

Greenpeace International

Submission to the Convention on Biological Diversity

Advice on environmental impacts of transgenic forest trees for consideration by the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA)

at its 13th meeting, to consider and assess the potential environmental, cultural, and socio-economic impacts of genetically modified trees on the conservation and sustainable use of forest biological diversity

Prepared by Benno Vogel, MA

For Greenpeace International

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Introduction

In 2002 the first transgenic forest trees were marketed in China. Over 250 experimental releases of transgenic forest trees have been conducted worldwide to date. The research is driven primarily by private companies from developed nations, including some of the world's largest companies in the pulp and paper industry. These companies also hold most of the patents on engineering methods and genetic resources. The focus of present research is on species that can be marketed on a global scale, and on properties to increase productivity of tree plantations and facilitate pulp and paper production.

There is wide spread concern about detrimental effects of genetically engineered trees on the environment. Transgenic annual crops are already known to have detrimental effects on wild-life communities and ecosystems. For a number of reasons, the risk of harmful environmental effects is considerably greater in the case of transgenic forest trees.

- forest trees have very long lifespans (up to several hundreds of years),
- forest trees are relatively undomesticated and can thrive in natural environments without human intervention,
- forest trees often produce copious amounts of seeds and pollen, which will travel long distances,
- some forest trees can reproduce vegetatively,
- most forest trees are outbreeders and interbreed with related wild species,
- forest trees are often dominant species in their ecosystem and support a large web of organisms that rely on them, either directly or indirectly, as their ultimate source of nutrients.

Transgenic forest trees are very likely to have long-term impacts on the environment and biodiversity. This submission provides evidence on ecological risks associated with transgenic forest trees, which are significant and likely to prove unmanageable and irreversible.

Greenpeace is opposed to the release of genetically engineered organisms into the environment at the present state of knowledge and calls for a ban on the release of transgenic trees. As an interim measure a global moratorium on commercial releases and on larger scale experimental releases is recommended.

Environmental impacts of transgenic forest trees

Outcrossing and propagation

Although transgenic forest trees are largely intended to be grown on plantations, their effects will not be confined to these. Since they propagate via seeds as well as vegetatively via shoots, pass on their genes to wild relatives by hybridisation and could also transfer their transgenes to micro-organisms, the direct impact of transgenic trees will not be confined to plantations, but also affect semi-natural and natural ecosystems. Once they have escaped the original confinements, it will not longer be possible to retrieve transgenic forest trees and their foreign genes.

Invasion through seed dispersal

Trees used for forestry purposes are largely undomesticated, having been subjected to little breeding activities, and are therefore highly capable of surviving in natural or semi-natural ecosystems without human intervention. There are numerous examples of coniferous and deciduous trees from plantations invading unmanaged habitats (e.g. Johnson & Kirby 2001, Richardson 1998). This led to ecological problems, particularly when the species involved were not indigenous to the region. Some of the most widespread and harmful invasive trees include species of the genera *Pinus*, *Pseudotsuga*, *Robinia* and *Salix* (Richardson & Petit 2006). Species of these genera are among those subject to genetic engineering research and experiments.

Experiences with non-indigenous trees suggest that transgenic trees will escape from plantations and cause problems in natural and semi-natural habitats. Especially where trees are intentionally or unintentionally altered with transgenes that may increase their fitness they could become more invasive, invade new habitats and cause a loss in biodiversity and ecosystem functions (Andow & Zwahlen 2006).

The escape of transgenic trees can be neither prevented nor controlled. Trees usually produce a very large number of seeds. While the majority of these seeds is usually deposited in the closer vicinity smaller amounts can spread across very large distances.

Wind and water can carry seeds from trees across great distances. Birds, bats, squirrels and red deer also help trees to conquer distant habitats (Nathan 2006, Richardson et al. 2000). In this way, conifer seeds can travel dozens of kilometres (Nathan et al. 2002). Loblolly pine (*Pinus taeda*) seeds can be carried up to 30 kilometres by the wind (Williams et al. 2006).

Long-distance escape via pollen flow

While transgene dispersal via seeds is worrying, the potential spread of foreign genes through hybridisation with wild relatives is even more alarming (Trakhtenbrot et al. 2005). The escape of transgenes into wild populations could alter the genetic resources of wild relatives and thereby contaminate native germplasm that ought to be protected (Williams 2005, Vanden Broeck et al. 2005). Hybridisation with wild relatives could lead to increased weediness or

the invasion of new habitats by the wild population. In addition, native species with which the wild plant interacts (including herbivores and other plant species in the community) could be adversely affected by transgenic-wild plants (Pilson & Prendeville 2004).

