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Evaluation of Adaptive Fitness of Indian Teak (Tectona grandis L. F.) Metapopulation through Inter Simple Sequence Repeat Markers

Authors : Vivek Vaishnav, Shamim Akhtar Ansari

Abstract : Teak (Tectona grandis L.f.) belonging to plant family Lamiaceae and the most commercialized timber species is endemic to South-Asia. The adaptive fitness of the species metapopulation was evaluated through its genetic differentiation and assessing the influence of geo-climatic conditions. 290 genotypes were sampled from 29 locations of its natural distribution and the genetic data was incorporated with geo-climatic parameters. Through Bayesian approach based analysis of 43 highly polymorphic ISSR markers, six homogeneous clusters (0.8% genetic variability) were identified. The six clusters were found with the various regimes of the temperature range, i.e., I - 9.10±1.35^{0}C, II -6.35±0.21^{0}C, III -12.21±0.43^{0}C, IV - 10.8±1.06^{0}C, V - 11.67±3.04^{0}C, and VI - 12.35±0.21^{0}C. The population had a very high percentage of LD (21.48%) among the amplified loci possibly due to experiencing restricted gene flow as well as co-adaptation and association of distant/diverse loci/alleles as a result of the stabilized climatic conditions and countless cycles of historical recombination events on a large geological timescale. The same possibly accounts for the narrow distribution of teak as a climax species in the tropical deciduous forests of the country. The regions of strong LD in teak genome significantly associated with climatic parameters also reflect that the species is tolerant to the wide regimes of the temperature range and may possibly withstand global warming and climate change in the coming millennium.

Keywords : Bayesian analysis, inter simple sequence repeat, linkage disequilibrium, marker-geoclimatic association
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