GEONOMIC APPROACHES FOR INCREASING SUSTAINABLE BIOMASS HARVEST IN SOURTHERN FORESTS

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A wealth of genomic sequence information and tools has become available in recent years for loblolly pine (Pinus taeda) and an increasingly wider array of other conifer species. These powerful technologies open a wide range of new opportunities to address both short-term and long-term challenges to productivity in southeastern conifer forests. In this presentation we will touch on three case studies in which various genomic tools are being used to address specific problems in loblolly pine. In the first example, spotted DNA microarrays have been used to follow gene expression patterns in different clones of loblolly pine responding to water stress. The work identified networks of genes that responded to water stress in a coordinated fashion, and also identified so-called hub genes that may be master regulators of these network responses. Such hub genes have been recognized as important breeding targets for improvement programs. In the second example, a truncated microarray experiment was used to identify biomarker genes whose expression was induced when loblolly pine was exposed to venom injected into pine trees by the invasive exotic woodwasp, Sirex noctilio. Quantitative PCR assays for these biomarker genes were used to demonstrate that Monterey pine (Pinus radiata) is about 100-fold more sensitive to the venom than is loblolly pine, and that sensitivity varies by genotype within these two pine species. These findings set the stage for breeding resistance against S. noctilio into loblolly pine, which may be important now that S. noctilio has become established in North America. Finally, we will revisit an old study of differential gene expression in compression and opposite wood, and use a new database of transcribed gene sequences for loblolly pine to identify genes whose expression is most affected in these different reaction woods. The results highlight genes that contribute to the undesirable qualities of compression wood, and may provide additional targets for advanced breeding efforts.