

***trnL-trnF* Intergenic Region Polymorphisms Reveal Chloroplast Paternal Inheritance
Among Three *Pinus* Species**

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The inheritance patterns of the chloroplast genomes of *Pinus echinata*, *Pinus taeda* and *Pinus elliottii* were investigated through *trnL-trnF* intergenic spacer polymorphism analysis. The DNA sequences of this spacer differ among these three closely related *Pinus* species. A modified 'cold' PCR-SSCP (single-strand conformation polymorphism) analysis of this spacer shows that the artificial hybrids (F1) from the cross, *Pinus echinata* (seed parent) x *Pinus taeda* (pollen parent), exhibit the *Pinus taeda* profile. The nine putative hybrids between *Pinus echinata* and *Pinus taeda*, previously identified by the IDH allozyme marker, presented the *Pinus echinata* profile. Nondenatured polyacrylamide gel electrophoresis of the *trnL-trnF* intergenic spacer demonstrated that the artificial hybrids (F1) from the cross, *Pinus elliottii* (seed parent) x *Pinus echinata* (pollen parent), present the *Pinus echinata* profile. These results confirmed that the chloroplast genome is paternally inherited in the genus *Pinus* and that *Pinus echinata* sired all of the putative hybrids between *Pinus echinata* and *Pinus taeda*. The significance of the *trnL-trnF* intergenic region polymorphism and our modified 'cold' SSCP protocol for population genetic studies is discussed.