INTRODUCTION

Bamboos are vital to many Asian economies, having important uses ranging from domestic items to rural housing and raw materials for industry. The overexploitation and genetic erosion of bamboo species have made it necessary to preserve germplasm (Ramanayake 2006), whose classification and identification requires greater attention.

The vegetative character used for identification are the lack of basic knowledge of the biology and genetics of bamboo. This is the direct result of the unusual life cycle of bamboo. Among bamboo species, the vegetative growth varies from 1 to as much as 120 years and some species have never been known to flower (Ramachandran et al. 2007). Taxonomic studies that rely on floral morphology are therefore limited. The bamboo inflorescence is an area of morphology with serious problems of interpretation. The inflorescence type, somelautant and interauctant, that has been used in defining genera is not easy to interpret (Li 1997). Although Stapleton (1997) forwarded a modern interpretation, it has not been widely adopted as it radically alters the traditional terminology. According to Watson and Dallwitz (1992), description of bamboo species will not be possible until the descriptive terminology of inflorescence and spikelet morphology are standardized.

The vegetative character used for identification are likely to be subtle and variable in most cases, it is difficult to say how much they reflect the true evolutionary history of these plants (Wu 1962; Ohnberger 2002). Therefore, molecular-based approaches were undertaken to establish phylogenetic relationships in temperate bamboos targeting either the nuclear genome (Friar and Kochert 1994; Kobayashi 1997) or nuclear r-RNA gene sequences (Hodkinson et al. 2000; Guo et al. 2001).

Since its discovery (Williams et al. 1990), Random Amplified Polymorphic DNA (RAPD) technique has been successfully employed in the evaluation of genetic relationships in several plant species, including bamboo (Gielis et al. 1997; Nayak et al. 2003; Rout 2006; Das et al. 2006; Ramanayake et al. 2007).

In this paper, we demonstrated the use of RAPD in bamboo identification as well as determining genetic diversity and relationships between selected 26 bamboo species.
with initial strand separation at 94°C for 3 min, followed by annealing at 37°C for 1 min and extension at 72°C for 1 min. After 35 cycles there was a final extension at 72°C for 10 min. Amplification products were electrophoresed in 1.6% agarose gel and stained with ethidium bromide. Each set of reactions was repeated in triplicate and only the reproducible bands were included in the analysis.

**Statistical analysis**

Evaluation of variation in the RAPD profile was performed by calculating the individual band frequency for each species. Polymorphism was scored for the presence (1) or absence (0) of bands. Cluster analysis was performed on the similarity matrix based on Jaccard’s similarity index by the UPGMA method. All computations were performed with NTSYS-PC version 2.1 (Rohlf 1993).

**RESULTS AND DISCUSSION**

Fifty, 10-mer random primers of OPM, OPH, OPO, OPB, and OPB series were tested for their ability to produce polymorphic bands. Primers resulting in monomorphic, too complex and irreproducible patterns were excluded from the studies. Ten primers were selected for further studies. The total number of scorable bands amplified using these 10 primers was approximately 58. Thus the average number of bands amplified per primer varied between 6 and 9 of the 10 primers was approximately 58. Thus the average number of scorable bands generated per primer varied between two to eight. Of the 10 random primers, the percentage polymorphism was greatest in OPH 19 (88.88%) (Fig. 1), followed by OPM 16 (75.01%). Least polymorphism was found in OPO 10 (33%). Cluster analysis (Fig. 2) was performed based on the banding pattern obtained utilizing all 10 primers. Species like D. stocksii and O. stocksii were clustered together. Similarly, D. strictus, D. hamiltonii and D. asper had similar banding patterns and thus they appeared in a single cluster. In case of Bambusa species, B. nutans, B. vulgaris and B. mugalba showed similarity and are inferred as closely related species.

RAPD results support the position of *Thysostachys* within Bambusinae as a genus distant from *Bambusa*. This result is also confirmed by the AFLP studies (Loh 2000). The two different clusters of *Bambusa* spp. suggest that the genus *Bambusa* is polyphyletic and highlights the potential of RAPD to assess the variation and relationships within this genus. The two *Dendrocalamus* spp. examined were very different to *D. brandisii* falling within the *Bambusa* cluster. *D. giganteus* showed the least genetic similarity to any of the *Bambusa* species examined. The relationship between these species has been studied and split into several genera (Li 1997). Currently the genus *Dendrocalamus* is used in a broad sense (Li 1997; Wong 1995). At one ex-

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**REFERENCES**


Hodkinson TR, Renvoize SA, N’Chonghaile G, Stapleton CMA, Chase...
RAPD analysis of 26 bamboo genotypes. Eevera et al.


