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Indiana's Forest Legacy Program Valuable, Beautiful Forests — Forever

PART #1

U.S. Senator Dick Lugar, and State Forester Burney Fischer recently announced Indiana's acceptance into the Forest Legacy Program of the U.S. Forest Service.

The Forest Legacy program purchases development rights to help protect environmentally sensitive forest lands from being developed for commercial, residential or other non-forest uses. The Indiana program is administered by the Indiana DNR, Division of Forestry and is funded largely by the United States Department of Agriculture (USDA) Forest Service.

The Forest Legacy program will help the State acquire and administer conservation easements, or development rights, from willing forest landowners. The owners retain all other rights, including the right to manage timber and sell or bequest the remaining rights. While ownership remains in private hands, the permanent conservation easement would ensure that the land would remain forested for future generations. The land would also remain taxable on the property tax roles at some level.

Indiana program targets six areas in the state where forest lands are threatened with deforestation. Of Indiana's 4.4 million acres of forest land, 87% is privately owned. Economic pressures on forest landowners have prompted the splitting of ownerships and the sale of land to developers for shopping malls, houses or other non forest uses.

"Hoosier forest lands provide recreational opportunities and multiple environmental benefits such as water quality, wildlife habitat and protection of endangered species", said Lugar, who owns and operates his family's 604 acre corn, soybean and tree farm in Marion county. "The Forest Legacy Program will help conserve its important forest heritage."

PART #2

Questions Commonly Asked about Indiana's Forest Legacy Program

- Q:** Can the way the forest is managed, and what it is used for, change after it's entered in the Forest Legacy Program?
- A:** Yes. As long as the new use is compatible with the long-term sustainability of the forest, the forest stewardship plan can be amended.
- Q:** Can I build a house, or make other improvements within the easement area?
- A:** No. Any part of the property that you may want to use for improvements should be excluded from the easement area at the time the parcel enters the program.

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APPLICATION OF ADVANCED TECHNOLOGIES FOR IMPROVEMENT OF HARDWOOD FORESTS

Charles H. Michler, Director of Hardwood Tree Improvement and Regeneration Center

Hardwood tree improvement in Indiana is on the brink of entering the 21st century with the recent initiation of the Hardwood Tree Improvement and Regeneration Center (HTIRC) at Purdue University. At a time when midwestern agriculture has enthusiastically embraced genetically modified insect and herbicide resistant corn and soybean crops and all the human genes are close to being sequenced through the human genome project, we can now begin to envision similar advancements of gene discovery and the applications thereof to genetic improvement with hardwood trees.

Purdue University Department of Forestry and Natural Resources, Indiana Department of Natural Resources Division of Forestry, Indiana forest industry and the USDA Forest Service have entered into a unique partnership whereby funds, facilities, and expertise will be shared and leveraged to create a center with a unified vision for the sole purpose of applying advanced biological technologies to hardwood tree improvement for enhanced forest productivity. Each group brings to the table unique abilities that will allow the HTIRC to develop new technologies and products and then deliver them to nurseries, landowners and public agencies through development of low cost improved seed and seedlings.

The USDA Forest Service scientists under the direction of Center Director, Charles Michler already have a proven track record in this type of research. His unit in Rhinelander, Wisconsin was the first in the world to genetically modify a tree. In this case, it was hybrid poplar that was engineered for herbicide resistance. This effort was an early example of university, federal and industry collaboration albeit much less formalized and on a much smaller magnitude than the arrangement that has been created at Purdue. Recently, these same techniques developed in Rhinelander have been applied commercially by forest industry in the Pacific Northwest through a research consortium of 23 member paper companies, nurseries, and federal agencies administered at Oregon State University. As a result, Roundup™ and leaf beetle resistant cottonwoods have been undergoing field testing for 3 years now and appear to be good candidates for deployment in clonal fiber farms.

More recently, Michler's Rhinelander unit has developed new technologies for eastern white pine. Scientists in his program have developed tools by which genes for blister rust resistance can be identified in rust resistant families. Upon identification of these unique genes, techniques developed through his personal research program can be employed to insert these genes into superior white pine trees that lack these genes for resistance. Even more important, he has developed techniques to produce hundreds of thousands of these new trees in the laboratory through a process that induces pine cells to form artificial embryos. These embryos can then be stimulated to germinate like seeds and grow into normal seedlings. Instead of having one tree that is improved, many improved individuals can be produced over a short period of time.

