CHARACTERIZATION OF BAMBOO ELITE CLONES FROM WESTERN GHATS OF INDIA USING RAPD MARKERS

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Summary
The elite clones of *Dendrocalamus strictus* and *Bambusa bambos* from Western ghats of India were analysed using random amplified polymorphic DNA markers. Out of 80 random primers, 42 in *D. strictus* and 32 in *B. bambos* produced polymorphic banding patterns. The results indicated a genetic similarity range of 61.40% to 84.23% in *D. strictus* while 51.58% to 93.11% in *B. bambos* and cluster analysis grouped eleven clones of each species into three major groups.

Keywords
Bamboo, RAPD markers, *Dendrocalamus*, *Bambusa*, Western ghats

Contribution
India is rich in biodiversity and has a wide spectrum of habitats from tropical rainforests to alpine vegetation and from temperate forests to coastal wetlands. About a third of the country's recorded flora are endemic and are concentrated mainly in the North-East, Western ghats, North-West Himalaya and the Andaman and Nicobar islands. Western ghats of India are known for their valuable biodiversity and has been considered as one amongst the top most important eight hotspots in the world [1]. This hotspot of biodiversity is a treasure house of genetic resources of many plant species including bamboos. The economy of India and so also of many Asian countries depends on bamboos and their uses are not only in domestic items but also in rural housing and raw materials to several industries. Out of several species of bamboos, *Dendrocalamus strictus* and *Bambusa bambos* are extensively found in Western ghats. In a study supported by IPGRI, elite clones of *Bambusa bambos*, *Dendrocalamus strictus* have been identified previously based on morphological characteristics like clump size, number of culms, culm height etc. In the present study, molecular diversity in the identified clones is being investigated using random aplified polymorphic DNA (RAPD) markers.

The previously identified elite clones of bamboo in the Western ghats were used for molecular characterization. Leaf samples of *Dendrocalamus strictus* were collected from the forest ranges of transects Barchi (Brc-1, Brc-2, Brc-3, Brc-4), Kerwad (Krd-1, Krd-2, Krd-3) and Tatawanagi (Ttg-1, Ttg-2, Ttg-3, Ttg-4) while samples of *Bambusa bambos* were from Dandeli (Dnd-1, Dnd-2), Badekhanshirda (Bde-1), Kogilbana (Kog-1, Kog-2, Kog-3), Arashinageri (Ars-1, Ars-2, Ars-3) and Bapeli (Bap-1, Bap-2). The DNA was isolated using the CTAB method [2]. A set of 80 random primers selected from OPJ, OPO, OPD, OPA, OPE, OPP, OPK and OPN kits (Operon Technologies, Inc. USA) were used in the study. The protocol for RAPD-PCR amplification of DNA [3] was followed with minor modification of thermal cycles as: 94 ˚C for 5 min; 40 cycles of 94 ˚C for 1 min, 36 ˚C for 1 min, 72 ˚C for 1 min; 72 ˚C for 5 min; 4 ˚C end. The amplifications were carried out on an Eppendorf Master

gradient cycler (Eppendorf AG, Germany) and the products were seperated by 1.5% agarose electrophoresis in 0.5x TBE buffer at 200 V for 2 h. The primers which produced polymorphic bands were used for scoring present (1) or absent (0) and matrix data was analysed using the standard procedure in NTSYS Pc2 package.

The results of present study indicated that out of 80 primers, 42 primers in *D. Strictus* and 32 primers in *B. Bambos* exhibited good polymorphism. The maximum genetic similarity of 84.23% was observed between Ttg-1 and Krd-3 while the lowest genetic similarity of 61.40% was between Brc-3 and Ttg-3 in *D. Strictus* (Table 1). The dendrogram of the pooled data showed three major clusters, the first cluster comprising of Brc–1, Brc–2, Brc–4, Krd–1, Krd–2, Krd-3, Ttg–1, Ttg-2 and Ttg-4, the second with Brc-3 and the third cluster with Ttg–3 clone.

Table-1: Genetic similarity (%) based on pooled data of RAPD profiles in D. strictus

	Brc-1	Brc-2	Brc-3	Brc-4	Krd-1	Krd-2	Krd-3	Ttg-1	Ttg-2	Ttg-3	Ttg-4
Brc-1	100										
Brc-2	83.61	100									
Brc-3	68.44	72.77	100								
Brc-4	73.90	76.84	75.47	100							
Krd-1	69.23	77.75	72.19	77.00	100						
Krd-2	69.40	74.50	64.87	75.12	76.09	100					
Krd-3	71.60	72.16	69.92	74.12	72.59	74.25	100				
Ttg-1	71.09	72.68	72.00	75.77	71.61	72.82	84.23	100			
Ttg-2	67.59	68.94	67.24	73.74	68.69	68.88	72.34	77.34	100		
Ttg-3	69.27	70.55	61.40	71.54	68.71	70.02	65.41	69.63	65.04	100	
Ttg-4	67.69	71.39	66.84	73.90	69.74	68.89	72.59	76.72	77.00	68.15	100

Table-2: Genetic similarity (%) based on pooled data of RAPD profiles in B. bambos

	Dnd-1	Dnd-2	Bde-1	Kog-1	Kog-2	Kog-3	Ars-1	Ars-2	Ars-3	Bap-1	Bap-2
Dnd-1	100										
Dnd-2	87.54	100									
Bde-1	93.11	89.03	100								
Kog-1	90.23	86.09	91.61	100							
Kog-2	67.21	63.41	69.29	65.04	100						
Kog-3	89.63	88.15	92.30	90.78	68.54	100					
Ars-1	88.51	89.70	88.67	88.37	63.67	89.76	100				
Ars-2	85.71	81.40	86.68	83.50	66.37	85.01	86.61	100			
Ars-3	85.71	82.19	86.66	84.93	66.10	87.07	83.16	85.09	100		
Bap-1	55.55	51.58	56.76	56.10	77.57	54.70	53.63	55.88	58.76	100	
Bap-2	70.68	68.50	72.51	69.29	72.72	75.78	69.56	65.82	72.13	68.20	100

The maximum genetic similarity of 93.11% was observed between Dnd-1 and Bde-1 while the lowest genetic similarity was between Bap-1 and Dnd-2 (51.58%) in *B. Bambos* (Table 2). The dendrogram in this species also showed three major clusters, the first having Dnd-1, Bde-1, Kog-3, Kog-1, Dnd-2, Ars-1, Ars-2 and Ars-3, the second Bap-2 and the third comprising of Kog-2 and Bap-1 clones. The study shows usefulness of RAPD markers in studying genetic similarity in bamboo and the financial support has been provided by NATP-CGP project of ICAR, New Delhi.

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