Center for Tree Genetics (CTG)

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Method for Identifying Genes Controlling Growth of Trees

Manipulation of plant stature has long been a major goal in agronomy, horticulture, and silviculture. Trees of short stature can provide substantial benefits for urban forestry and wood products industries. CTG researchers have established a method for identifying genes that affect the growth and development of trees. This research has resulted in the first identification of a gene underlying an unusual tree form and size. The difficult biology and genetics of trees, including their long generation time, has impeded such efforts in the past. Control of plant stature and form previously required the use of plant growth regulators or classical plant breeding. It is difficult to obtain through classical breeding the healthy dwarf plants of the variety needed for large-scale commercial deployment. The new method, using "activation tagging," allowed CTG to circumvent several roadblocks. Center research on creating an activation-tagged poplar population is finding application, according to a Weyerhaeuser representative. This work is expected to provide numerous new genes for exploring and manipulating the development and physiology of trees.

Furthermore, CTG researchers identified a gene that controls tree size in a dominant manner, enabling the size of any tree to be reduced via over-expression of this gene. This result could provide a valuable new way to reduce tree size for uses in urban and orchard environments, and can be used as a tool to provide a high degree of biosafety to linked transgenes that derive from other species. This work appears to be the first case of successful forward genetics - where a gene has been isolated based on a mutant phenotype - in a tree. For more information, contact Steven Strauss, 541-737-6578; e-mail: Steve.Strauss@orst.edu.

Precocious Flowering in Populus

Federal regulators have made it clear that a transgene confinement system must be developed before genetically engineered trees can be deployed commercially. Center researchers are attempting to genetically engineer reproductive sterility as a way to satisfy this requirement. In order to test the efficacy of the genetic constructs inserted in the poplar genome for their ability to impart sterility, researchers must wait for flowering to occur. The long delay before the onset of flowering in poplars (they have a juvenile period of five to seven years) and their resistance to various conventional flower-induction treatments have been serious impediments to engineering sterility. CTG obtained a genotype of Populus alba from a colleague at the University of Tuscia (Viterbo, Italy) that flowered nine months from when the seed was sown. Vegetative propagules from this line remained true to type (i.e., they flowered in nine months). However, this genotype had to be regenerated in vitro, and grown under aseptic conditions, before APHIS would allow it to be imported into the U.S. The regeneration process caused this genotype to lose its ability to flower early. CTG experimented with a variety of inductive treatments and discovered one that restored the early-flowering phenotype. Center researchers now have an effective model system for testing sterility constructs, without having to conduct lengthy, expensive field trials. For more information, contact Rick Meilan, 765-496-2287; e-mail: rmeilan@fnr.purdue.edu.