There is a high risk of transgenic forest trees hybridising with their wild relatives, mainly for three reasons:

- (1) most forest tree species are undomesticated outbreeders that will readily interbreed with related species;
- (2) gene flow is often mediated by a copious production of wind-borne pollen that may travel large distances;
- (3) transgenics are likely to be used in close proximity to interfertile populations of natural or feral origin (van Frankenhuyzen & Beardmore 2004).

Several authors indicate that pollen of some tree species can travel hundreds of kilometres. Birch pollen has been found on the treeless Shetland Islands, originating from forests more than 250 kilometres away and across the sea (Tyldesley 1973). Long-distance dispersal of coniferous seed can occur as far as 600 to 1200 km from the source (Katul et al. 2006, OECD 1999, Di-Giovanni et al. 1996). For pine and spruce pollen, transport distances of up to 3000 km have been recorded under rare conditions (Campbell et al. 1999).

As experimental data on the viability of pollen dispersed over long distances are lacking for most tree species, it remains unclear whether the effective pollination distance is lower than the recorded travel distances (Katul et al. 2006, Williams 2006). For Norway spruce (*Picea abies*) and Scots pine (*Pinus sylvestris*), available data indicate that pollen in the atmosphere remains viable long enough to permit long-distance gene flow through pollen migration (OECD 2002). In the case of pine and spruce it is very likely that large amounts of pollen will remain viable at least after mesoscale transport of around 60 km (Katul et al. 2006, Di-Giovanni et al. 1996).

Transgene escape to microbes

Since plant DNA can be released into the soil through decomposing plant tissue (such as pollen, leaves and roots), transgenes may escape from genetically modified trees to soil microbes. In transgenic annual crops, horizontal gene transfer from plants to microbes has been shown to be possible under favourable experimental conditions, though at a low frequency (e.g. de Vries et al. 2004, Kay et al 2002, Nielsen et al 2000, Gebhard & Smalla 1998). Since monitoring efforts so far have failed to observe such transfer events in the field, horizontal gene flow from plants to microbes is believed to be rare in nature. However, current methods for monitoring horizontal gene transfer are fraught with difficulty and too insensitive to detect transfer events. Hence, corresponding frequencies and risks may be higher than assumed (Nielsen & Townsend 2004, Heinemann & Traavik 2004). Since DNA from long-living trees will enter the soil far more often than that of annual plants, the probability of gene transfer may be increased. A single study regarding tree to microorganism horizontal gene transfer has been published so far. This study investigated whether the genes of transgenic poplars were transferred to a single microorganism, the ectomycorrhizal fungus *Amanita muscaria* (Zhang et al. 2005). In this case, no evidence of gene transfer was found. In view of the vast number of known and unknown soil bacteria and symbiotic microorganisms which may be in direct or indirect contact with a tree over its live span, this may not be reassuring.

One pathway of gene transfer from trees to microbes is via *Agrobacterium tumefaciens*. *A. tumefaciens*-mediated transformation methods have been developed for a number of important forest species (e.g. *Pinus radiata*, *P. strobus*, *P. glauca*, *Picea abies*, *Betula pendula*, *Populus nigra*, Eucalyptus species). Previous studies with crops have shown that *A. tumefaciens* can persist in transgenic plants after transformation (e.g. Dominguez et al. 2004, Barrett et al. 1997, Matzk et al. 1996, Mogilner et al. 1993). It has been shown with non-recombinant bacteria that horizontal gene transfer is possible from inoculated bacteria to endophytic bacteria associated with poplars (Taghavi et al. 2005). In field-grown transgenic trees, persistent recombinant agrobacteria could transfer their transgene(s) to other microorganisms, especially to endophytic bacteria and, if released via the roots, to soil bacteria. As the probability of horizontal gene transfer increases over time, the persistence of *A. tumefaciens* in transgenic trees is of significant ecological relevance, as it may persist in the environment of plantation forests for several decades.

