## **RESEARCH ARTICLE**

# Establishment of Phylogenetic relationship on the basis of SDS-PAGE among the *Dioscorea* species under section Opsophyton, Enantiophyllum and Lasiophyton from Melghat Tiger Reserve Maharashtra, India.

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#### ABSTRACT

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**Copyright: (** Author(s), This is an open access article under the terms of the Creative Commons Attribution-Non-Commercial - No Derives License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made. A crude protein extract when fractionated on a suitable gel medium produces a spectrum of bands which is diagnostic for the species. For each species at least 10 locations were selected. Protein samples were extracted in 50 mM Tri-HCl buffer (pH 8.3) to added 10 mM 2-Mercaptoehanol. Vertical polyacrylamide gel electrophoresis (SDS-PAGE) was carried out for separation of proteins, using crude extract. The 15% Gel caste was used for the separation of proteins. Genetic similarity (GS) between individuals was estimated and the matrix was subjected to Unweighted Pair Group Method for Arithmetic average analysis (UPGMA) to generate dendrogram using average linkage procedure. It was evident that these five species were in two clusters. *D. bulbifera, D. oppositifolia, D. hispida,* and *D. pentaphylla* formed a distinct cluster (cluster-I), while *D. belophylla* was completely out-grouped and formed cluster II. Although, *D. bulbifera* and *D. oppositifolia* were placed nearer to each other, they did not pair and hence, were placed in two different sub-clusters (sub-cluster I and II). In this cluster *D. hispida* and *D. oppositifolia* was grouped together and formed sub-cluster III. The *D. belophylla* was distantly related with remaining four species.

Keywords: Dioscorea, Dioscoreaceae, SDS-PAGE, Protein Profile, Phylogenetic analysis.

## **INTRODUCTION**

The Melghat Tiger Reserve (MTR) is located on southern offset of the Satpura hill ranges in central India, called Gawilgarh hills in the Maharashtra. The family Dioscoreaceae is a natural group of tuber forming, tropical vines. The family is divided into two tribes: the Dioscoreae, including six genera all of which have unisexual flowers, and the Stenomeridae with three genera which produce hermaphroditic flowers (Smith, 1937).

The present investigator was very much impressed by the work carried out by Prain and Burkill in India as well as abroad. Burkill spent 58 years of his life on the study of world Dioscoreaceae (Burkill, 1960). Under the family Dioscoreaceae, the section Combilium includes *D. aculeata*, section Lasiophyton with *D. pentaphylla* and *D. triphylla*, Opsophyton with *D. bulbifera* and the last section Enantiophyllum represented by *D. wallichii*, *D. anguina*, *D. belophylla*, *D. glabra* and *D. alata* (Duthie, 1960). These sections were introduced earlier by Prain and Burkill (1936) who were the basic contributors on the taxonomy of Dioscoreaceae. The genus *Dioscorea* in the

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forests of MTR is represented by five species namely, in the section Opsophyton includes species such as *D. bulbifera*; however section Enantiophyllum includes *D. oppositifolia* and *D. belophylla* and in the section Lasiophyton accomodate *D. hispida* and *D. pentaphylla* (Patel, 1968; Dhore and Joshi, 1988). Marked diversity was observed among the five species of the genus *Dioscorea* in MTR and also within individuals of the same species except *D. hispida*.

Protein electrophoresis has provided a new approach to the problems of species relationships (Johnson and Hall, 1965). SDS-PAGE technique was for the first introduced by Laemmli (1970). The proteins and enzymes are the important parameters in order to study molecular taxonomy (Anu and Peter, 2003). The proteins as primary gene products are good markers of genetic variations (Odeigah *et al.*, 1999).

Dioscoreales have been the centre of attraction for plant systematists for many years. Salient features of Dioscorea viz. reticulate venation, nervation between primaries reticulate, ring vascular bundles, lateral position of the pistil, and second delayed cotyledon render the genus Dioscorea interesting for tracing possible phylogenetic relationship between Monocotyledons and Dicotyledons (Dhalgren et al., 1985; Brunnschweiler, 2004). By considering above character the present investigation intends to undertake in order to perform morphological character optimization, correlation of phenetic similarities with the genetic similarity and establishment of genetic relationship among genus Dioscorea from MTR. In relation to the above, the following parameters were undertaken to study genetic relationship between the five species of Dioscorea for to study inter-relationship based on morphology and protein profile.

## **MATERIALS AND METHODS**

A total five individuals were randomly collected from each location on geographical and morphological basis as mentioned earlier. For each species at least 10 locations were selected. Tubers were cleaned with distilled water, pealed and cut into small strips. Small part measuring 1 gm from one location, thus samples from 10 locations were, dried at room temperature for 12 hours and transferred to oven at 55°C for 24 hours, then grinded into fine powder in pestle and mortle. Tuber powder (200 mg) was taken from the above composite bulk and was homogenated at room

temperature with 50 mM Tri-HCl buffer (pH 8.3) to added 10 mM 2-Mercaptoehanol, (Harvey and Boulter, 1983) and placed at 0°C for 24 hours and then subjected to centrifugation at 13000 rpm for 15 min at 4°C. The supernatant was transferred to 2 ml microcentrifuge tube containing 100 mg powder from bulk homogenate. The procedure was repeated twice. Protein electrophoresis was worked out according to the method of Laemmli (1970). Vertical polyacrylamide gel electrophoresis (SDS-PAGE) was carried out for separation of proteins, by using 15% Gel caste. Staining was performed by applying comassive brilliant blue stain R-250. Only the clear, unambiguous bands were considered for the preparation of unitary matrix by applying the method outlined by Nei and Li (1979). The phylogenetic analysis was carried out by using NTSYS-pc version 2.0 (Rohlf 1987) to generate similarity coefficient. The matrix was subjected to Unweighted Pair Group Method for Arithmetic average analysis (UPGMA) (Sokal and Micluner, 1958) to generate dendrogram using average linkage procedure.