Michler's unit has also been on the leading edge of development of white pine molecular genetic markers. These are not genes, but rather are unique pieces of non-coding DNA located between genes that can be used to "mark" locations on chromosomes near genes for important traits. These markers can be used in several ways. First, markers can be developed that associate with a gene or genes for an important trait such as anthracnose resistance. Then this marker can be used to actually find that gene on a particular chromosome and isolate it. Once isolated, it can be introduced into another tree having other superior traits in which you would like to complement with your new gene. Second, markers can be used to study populations of tree species. For example, if we wanted to study whether high-grading had resulted in loss of genetic quality in a stand, we could use our markers to "fingerprint" the genetic make-up of an unmanaged stand and compare that to the "fingerprint" of the high-graded stand. If we found a loss of markers through this forest management strategy, we could predict the loss of genetic quality and genetic variation. Third, markers

can be used to "mark" genes that we desire in improved seedlings in seed orchards. If we have a marker for a trait such as gypsy moth resistance in a red oak tree that we are using as a parent tree for sexual mating, then we can easily take a tissue sample from seedlings that were derived from that cross and test for that marker. If that particular seedling has the marker, then it has inherited that gene from the parent tree. This type of testing is not unlike having blood samples analyzed in a hospital laboratory.

Last, we have developed techniques that could be applied to tree forensics. Tree theft is extremely costly to the forestry community and some federal forest managers estimate the annual value of timber lost to theft in the US exceeds the proceeds from federal timber sales. Not unlike DNA analysis used in a recent nationally televised trial of a professional football celebrity, we can use markers to produce a DNA fingerprint from a tree stump and match it to wood fibers retrieved from a suspect's tree, chains, vehicles, or stolen logs.

The HTIRC plans to focus its initial work on improvement of northern red oak and walnut and much of the research emphasis will differ for plantation versus trees for natural forests. Midwestern hardwood species are basically wild species that have not been domesticated. The potential for increased productivity is huge. While we may not see the increase in productivity that has taken corn production from 20 bushels per acre to over 300 bushels, we can still expect to obtain significant increases. Commercially, we can also expect the value of increased hardwood productivity to rise significantly from small gains in wood productivity and quality. Using a conservative example, a 1% increase in annual production of quality northern red oak would result in an annual revenue increase of \$1-5 million based on the value and quality of red oak logs that entered Indiana mills last year. Although not

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We tested stands that had undergone clearcuts and shelterwood cuts and compared the genetic variation of tree seedlings in those stands to that of unmanaged virgin stands. Our results showed that no loss of genetic variation had occurred which insured that the Menominee Forest Enterprises could maintain their forest certification for production of green products.

APPLICATION OF ADVANCED TECHNOLOGIES FOR IMPROVEMENT OF HARDWOOD FORESTS

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hardwoods, through tree improvement efforts in New Zealand with radiata pine, typical pine families show increased wood volume of 12-41% just in the first generation of improvement. This example is useful to portray the potential for tree improvement although this rate of volume increase with radiata pine is probably not desirable or obtainable with many hardwoods while at the same time maintaining desirable wood structural characteristics.

Before we can implement many of the new gene technologies for tree improvement, we will need to develop new propagation, production and delivery systems to complement current methods of grafting, cutting propagation, wild seed collection and seedling production. As mentioned above for eastern white pine, we will need to develop (tissue culture) propagation methods so that we can introduce our new genes into tree cells, induce these cells to form artificial embryos (somatic embryos), and germinate these embryos into improved seedlings. These same propagation methods can be used to produce many new copies of superior trees that we find in wild or in known existing tree populations and allow us to multiply a particular tree more quickly than by current grafting methods.