So far, only one study has been published dealing with the persistence of *A. tumefaciens* in transgenic trees. In this small study with transgenic spruce and pine, no *Agrobacteria* were detectable in the plant tissue. However, the authors were unable to rule out that some *Agrobacteria* remained undetected (Charity & Klimaszewska 2005). In a literature review, Ulrich et al. (2006) mention unpublished results showing that recombinant *A. tumefaciens* can persist in transgenic poplars for at least one year after transformation.

Biocontainment

In order to prevent transgene escape, various attempts have been made to prevent trees from forming either pollen or seeds. Although the development of sterile trees is as yet in its infancy, it is questionable whether such containment systems will ever be able to completely prevent gene escape once transgenics are deployed over large acreages and in full rotation (van Frankenhuyzen & Beardmore 2004, Mayer 2004). Due to the potential instability of transgenes, total sterility of every single tree in large plantations is highly unlikely even where the stability of transgenes is generally very high. Especially where the transgenic trait confers a fitness advantage, only a few escaped seedlings can cause colonization and transgene introgression into wild populations may occur even where gene flow is extremely limited (Richardson & Petit 2006, Lee & Natesan 2006, Williams & Davis 2005).

Ecosystem impacts

Although studies on annual transgenic crop plants are limited, they have shown that environmental impacts on ecosystems above and below ground are possible (Snow et al. 2005). Potential impacts on communities and ecosystems could be especially severe when caused by dominant species such as trees. Forest trees often dominate natural habitats or forest ecosystems and support large webs of organisms which rely on them, either directly or indirectly, as their ultimate source of nutrients. Thus, transgenes in tree species are likely to have cascading effects on the rest of the community and the ecosystem.

Experiments on the environmental impacts of transgenic trees have been rare. But data on non-transgenic *Populus*, *Eucalyptus* and *Pinus* species show that genes from individuals and populations have an “extended phenotype”,

meaning that their genetic makeup can affect communities and ecosystems (for reviews see Whitham et al. 2006, 2003).

Negative impacts on ecosystems may also result from forest plantation practices. Plantation forests are often less favourable as habitats for a wide range of wild species, particularly in the case of even-aged, single-species stands involving exotic species (Hartley 2002). Some of the consequences of plantations for the environment will be affected by attributes of the tree species used. Many consequences will also depend on plantation practices. Forest biotechnology may become another driver for inappropriate plantation development and transgenic trees may exacerbate the ecological consequences of current forestry practices. For example, converting native forests to transgenic plantations will have negative implications for biodiversity. Similarly, the conversion of native grasslands or savannah to transgenic plantations would have negative effects on biodiversity (Hayes 2001).

Potential environmental impacts of the most frequently engineered traits in forest trees are discussed below.

Low-lignin trees

Lignin-reduced transgenic trees are likely to have multiple environmental side effects since lignin has diverse functions in forests.

Changes in lignin content could affect soil structure and fertility by accelerating the decomposition of organic matter (Talukder 2006, Campbell & Asante-Owusu 2001). This may result in increased CO₂ emissions and may negatively affect below-ground carbon sequestration, possibly contributing to atmospheric concentrations of greenhouse gases (Talukder 2006). Furthermore, more rapid decomposition of transgenic low-lignin organic material could negatively affect populations of organisms colonising slowly-rotting timber (Talukder 2006).

Increased invasiveness may be another result. At least one set of gene constructs used for lignin modification has been reported to enhance growth in transgenic aspen trees (see *Secondary phenotypic effects*).

Reduced lignin content may also lead to increased population growth of insect defoliators. This could negatively affect biodiversity and also increase the need for agrochemical use (Johnson & Kirby 2001).

So far, two field studies have been published dealing with the ecological risks of a low-lignin transgenic tree. In a field trial with transgenic poplars, interactions with leaf-feeding insects, microbial pathogens and soil organisms were unaltered, but, as expected, the rate of decomposition of transgenic roots was enhanced (Pilate et al. 2002). No changes in decomposition were found with woody trunk material from the same field trial, but the results of this study are tentative, because the data were limited (Tilston et al. 2004).

Fast-growing trees

Fast-growing transgenic trees allowing for shorter rotation management in plantations may decrease the opportunities for colonisation by poorly dispersed, late-successional plant species. Short rotations could also limit the extent to which structurally complex understorey development will occur, which may in turn limit the suitability of plantations for certain wildlife species. In addition, fast-growing trees may well sequester more, and therefore

recycle fewer, nutrients and water, and this could have a deleterious long-term effect on site productivity (Asante-Owusu 1999).