## **RESULTS AND DISCUSSION**

Two procedures were followed, one with 50 mM Tris-HCl buffer (pH 8.3) to which 10 mM  $\beta$ -mercaptoethnol and second with 50 mM Tris-Glycine buffer (pH 8.3) with 10 mM  $\beta$ -mercaptoethnol was added. Storage proteins were soluble maximally in Tris-HCl buffer because of its high ionic strength.



Lane1- Molecular wt. Marker, L2- D.bulbifera, L3- D.oppositifolia, L4- D.hispida, L5- D.pentaphylla, L6- D.belophylla



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Species	D. bulbifera	D. oppositifolia	D. hispida	D. pentaphylla	D. belophylla
D. bulbifera	1				
D. oppositifolia	0.76	1			
D. hispida	0.66	0.75	1		
D. pentaphylla	0.75	0.82	0.84	1	
D. belophylla	0.60	0.54	0.46	0.42	1
			-		— D. bulbifera — D. oppositifolia — D. hispida — D. pentaphylla
0.00	0.25	0.50		0.75	— D. belophylla —

Table 1: Nei and Li similarity coefficient of SDS-PAGE

Fig. 2: Dendrogram showing genetic relationships between Dioscorea spp.

The five species of the genus *Dioscorea* were analyzed for proteins by 15% SDS-PAGE. Dormant tubers were taken for protein profile study. The tuber storage protein profile of five species of Dioscorea showed 11 stable bands, out of which 2 bands were monomorphic and 9 were polymorphic. The SDS-PAGE profile produced on an average 8 bands per species (fig. 1.). The highest similarity index was observed in D. hispida-D. pentaphylla (0.84) and the lowest in D. pentaphylla-D. belophylla (0.42). From similarity matrix (Table 1.) the dendrogram was constructed by using UPGMA method. It was evident that these five species were in two clusters. D. bulbifera, D. oppositifolia, D. hispida, and D. pentaphylla formed a distinct cluster (cluster-I), while D. belophylla was completely out-grouped and formed cluster II. Although, *D. bulbifera* and *D. oppositifolia* were placed nearer to each other, they did not pair and hence, were placed in two different sub-clusters (sub-cluster I and II). In this cluster D. hispida and D. oppositifolia was grouped together and formed sub-cluster III. The *D. belophylla* was distantly related with remaining four species (Fig.2).

The genus *Dioscorea* of MTR exhibited more diversity in morphology and protein profile as a biochemical marker used in present study was able to establish genetic relationship in the five species of MTR as well as for the taxonomic circumscription. Significant diversity was detected within the germplasm of *Dioscorea* spp. by isozyme pattern (Mignouna and Dansi, 2003). Cultivars of *Dioscorea cayenensisrotundata* complex can be distinguished based on their morphological traits and/ or their isozyme pattern (Mignouna *et al.*, 2002).

From dendrogram it was evident that these five species fell in to two clusters. The species *D. bulbifera*, *D. oppositifolia*, *D. hispida*, and *D. pentaphylla* formed a distinct cluster (cluster-I), while *D. belophylla* was

completely out-grouped and formed cluster II. The juvenile leaf of D. oppositifolia resembled with the mature leaf of D. bulbifera, moreover cormous head of D. oppositifolia apparently resembled with the tuber of D. bulbifera. In the dendrogram generated by SDS-PAGE these two species were placed nearer to each other but did not cluster, D. bulbifera of section Opsophyton was placed under sub-cluster I and D. oppositifolia of section Enantiophyllum under subcluster II. In the genus Brachypodium, B. mexicanum of section Brachypodium and B. distachyon of section Trachynia were clustered together in dendrogram generated on the basis of SDS-PAGE (Khan, 1992). In present investigation D. belopylla and D. oppositifolia of Enantiophyllum gets separated from each other. Similarly, cultivars of *D. rotundata* (white yam) and *D.* cayenensis (yellow yam) of section Enantiophyllum clearly separated from each other in dendrogram generated on the basis of isozymes (Mignouna et al., 2002). In the cluster I, D. hispida and D. oppositifolia of section Lasiophyton grouped together and formed sub-cluster III. The tripinnately compound leaf species D. hispida and D. dumetorum grouped together in the dendrogram generated on the basis of rbcL gene; D. pentaphylla and D. hispida placed nearer to each other on the dendrogram generated by *atpB* (Caddick *et al.*, 2002). Morphological analysis brought D. oppositifolia and D. hispida under compound leaf clade (Wilkin et al., 2005). The D. belophylla of section Enantiophyllum was distantly related with remaining four species in the forest of MTR.

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