RFLP MAPPING OF THE LOBLOLLY PINE (*Pinus taeda* L.) GENOME

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A genetic linkage map of loblolly pine (*Pinus taeda* L.), a commercially important forest species, is being developed using restriction fragment length polymorphisms (RFLPs) as molecular markers. The genome of loblolly pine ($2x=2n=24$) is very large (10E10bp), which presents some difficulty in detecting single-copy sequences on Southern blots. Recombination size has been conservatively assessed at 2,000 cM; therefore, 20 cM-saturation can be achieved with 200-300 RFLPs. A single 3-generation pedigree, obtained from a commercial tree breeding program, was selected to construct the map. This pedigree was chosen on the basis of its high level of heterozygosity, as determined from isozyme and RFLP analyses. Several restriction enzymes were chosen for their ability to digest loblolly pine genomic DNA and reveal polymorphisms. Random cDNA clones are currently being screened to identify RFLPs in the parent lines. Thus far, approximately 30% of the clones have revealed polymorphisms. These clones will be used for segregation analysis of RFLPs in progeny DNAs. The completed map will be valuable in understanding the structure and organization of the loblolly pine genome, as well as assisting in the genetic improvement of this species.