Insect-resistant trees

A number of transgenic insect-resistant forest trees have been developed so far, and two such varieties of poplar have been commercialised in China. No peer-reviewed publications are available about their potential effects on non-target organisms. The fact that such effects are possible is apparent from experiences with annual crop plants. Laboratory trials suggest that insect-resistant transgenic crops often have a significant harmful effect on natural enemies such as predators and parasitoids (Lövei & Arpaia 2005). Similar effects have also been observed in the soil. Bt-crops can affect the bacterial community, the establishment of ectomycorrhizal fungi, earthworms and soil respiration (Castaldini et al. 2005, Zwahlen et al. 2003). Compared to annual crop plants, insect-resistant trees offer scope for new harmful scenarios. If transgenic Bt-poplars were planted in riparian areas, their leaves would enter the rivers and streams, with unforeseeable consequences for the aquatic communities there (LeRoy et al. 2006, Close 2005).

There are at least two ways in which transgenic insect-resistant trees might lead to increased pesticide use. First, although target pest populations may be reduced by a transgenic insect-resistant trait, this might allow other, previously rare, secondary pest species to flourish, leading to an increased need for chemical control (Johnson & Kirby 2001). This issue has received very little attention within the forestry context to date.

Second, a trend towards increased insecticide use may also result when target insects develop resistance (Johnson & Kirby 2001). In long-lived forest trees, selective pressure will be strong and more difficult to manage than in annual crops (van Frankenhuyzen & Beardmore 2004). The only two studies involving a forest insect (the poplar pest *Chrysomela tremulae*), showed an initial frequency of the allele conferring resistance to be surprisingly high, suggesting that without management strategies resistance may be rapidly selected (Wenes et al. 2006, Génissel et al. 2003).

Fungi-resistant trees

It is possible that the introduction of non-specific fungal resistance in transgenic trees could affect decomposer ecosystems in plantations (Johnson & Kirby 2001). To date, only one field trial has been published dealing with non-target impacts of fungi-resistant trees. Vauramo et al. (2006) analysed the decomposition process of leaf litter from chitinase transgenic silver birches and the effects on the decomposer populations. No effects were detected on the decomposability of the litter in the soil. However, the duration of the experiment may well have been too short to reveal long-term differences in decomposition (Vauramo et al. 2006).

Herbicide-tolerant trees

Residual native vegetation within planted forest stands is most important to biodiversity (Hartley 2002). Herbicides affect forest biodiversity by causing a decline in plant species diversity, altering the vegetative structure, and

potentially changing plant successional trajectories. Until now, some plantations contain a high proportion of the native woody plant species found on unplanted stands, due to incomplete elimination (Hartley 2002). This could well change in the future, if genetically modified trees tolerant to broad-spectrum herbicides were to be widely used. Such plantations would be less attractive for species of birds and invertebrates that rely on the habitat of young plantations, with its combination of young planted trees and diverse wild plants that support the food webs on which they rely (Johnson & Kirby 2001).

Sterile trees

Sterile transgenic trees raise new concerns in terms of their impact on biodiversity (Valenzuela et al. 2006). Pollen, nectar, seeds and fruits of plantation trees are elements of the woodland food web and are important in maintaining biodiversity. Plantations of sterile trees will be devoid of birds, insects and mammals that rely on seeds, pollen or nectar for food. Thus, sterility could result in cascading ecological effects and could disrupt population dynamics, with severe repercussions for neighbouring natural ecosystems (Mayer 2004, Hayes 2001, Johnson & Kirby 2001).

Research into sterile seed production would also contradict Decision V/5, section III (Genetic use restriction technologies) of the 5th Conference of Parties, as confirmed by the 8th Conference of Parties in Decision VIII/23.

Secondary phenotypic effects of genetic modification

An issue that is particularly relevant for long-lived plants like trees is the possibility of inadvertent effects arising from the transformation process. These unintended effects can be caused by the transgene's location in the genome, by effects of the transgene on other traits (pleiotropy), by interactions between the transgene and native genes (epistasis), and by somaclonal mutations that occur during tissue culture (NRC 2004). Effects may be subtle and may not appear until a particular stage of growth or in response to specific environmental conditions (RSC 2001). Most importantly, secondary phenotypic effects are unpredictable and may cause unintended environmental side effects.

