

# Community and Ecosystem Consequences of Genetically Engineered Organisms

Thomas G. Whitham, Regents' Professor  
Department of Biological Sciences &  
Director, Merriam-Powell Center for Environmental Research  
Northern Arizona University  
Flagstaff, AZ 86011  
[Thomas.Whitham@nau.edu](mailto:Thomas.Whitham@nau.edu)

## Summary of the presentation by Thomas G. Whitham at the July, 2003 meetings on "Genetically Engineered Forest and Fruit Trees" sponsored by USDA/APHIS in Riverdale, MD

In developing policies on the use and/or release of genetically engineered organisms, our research on *Populus*, *Eucalyptus* and *Pinus* has demonstrated several major factors that need to be considered.

**First, in evaluating the potential release of genetically engineered organisms, it is crucial to evaluate their impacts on the community and ecosystem. The primary reason for this statement is the fact that genes in individuals and populations have "extended phenotypes", which are defined as the effects of genes on the community and ecosystem (Whitham et al. 2003).** This is not just a theoretical effect, it has been clearly demonstrated in *Populus* (Whitham et al. 2003), *Eucalyptus* (Dungey et al. 2001), and *Pinus* (Brown et al. 2001, Whitham et al. 2003). The following example illustrates this point. Using experimental crosses of known pedigree, we found that a single QTL (Quantitative Trait Loci) accounts for a significant portion of the phenotypic variation in the production of condensed tannins in cottonwood leaves. Using these same cross types, Driebe and Whitham (2000) showed that the "traditional phenotype" of condensed tannins varied ~4X among *Populus fremontii*, *P. angustifolia*, and their F<sub>1</sub> and backcross hybrids. These phenotypes have "extended phenotypes" that go beyond the individual and population to affect community and ecosystem-level processes (Whitham et al. 2003). Because condensed tannins slow decomposition, tannin concentrations explained 63% of the variation in litter decomposition in an aquatic system (Driebe and Whitham 2000) and 57% of the variation in N mineralization in the soil (Schweitzer et al. 2004). Condensed tannins also affect the foraging of beavers, an ecosystem engineer. Beavers avoid felling tree genotypes high in condensed tannins, which then affects the rest of the community (Bailey et al. in review). These studies demonstrate direct links between a mapped trait and both community and ecosystem-level processes. Importantly, because lignin concentrations are often highly correlated with condensed tannins, it is likely that the current industry desire to reduce lignin concentrations in genetically engineered poplars will have community and ecosystem-level effects that may be similar to those described above for tannins.

These findings have immense implications for the trees, the thousands of species that are dependent upon them for survival, and for the ecosystem. Thus, before

genetically engineered organisms are released, it is important to evaluate the extended phenotypes of these genes on the community and ecosystem.

**Second, the impacts of genetically engineered organisms on the community and ecosystem are especially important to consider when they affect dominant and/or keystone species (Whitham et al. 2003).** By definition, dominant (i.e., species that dominate a natural environment or agro ecosystem) and keystone species (i.e., organisms that have disproportionate effects relative to their biomass such as beavers or pathogens) are community drivers. For example, in *Pinus*, we have found that resistance and susceptibility traits to a keystone moth affects the distribution of nearly 1000 other species including birds, mammals, insects, mycorrhizal mutualists and decomposers (Brown et al. 2001, Whitham et al. 2003, Kuske et al. 2003). Thus, genes in dominant species (e.g, pines) and/or keystone species (e.g., moths) are likely to have cascading effects on the rest of the community and ecosystem. Because many genetically engineered organisms may be considered dominant or keystone species, their impacts on the community and ecosystem need to be critically evaluated.

**Third, it is crucial to evaluate the impacts of gene flow from genetically engineered organisms into native populations. In addition to other protocols that are currently recognized, we recommend analyzing the potential for gene flow using native populations.** By analyzing native populations of the species that is being genetically engineered, we can detect how much introgression has occurred over a much longer period of time than what might be observed over a few years next to a plantation. Such analysis of introgression in the wild represents a more realistic evaluation of what will eventually occur once genetically engineered organisms are released. Our studies of natural hybridization between Fremont cottonwood (*Populus fremontii*) and narrowleaf cottonwood (*P. angustifolia*) represent such an example. We found that Fremont cpDNA and mtDNA were found throughout the geographic range of narrowleaf cottonwood, and that 20% of the nuclear markers of Fremont cottonwood introgressed varying distances (some over 100 km) into the recipient species' range (Martinsen et al. 2001). These studies argue that there is a high potential for the genes in genetically engineered poplars to spread into native poplars and that the widespread release of modified trees could affect most poplars in the US.

