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### Whole Genome Shotgun And BAC Sequences In Loblolly Pine (*Pinus taeda* L.): The Majority Of The 22-Gb Genome Appears To Be Highly Diverged And Nested Repetitive Elements.

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The large size of pine genomes (20-40 Gb) has long precluded large-scale genomic sequencing in this ecologically significant family of conifers. Further complicating genomic exploration, all pines have 24 similarly sized chromosomes ( $n=12$ ) that show no evidence of recent genome duplication or polyploidy. The pine genomes show a high degree of synteny, which has permitted comparative mapping in these massive genomes. This implies that a genome assembly for one species could essentially serve as a reference genome against which to assemble other pine genomes or regions therein, accelerating studies within the *Pinus* genus. Further sequencing of the loblolly pine genome will be greatly assisted by a description of the noncoding, or repetitive, component. In this study, we describe the complex nature of the repetitive fraction of the loblolly pine genome. Using a combination of sequencing platforms and innovative sequence analyses, we show that the genome contains very few identical repeats. We report that the exceptionally large noncoding fraction of the genome will not likely pose the problems in assembly seen in other large genomes such as human and maize. Bacterial artificial chromosome assemblies and whole genome shotgun sequences representing 7.6% of the loblolly pine genome indicate that (1) next-generation sequencing technology can be used to assay a large complex genome, (2) money is the primary obstacle to sequencing the pine genome, and (3) using a combination of sequencing platforms is a plausible approach to reducing the cost of sequencing the genome of loblolly pine.

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