MICROSATELLITE VARIATION IN LOBLOLLY PINE CHLOROPLASTS

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Abstract. Organelle genomes can provide a different and useful perspective on genetic variation in organisms. A special feature of organelle genomes is uniparental haploid inheritance without recombination. In animals, high levels of genetic variation in mitochondrial genomes has made it possible to describe within species phylogenetic trees that could reflect population history and evolutionary divergence. However, plant organelle genomes have been less useful because plant mitochondria are more complex and chloroplasts have low levels of DNA sequence variation. PCR-based "microsatellite" markers from genomic DNA are based on simple sequence repeats (i.e., repeated sequences of single nucleotides or dinucleotides or trinucleotides) that often show high levels of variation in repeat number. In pine, the chloroplast genome (approximately 120 kb) is inherited through the pollen parent and contains 20 microsatellite regions. We found that the gene diversity of loblolly pine cpDNA microsatellite markers is relatively high, suggesting that cpDNA microsatellite markers could distinguish individuals and be useful for assessing paternity in seed orchards and natural populations.

Keywords: *Pinus taeda,* microsatellites, paternity, chloroplast