**Fourth, it is important to recognize that a beneficial trait under one set of conditions can become a deleterious trait under another set of conditions (e.g., gene by environment interactions). The recognition that genetically engineered organisms will interact with many other species to produce potentially unexpected outcomes is crucial to any prudent evaluation and management policy.** For example, Ruel and Whitham (2002) found that the tree genotypes that grew fastest during the first 50 years of their life were the slowest growing trees for the next 100 years of their life. This reversal in outcome is likely an ontogenetic change in gene expression that would only be uncovered in long-term field trials. Similarly, van Ommeren and Whitham (2002) found that in a 2-way interaction, mistletoe on juniper was a classic example of a parasitic association. However, when the seed dispersing birds were included in the analysis as a 3-way interaction, mistletoe could be a mutualist of juniper because it attracted more seed dispersing birds that benefited juniper. Unfortunately, these reversals in interpretation occur with alarming frequency. In a survey of 100s of published studies, Bailey and Whitham (unpublished data) found that when more factors were included in

an experimental testing design, there was a nearly 90% probability that one of more major factors of interest would reverse with time, space, and/or the number of species included in the study. This is largely driven by the interactions of species with one another and their environment. The importance of such reversals is especially important when management decisions are involved; management decisions that ignore interaction effects of space, time and species number run a high risk of making decisions have the opposite effect of what is intended. Because important ecological factors commonly interact resulting in variable patterns, empirical field tests are required to confirm the generality of results across temporal (e.g., short vs. long-term), and spatial scales (e.g., local to landscape), and with increasing biocomplexity (e.g., interactions with other species). We feel such reversals are also likely to occur with the release of genetically engineered organisms. To avoid this pitfall, careful evaluation is needed under realistic settings.

**Taken in combination, the above four scientific findings argue that it is important to evaluate genetically engineered organisms from a community and ecosystem perspective. This perspective is crucial because it considers the realistic setting under which genetically engineered organisms are likely to interact with many other species in nature. Most importantly, it is doable. The scientific methodology is available and it is realistic to evaluate. It cannot be argued that it is a project “killer” because the success of the approach has been demonstrated in the following cited studies.**

#### **References Cited**

- Schweitzer, J.A., J.K. Bailey, B.J. Rehill, G.D. Martinsen, S.C. Hart, R.L. Lindroth, P. Keim, and T.G. Whitham. 2004. Genetically based trait in a dominant tree affects ecosystem processes. *ECOLOGY LETTERS* (in press).
- Bailey, J.K., J.A. Schweitzer, B.J. Rehill, R.L. Lindroth, G.D. Martinsen, P. Keim, and T.G. Whitham. 2003. Beavers as molecular geneticists: A genetic basis to the foraging of an ecosystem engineer. *ECOLOGY* (in press).
- Kuske, C.R., J.D. Busch, L.O. Ticknor, C.A. Gehring, and T.G. Whitham. 2003. The pinyon rhizosphere, plant stress, and herbivory affect the abundance of microbial decomposers in soils. *MICROBIAL ECOLOGY* 45:340-352.
- Whitham, T.G., W.P. Young, G.D. Martinsen, C.A. Gehring, J.A. Schweitzer, S.M. Shuster, G.M. Wimp, D.G. Fischer, J.K. Bailey, R.L. Lindroth, S. Woolbright, and C.R. Kuske. 2003. Community and ecosystem genetics: A consequence of the extended phenotype. *ECOLOGY* 84:559-573.
- van Ommereen, R.J., and T.G. Whitham. 2002. Changes in interactions between juniper and mistletoe mediated by shared avian frugivores: parasitism to potential mutualism. *OECOLOGIA* 130:281-288.
- Ruel, J., and T.G. Whitham. 2002. Fast-growing juvenile pinyons suffer greater herbivory when mature. *ECOLOGY* 83:2691-2699.
- Brown, J.H., T.G. Whitham, S.K. Morgan Ernest, and C.A. Gehring. 2001. Complex species interactions and the dynamics of ecological systems: long-term experiments. *SCIENCE* 293:643-650.
- Martinsen, G.D., T.G. Whitham, R.J. Turek, and P. Keim. 2001. Hybrid populations selectively filter gene introgression between species. *EVOLUTION* 55:1325-1335.
- Dungey, H.S., B.M. Potts, T.G. Whitham, and H.-F. Li. 2000. Plant genetics affects arthropod community richness and composition: evidence from a synthetic eucalypt hybrid population. *EVOLUTION* 54:1938-1946.
- Driebe, E., and T.G. Whitham. 2000. Cottonwood hybridization affects tannin and nitrogen content of leaf litter and alters decomposition. *OECOLOGIA* 123:99-107.