



Genetic diversity in fragmented populations of *Populus talassica* inferred from microsatellites: implications for conservation

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Genet. Mol. Res. 15 (2): gmr.15027899

Received October 22, 2015

Accepted January 18, 2016

Published May 25, 2016

DOI <http://dx.doi.org/10.4238/gmr.15027899>

ABSTRACT. *Populus talassica* Kom. is an ecologically important species endemic to central Asia. In China, its main distribution is restricted to the Ili region in the Xinjiang Autonomous Region. An understanding of genetic diversity and population structure is crucial for the development of a feasible conservation strategy. Twenty-six high-level simple sequence repeat (SSR) markers were screened and used to genotype 220 individuals from three native populations. A high level of genetic diversity and low population differentiation were revealed. We identified 163 alleles, with a mean of 6.269 alleles per locus. The observed and expected heterozygosities ranged from 0.472 to 0.485 (with a mean of 0.477), and from 0.548 to 0.591 (mean 0.569), respectively. Analysis of molecular variance revealed 93% variation within populations and

7% among populations. A model-based population structure analysis divided *P. talassica* into two groups (optimal $K = 2$). These genetic data provide crucial insight for conservation management.

Key words: *Populus talassica*; Genetic diversity; Population structure; Microsatellite