Several examples of unintended phenotypic effects in genetically modified trees are known. For example, in transgenic aspens which had been downregulated in their expression of a gene for the lignin biosynthetic pathway, Hu et al. (1999) made the surprising observation that the transgenic trees displayed substantially enhanced growth compared with wild-type plants. The enhanced growth rate may enhance the invasiveness of the transgenic aspen trees (Talukder 2006).

Transgenic hybrid aspens that overexpressed a key regulatory gene in the biosynthesis of gibberellin had improved growth rate and biomass, as expected, but they also had more numerous and longer xylem fibres than the wild-type plants (Eriksson et al. 2000).

Ralph et al. (2001) reported the production of unanticipated benzodioxane structures in lignins of transgenic O-methyltransferase-deficient poplars. Changes in lignin structures as a result of genetic modifications could have a

detrimental effect on natural forests where microbial degradation of plant materials (i.e. leaves, roots, limbs etc.) is an important aspect of the nutrient cycle (Sariyildiz 2003).

In the first field study on mycorrhization in transgenic trees, one of the transgenic aspen clones displayed depressed mycorrhization because of minute physiological modifications not directly related to the function of the inserted gene (Kaldorf et al. 2002; see also Hoenicka & Fladung 2006). These results indicate that secondary phenotypic alterations can result in unpredictable changes in the tree's ability to form mycorrhizal associations.

Tiimonen et al. (2005) have produced transgenic silver birch lines in order to modify lignin biosynthesis. In controlled feeding experiments, the leaves of the transgenic birch lines were fed to insect herbivores. The feeding preferences of these herbivores differed between the tested lines, however these differences could not be directly linked with lignin modification. They may, however be caused by transgene side effects (Tiimonen et al. 2005).

In microcosm experiments with leaves of birches (*Betula pendula*) transformed to produce chitinase from sugar beet, Kotilainen et al. (2005) observed a higher decomposition rate of transgenic leaves and a negative response of nematodes to transgenic leaf litter. The explanation for these observations remains open, but it seems that the genetic modification has a pleiotropic effect on the chitinase leaves, thus altering the structural components of the leaves. Pleiotropic effects influencing the quality of plant litter can result in significant changes in the ecosystem, since the functioning of soil processes reflects the growth of above-ground biota (Wardle et al. 2004, Donegan et al. 1997).

Unintended changes in plant physiology, anatomy and metabolism as a result of the genetic engineering process challenge the risk assessment procedures for transgenic trees, since tests cannot rule out unexpected and unpredictable secondary phenotypic effects. For example, small unintended effects may remain undetected because they may depend on cumulative action, specific environmental conditions, or introgression into different genetic backgrounds. Ecological consequences may not be evident until after several years of growth.

Short case studies

Transgenic poplars – uncontrollable long-distance distribution

The commercial era of genetically modified trees began in 2002, when two transgenic poplars were licensed for sale in China – a black poplar (*Populus nigra*) with a Bt gene (Hu et al. 2001) and a double transgenic hybrid poplar having both a Bt gene and a proteinase inhibitor gene (Tian et al. 2000). Some 1.4 million cuttings are reported to have been planted. However it is no longer possible to determine precisely where the transgenic poplars are now growing. Their cultivation seems to be no longer under systematic control (Wang 2004, Pearce 2004).

Poplar varieties are the most common species worldwide to be genetically modified (FAO 2004). The reason they are the tree of choice is that they can be vegetatively propagated, they grow rapidly and have a world wide geographic distribution (Mayer 2004). If transgenic poplars are commercialised and used, their biology will

inevitably lead to their escaping into natural or semi-natural habitats. Poplars are dioecious and must therefore necessarily outcross. As they are wind-pollinated, outcrossing occurs over long distances. Natural hybrids are regularly found wherever different species of poplar come into contact with each other (Vanden Broeck et al. 2005, OECD 2000).

A fully-grown poplar tree can produce up to 50 million seeds a year (OECD 2000). The seeds are primarily carried by wind and water, and are designed so as to be widely distributed and hence permit large migration rates (OECD 2000). The possibility of vegetative propagation is also important for its spreading. Thus poplars can spread through sprouting from roots and stumps, as well as adventitious shoots and root suckers, and so colonise new habitats (Fladung et al. 2003). In some poplar species there is also evidence of cladogenesis, in which short shoots abscise and can be carried long distances on watercourses and subsequently take root (Vanden Broeck et al. 2005). In short: transgenic poplars will spread in an uncontrolled fashion, covering large distances in the course of time. In the United States, for example, introgression has been observed across distances of over 100 km (Martinsen et al. 2001).

