



EVALUATING PHYLOGENY AMONG 34 EASTERN INDIAN BAMBOO SPECIES USING CHLOROPLAST DNA BARCODE MARKERS

SANJAY SINGH^{1*}, AMRITA SINHA² AND KANCHAN KUMARI²

¹ Scientist F and Head, Forest Research Centre for Eco-Rehabilitation
3/1 Lajpatrai Road, Prayagraj-211002, U.P., India

² Indian Institute of Natural Resins and Gums
Tata Road, Namkum, Ranchi - 834010, Jharkhand, India

*Corresponding author email: sanjay.drsingh@gmail.com

ABSTRACT: The performance of three chloroplast markers viz. *rbcL*; *mat K* and *rpoC1* was evaluated for DNA barcoding purpose and complementary construction of phylogenetic relationship among the 34 species of eastern Indian selected bamboo species. The study provides comparative assessment of universality, resolvability and benefits of combining loci for three candidate plastid barcoding markers in bamboos. The primer pairs resulted in 100% PCR amplification and sequencing success. Unambiguous monomorphic amplicons of molecular weights 738 bp for *rbcL*; 930 bp for *mat K* and 450 bp for *rpoC1* were obtained, respectively. The best substitution models were selected for generation of dendrograms along with their rates among sites and gap/missing data. Genetic similarity of *B. polymorpha* and *P. aurea* was exhibited in dendrograms generated by individual markers and dendrogram generated by three markers together indicated that these barcode markers do not suffice the purpose of discrimination between these two species. However, close affinity between these species placed in most taxonomic classifications in different sub-tribes warrants further introspection. Similarly barcode marker *rbcL* alone as well as the information from all the three markers combined ascertained the close proximity of *Bambusa nana* and *Schizostachyum pergracile*. As a single DNA barcode, the three plastid DNA markers provided low species discrimination. However, the universality and sequencing success proved barcoding proved their suitability in barcoding.

Key words: Amplification, barcoding, phylogeny, sequencing, universality

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INTRODUCTION

Bamboos are members of subfamily Bambusoideae within the grass family Poaceae, which is monophyletic having early diverging lineages. Among bamboo species, the vegetative growth phase varies from 1 year to as long as 120 years, and some species have never been known to flower (Janzen, 1976). Because of this peculiar and uncertain nature of flowering, vegetative parts such as rhizomes, culms, culm sheaths, ligules, branching, and leaves have been traditionally used to classify and establish phylogenetic relationships among the bamboo genera (Ohrnberger and Goerrings, 2002; Isagi *et al.*, 2004; Sharma *et al.*, 2008). Taxonomic demarcation of woody bamboos at lower ranks, such as genera and species, is not well

resolved to date (Sharma *et al.*, 2008). Quite often, morphological characters are influenced by environment and are complex, limited in number, and state-specific in their expression, making an objective analysis difficult (Wu, 1962). This has led to the misclassification of bamboo genera and species due to phenotypic plasticity and genotypic variability of characters, overlooking of morphologically cryptic taxa which are common in many groups, constraints associated with morphological keys which are effective only at a particular stage of life or dependant on gender (Sreekumar *et al.*, 2008). In a nut shell, bamboo taxonomy remains in a state of flux with classification and subsequent reclassification of bamboo genera/species frequently resulting in confusion. Use