

DNA barcoding to discriminate *Dalbergia spp.* from western ghats Bhagwat R M, Dholakia B B, Balasundaran M*, Kadoo N Y and Gupta V S

National Chemical Laboratory, India *Kerala Forest Research Institute, India

The Western Ghats (WG) in India is amongst the 25 biodiversity hotspots identified in the world and well known for their rich and unique flora and fauna. Dalbergia [from the family of pea (Fabaceae)] is an important member of the WG flora; valued for decorative and often fragrant wood (rosewood, African blackwood, sisu) and is rich in aromatic oils. There is taxonomic confusion with respect to several Dalbergia species as these often have more than one species names. Hence, the size of the *Dalbergia* genus remains disputed. DNA barcoding is a modern biotechnological tool, which can distinguish species that look alike. It is well established in animals; however, a universally accepted barcode is still lacking in plants. Hence, the main objective of this study is to develop a unique barcode for quick, accurate and reliable species identification using the Dalbergia genus as a model system. Leaf samples from 15 accessions each, belonging to six validated Dalbergia species (D. melanoxylon, D. candenatensis, D. rubiginosa, D. latifolia, D. volubilis and D. paniculata) were collected from different locations in WG and DNA extractions have been carried out from these as well as characterized herbaria samples. A total of 37 primer pairs specific to several chloroplast genes (matK, rpoC, rpoB, rbcL, accD, ndhJ, ycf5 and trnH-psbA) as well as the nuclear ITS were evaluated on the samples and 16 of these have been standardized for the six Dalbergia species. We are currently analyzing six loci corresponding to matK, rpoc, rpoB, rbcl, trnH-psbA and nuclear ITS. We analyzed single locus as well as combinations of two loci to achieve species resolution. The initial results were obtained in MEGA software on the basis of NJ tree. Further work is in progress to achieve 100% species resolution and develop a successful barcode using other important genes either individually or in combination.