Plagiotropic vine length	26.74	27.95	20.61	35.67	23.04
13.	Plagiotropic leaf length	9.28	8.76	8.05	11.29	8.07
14.	Plagiotropic leaf width	7.30	6.75	6.45	7.43	6.25
15.	Plagiotropic leaf petiole length	3.70	4.03	4.80	4.38	4.69
16.	Leaf yield of laterals	31.40	32.87	28.16	45.36	35.99
17.	Leaf yield per vine	50.17	51.48	44.69	64.60	46.14
18.	100 leaves weight	280.16	194.64	147.59	310.35	110.89

Intra and inter cluster distances: The inter and intra cluster distances are depicted in Table 4 and Fig. 1. The inter and intra cluster distances were estimated based on total D^2 values. The maximum inter cluster distance was noticed between cluster IV and V (42044.54) showing that these two clusters are most divergent with maximum genetic distance or variation, which can be utilized in hybridization programmes to get heterotic advantage. The minimum inter cluster distance was between cluster I and II, which indicates that there is less genetic diversity among these two clusters. The maximum intra cluster distance was observed in cluster II and the minimum distance in cluster IV.

Table 3: Inter and intra cluster distances.

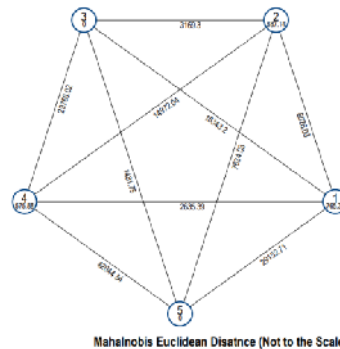| Cluster	I	II	III	IV	V
I	765.36	8026.03	18343.20	2635.39	29152.71
II		887.14	3169.3	14972.04	7634.03
III			0.00	29766.02	1481.75
IV				575.88	42044.54
V					0.00

Fig. 1. Cluster diagram.

In this experiment inter cluster distance was higher than the intra cluster distance which indicates that there is a homogeneity among the accessions within a cluster and heterogeneity between the clusters. So, we can use the accessions of different clusters for further crop improvement programme. The genotypes distributed randomly into different clusters based on morphological traits. The genotypes belonging to different geographic origin were included in same clusters. Differences in genetic constitution and the presence of unabated influence of environmental factors might be responsible for this type of clustering pattern. This might have been due to the free exchange of propagating materials from one place to another (Rahaman *et al*., 1997). These findings are in agreement with Kirankumar (2007); Priya *et al.* (2013) in betelvine.

CONCLUSION

The cluster analysis depicts the distance between and among the accessions. 17 accessions grouped into 5 clusters. In this study cluster (Tellaku Ponnuru and Swarna Kapoori) recorded the maximum diversity with respect to morphological variations. These accessions can be used for the purposes of high yielding traits as a male parent in the hybridization programme.

FUTURE SCOPE

The divergent accessions can be used for crop improvement especially as a male parent in hybridization programme.

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