# Gene Expression Profiling In Differentiating Xylem Of Loblolly Pine

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The formation of secondary xylem is a biological process of both ecological and economic importance. Over 40,000 xylem ESTs have now been sequenced from loblolly pine, the most important commercial forest tree species in the U.S. (web.ahc.umn.edu/biodata/nsfpine). Our goal is to learn more about regulatory, biosynthetic and cellular processes involved in secondary xylem differentiation by characterizing gene expression profiles. These studies aim at a broad understanding of the roles of newly discovered pine genes in secondary xylem formation and identifying candidate genes that potentially control specific wood properties. We are currently conducting preliminary experiments with ~350 abundantly expressed pine xylem ESTs; comparing glass slide microarray and membrane array systems to optimize methods.

The natural variability of wood properties affords opportunities to correlate transcript profiles with wood properties. For example, we are comparing transcript profiles of differentiating xylem at different times during the growing season, corresponding to early wood and late wood. Wood specific gravity is known to vary significantly between these two phases of xylem formation in loblolly pine. Cell wall thickness ranged from 3 µm (in early wood) to 8 µm (in the late wood) within a single growth ring and differential expression of specific ESTs may correlate with cell wall thickness. Other opportunities to investigate the relationship between wood properties and gene expression include comparisons of juvenile and mature wood, compression and normal wood, as well as the analysis and genetic variability among populations and in pedigree families.