



Sampling strategies for natural *Toona ciliata* populations

J. Liu and J.M. Jiang

Research Institute of Subtropical Forestry, Chinese Academy of Forestry,
Fuyang, China

Corresponding author: J.M. Jiang
E-mail: jiang_jingmin@163.com

Genet. Mol. Res. 15 (4): gmr15047751

Received March 29, 2016

Accepted June 6, 2016

Published October 17, 2016

DOI <http://dx.doi.org/10.4238/gmr15047751>

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

ABSTRACT. The genetic diversity and spatial autocorrelation of *Toona ciliata* populations were analyzed with eight microsatellite markers to determine an appropriate sampling strategy for the effective conservation of natural *T. ciliata* populations. The average number of alleles and effective number of alleles were 6.1 and 2.7, respectively. The mean expected heterozygosity was 0.6006. Overall, 96.6% of the genetic variation existed in two natural populations, which was concluded from the coefficient of genetic differentiation ($F_{ST} = 0.1854$). Therefore, two natural populations were selected for conservation and sampling. The mean effective number of alleles and expected heterozygosity increased with increasing sample number. The mean expected heterozygosity tended to be stable when the sampling number exceeded 30. The maximum value of expected heterozygosity was 0.4770 when the sampling number was 45. Therefore, 45 sampled individuals were sufficient for conservation and sampling. Similarity relationships existed between individuals within 240 m. There were marked differences among individuals over 240 m away. The distance

between individuals exceeded 240 m when natural populations were sampled.

Key words: *Toona ciliata*; Genetic diversity; Sampling strategy; Spatial autocorrelation analysis