We plan to use two technologies for gene insertion. The first utilizes a laboratory gene gun whereby tiny gold particles that are covered with our genes of interest are literally shot into the tree cells that are growing in a laboratory petri dish. When the tree cells divide, they incorporate the new genes into their chromosomes. The second method uses a bacteria (*Agrobacterium tumefaciens*) that normally causes crown gall disease. This bacteria is unique in that it naturally injects some of its own DNA into plant cells to induce the plant cells to divide and cause the crown gall. We can take advantage of this by placing our gene into the bacteria and have it do the work for us of inserting our new gene into tree cells. For both methods of gene insertion, we can trigger the newly transformed cells to divide and produce many new exact copies (clones), and then at some later point, induce each individual cell to form an artificial embryo. From one single transformed cell, we can produce thousands of new superior trees. Another application for the gene gun is to use it to blast genes into pollen. Then, we can use the natural delivery system of tree flower pollination under controlled greenhouse conditions to deliver our new gene into receptive flowers to produce genetically engineered seed.

Besides some of the more easy traits that can be improved such as insect, disease and herbicide resistance because the some of these genes are already known and their function is well studied, we can now begin to imagine how we could make desirable changes to traits such as tree architecture. For example, the ancestor of modern day corn, teosinte, was a short, branched annual fodder grass with little seed production and looked very different then what is grown today. If we apply that example to plantation hardwood species and if we imagine what might be our optimal end product that is efficient for harvest and milling, we could envision trees with very different features than what we grow today. The marketable product might be much shorter, but much wider in girth with few branches and highly efficient light-harvesting foliage.

For species in natural forests, we can use modern molecular genetic tools to identify trees with useful genetic variation that has been lost through past management practices, and we can provide

information that can direct future forest management for maintenance of robust genetic quality. For example, we can identify trees with genetic variation that has been lost in forests or woodlots that have been managed in a dysgenic manner (high-graded), and we can introduce those trees back into those forests to replenish the depleted gene pool. In addition, we can test trees with genetic markers in forests that are being regenerated under various management strategies to determine if these silvicultural practices are maintaining genetic diversity. We have applied this same technology with eastern white pine management on the Menominee Indian Reservation in Wisconsin. We tested stands that had undergone clearcuts and shelterwood cuts and compared the genetic variation of tree seedlings in those stands to that of unmanaged virgin stands. Our results showed that no loss of genetic variation had occurred which insured that the Menominee Forest Enterprises could maintain their forest certification for production of green products.

Another use of genetic markers is in determination of the need for seed zones for various species grown in state nurseries. We can test trees from various geographic zones within the growing region, and by the marker profile, can determine if the genetic makeup of trees from different ecological zones is significantly different enough to warrant development of separate seed orchards. In this case, use of genetic markers would provide only part of the evidence needed. In addition, we would have to plant trees in both ecological zones from seed gathered in each zone to insure that the trees had maintained their required fitness. If the trees had not maintained good growth characteristics, we could confirm the need for separate orchards.

Much like the human genome project, we plan to collaborate with other laboratories in the US to sequence what we call the functional genome of trees. These are the genes that have known functional roles in trees such as disease resistance, control of flowering, cellulose production, root structure, bark texture, and heartwood formation, but their location and sequence are unknown to us today. This is not a task we can do alone in a reasonable period of time because of the prohibitive cost of scientific gene sequencing equipment, high-powered computers for data analysis and labor costs. In addition, new federal programs to fund this work are needed, but the time is ripe for this to happen. The National Science Foundation is seeking congressional approval to increase plant genome funding in FY2000 to \$55 million. Although a program for trees is not included for next year, the director of the Plant Genome Initiative has indicated his interest in adding tree genome research to the program in upcoming years. In future years, once we can identify these 50,000 or so genes in trees, we can start to determine how we might want to further domesticate plantation forest trees and to more easily identify the superior trees in natural forests.

These technologies will allow us to meet future demands for quality hardwood trees and reduce the impacts of our unsustainable demands on natural forests. For reforestation on marginal farmland, in reclamation efforts and along riparian zones, we can insure that we are matching the characteristics of improved trees with the specific requirements of these sites. In doing so, we will insure the future protection of forests that provide irreplaceable recreational and environmental benefits such as carbon sequestration, wildlife habitat, and watershed protection. 🌱