

Characterization of Microsatellites in *Bambusa arundinacea* and Cross Species Amplification in Other Bamboos

Sumitra Nayak and Gyana Ranjan Rout*

Plant Biotechnology Division, Regional Plant Resource Center, Nayapalli,
Bhubaneswar – 751015, Orissa, India. E-mail: grrout@hotmail.com

* Author for correspondence and reprint requests

Z. Naturforsch. **60c**, 605–610 (2005); received January 30/February 23, 2005

Microsatellites, tandem repeats of short nucleotide (1–6 bp) sequences, are the DNA marker of choice because of their highly polymorphic, ubiquitous distribution within genome, ease of genotyping through polymerase chain reaction (PCR), selectively neutral, co-dominant and multi allelic nature. Six microsatellites, three polymorphic and three monomorphic, have been characterized for the first time in a bamboo species, *Bambusa arundinacea* belonging to the family Poaceae. The number of alleles per locus ranges from 2 to 13. Allelic diversity ranges from 0.041 to 0.870. Polymorphic information content (PIC) values for two loci were > 0.3 , an indicator of polymorphic allele. Cross species amplification has been tested in other 18 bamboo species. Monomorphic simple sequence repeats (SSRs) have been found to be cross amplified in most of the tested species while polymorphic ones in only three to four species. The utility of the SSR loci in genetic diversity study of *B. arundinacea* and other cross amplified bamboo species have been discussed.

Key words: Microsatellite, *Bambusa arundinacea*, Cross Species Amplification