

EVALUATION OF GENETIC DIVERSITY IN BAMBOO SPECIES THROUGH SDS-PAGE PROTEIN ANALYSIS

M.S. BHANDARI, R. KAUSHAL¹, R.L. BANIK² AND S.K. TEWARI²

Division of Genetics & Tree Propagation, Forest Research Institute, Dehradun (Uttarakhand)

ABSTRACT

Bamboos serve as multipurpose forest grass species. The success of bamboo as a commercially important forage species depends on the identification of genetically divergent materials of the plant and developing superior planting stock for the farmers. The phylogeny plays a crucial role in the evolution of species and superior germplasm. Twenty-two species of bamboo were evaluated for genetic diversity characterization through SDS-PAGE analysis. Based on electrophoretic pattern, banding pattern was established for 22 species. Also, on genetic diversity analysis, 22 species of bamboo were grouped into four clusters. Cluster IIBb had maximum number of species (9), cluster IIBa and cluster IIAb had four species each, whereas, Cluster IIAa and cluster IA had maximum of two and three species respectively. UPGMA (Unweighed Paired Group Mean Cluster Analysis) inferred that among *Bambusa* genera; species *B. bambusa*, *B. multiplex*, *B. vulgaris*, *B. balcooa*, *B. tulda*, *B. nutans*, *B. polymorpha*, *B. nutans* and *B. pallida* and among *Dendrocalamus* species *D. hamiltonii*, *D. giganteus*, *D. membranaceous* and *D. longispathus* were genetically similar having Jaccard's similarity coefficient ranged from 0.80-1.00.