

Identification of admixtures in *Melia dubia* germplasm as revealed by Bayesian analysis

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Melia dubia, an important agroforestry tree species, although it has its diversity hotspot in north-eastern states of India, it has been found to be dispersed in various other states as well. Therefore, to detect gene flow between populations, 185 genotypes from different geographical origins were sampled to identify and study the occurrence of admixtures using 60 Simple Sequence Repeats (SSRs) generating definite and reproducible bands. Bayesian structure analysis grouped genotypes into 6 (best $\Delta K = 6$) genetic groups. Through membership likelihoods ($Q > / < 0.60$), admixture analysis revealed 175 genotypes to be highly pure, whereas the remaining 10 were mixed indicating genetic mixing. The present study highlights the efficiency of SSRs for the molecular portrayal of *M. dubia* and assessing its genetic diversity for genetic improvement through effective breeding schemes.

Keywords: Admixture, Bayesian, membership likelihood, *Melia dubia*, mixing.

to examine whether *M. dubia* genotypes of a particular region/population are pure or are they admixed from different regions. This will put light on gene flow occurring between individuals of *M. dubia* which will further lead to better selection strategies for tree breeding programmes and will also generate a region-specific DNA fingerprint database of genotypes belonging to specific geographical origins. Utilising the basic principle of comparing likelihoods through Bayesian analysis, STRUCTURE is the first and prior step to examine population structures to infer origin of individuals, especially in the cases where population admixture occurred by designing membership coefficients across the genetic clusters obtained².

Methodology

Sample collection and DNA extraction

To detect admixtures in the studied existing populations of