

Summary of Comments by Dr. Charles Maynard
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Syracuse, NY
Presented at the USDA APHIS Public Meeting on
Engineered Forest and Fruit Trees
Riverdale, MD
July 8-9, 2003

Gene Flow

Most forest tree populations are massively buffered against introgression. Pollen and, subsequently, seed is produced in huge quantities by most commercially important tree species. Natural selection can also be extremely high. In a study with sugar maple in Wisconsin, more than six million viable seeds were released per acre in a single year. Less than 1% of the resulting seedlings were still alive at the end of three years and less than 1/10th of that population could be expected to reach maturity. And this was the seed crop from a single year. With such incredibly high fertility and intense natural selection, any mal-adaptive traits reaching natural stands through pollen or seed introgression from genetically enhanced plantations will be quickly eliminated.

Weediness/Invasiveness

Potential for weediness will have to be managed on a case-by-case basis. Both the tree species and trait being introduced will have to be considered. Given the massive pollen and seed production capacity of most tree species, any changes in weediness due to changes in fecundity are unlikely. More plausible is a change in weediness with introduced herbicide tolerance. This would be a possibility in cases where a tree species is considered a desirable crop by one landowner, but is considered a weed by other landowners. In such cases, the desirability of releasing an herbicide-tolerant transgenic tree would depend on the availability of alternative herbicides

Trial length

Full-rotation field trials are unnecessary to assess the safety and effectiveness of genetically enhanced trees. More than 50 years of progeny tests, provenance tests, species trials, and other genetics field trials with numerous conifer and hardwood species have clearly shown that (1) many traits can be assessed accurately as seedlings, (2) most traits can be assessed accurately by the time trees have reached approximately 1/4 of their commercial rotation age. It has been my personal observation that mal-adaptation actually shows up more quickly than ultimate superiority.

In terms of inadvertently knocking out important traits with the introduction of new genes, this can be easily assessed examining the sequences flanking the insertion by using procedures such as inverse PCR. It is a relatively simple process to locate exactly where a new gene has been inserted and sequence both directions from that insertion point. If identifiable genes have been disrupted, a different transformation event can be picked for field testing.