



Isolation and characterization of polymorphic microsatellite loci from *Zelkova schneideriana* Hand.-Mazz.

H.L. Liu^{1,2}, R.Q. Zhang¹, M.L. Geng³, J.Y. Zhu^{1,2} and J.L. Ma^{1,2}

¹College of Forestry, Central South University of Forestry and Technology, Changsha, Hunan, China

²Forestry Research Institute of Guangxi Zhuang Autonomous Region, Nanning, Guangxi, China

³Institute of Botany, Jiangsu Province and Chinese Academy of Sciences, Nanjing, Jiangsu, China

Corresponding author: R.Q. Zhang
E-mail: hanszhangriqing@csuft.edu.cn

Genet. Mol. Res. 13 (4): 10062-10066 (2014)

Received May 6, 2014

Accepted September 24, 2014

Published December 3, 2014

DOI <http://dx.doi.org/10.4238/2014.December.3.1>

ABSTRACT. *Zelkova schneideriana* is a highly valued hardwood species. An improved technique for isolating codominant compound microsatellite markers was used to develop simple sequence repeat markers for *Z. schneideriana*. A total of 12 microsatellite loci were identified. Overall, the number of alleles per locus ranged from 8-19, with an average of 11.75. Observed heterozygosity and expected heterozygosity values ranged from 0.109-0.709 and 0.832-0.929, respectively. Polymorphic information content is from 0.803-0.915, with an average of 0.854. These markers will be very important for future research related to the genetic diversity, population structure, patterns of gene flow, and mating system of this species.

Key words: Genetic diversity; Microsatellite loci; Simple sequence repeat; *Zelkova schneideriana* Hand.-Mazz. SSRs