Although the first transgenic poplars have already been commercialised, hardly any data have yet been collected as to what environmental effects this might have. However it is known from non-transgenic poplars that their genetic make-up does not only determine the tree's phenotype but also affects the environment, changing the composition of insect populations (Wimp et al. 2005, 2004), influencing the feeding preferences of beavers (Bailey et al. 2004b) or affecting decomposition processes in the soil (Schweitzer et al. 2004). Where the leaves of poplars are able to enter lakes and rivers, effects on aquatic communities may also occur (LeRoy et al. 2006).

The introduction of transgenic poplars could therefore have unpredictable effects on terrestrial and aquatic communities (LeRoy et al. 2006, Close 2005; see also Whitham et al. 2006). Another major concern associated with the growing of transgenic poplars is that foreign genes could enter indigenous poplars via hybridisation, contaminating genetic resources that ought to be protected (Vanden Broeck et al. 2005).

Transgenic pines – indefinite persistence of foreign genes

In economic terms, the genus *Pinus* is the most important group of trees in the world. Hence pine species are the second most frequently genetically engineered trees, after poplars. To date, no transgenic species of the genus *Pinus* has been commercialised, however companies like Arborgen, Scion and Genfor are working towards this goal. Genfor hopes to market transgenic Monterey pines in Chile in 2008 (Richardson & Petit 2006).

If transgenic pines are commercialised and grown on large areas, they will inevitably spread into natural and semi-natural habitats. Pines produce vast quantities of pollen and seeds, which can travel large distances. In the case of the Loblolly pine, for example, seeds are believed to spread more than 30 kilometres, and pollen up to 60 kilometres (Williams et al. 2006, Katul et al. 2006). The consequences of such spreading could be very serious – both in the northern hemisphere, where pines are indigenous, and in the south, where pines are often used in plantations.

In the north, pine species are among the ecologically most important trees. They play an important role in net primary production, forest structure, biogeochemical processes and water flow, and are in addition an important component of the food web (Richardson & Petit 2006). Since pine species therefore play a dominant role, escaped transgenes could have a cascading effect on the other communities and the ecosystem as a whole. The following, worrying example demonstrates just how far-reaching the effects could be: in non-transgenic *Pinus* it has been found that resistance and susceptibility traits to a keystone moth affects the distribution of nearly 1000 other species including insects, mammals, birds, mycorrhizal fungi and decomposers (Kuske et al. 2003, Witham et al. 2003, Brown et al. 2001).

In the southern hemisphere, a commercial utilisation of transgenic pines would in particular bear the potential risk of harmful invasions. Many pine species are highly invasive and no other gymnosperm family includes as many invasive species as the *Pinus* genus (Richardson & Reimánek 2004). One of the most harmful and aggressive species is the Monterey pine. It has already invaded native ecosystems in several regions in the southern hemisphere (Bustamante & Simonetti 2005, Richardson & Petit 2006). Nevertheless, Genfor is planning to market transgenic Monterey pines in Chile.

Huge Monterey pine plantations already exist there today. In Central Chile, for instance, the countryside is an artificial mosaic, in which patches of residual remnants of natural forest are surrounded by Monterey pine plantations (Bustamante & Simonetti 2005). If transgenic pines were used here, there would be a risk of their becoming even more invasive and penetrating into new habitats, where they could cause a loss in biodiversity and ecosystem functions (see also Ojeda 2005).

Pines demonstrate well the time dimensions over which possible environmental effects of transgenic plants need to be considered. Claire Williams of Duke University writes (Williams 2006): "Pines, among the oldest seed plant lineage on earth, have persisted for nearly 200 million years. Few advocates of transgenic pine plantations in the 21st century have considered this decision from the perspective of evolution. Many pine species have an open-ended hybridization system, so conditions can favor indefinite persistence of transgenes in neighboring or sympatric species."

Conclusions

The pursuit of genetic engineering in forest research is primarily corporate, shaped by the imperatives of private investment, market forces and government regulatory institutions (Williams 2005). As shown above, the commercial use of transgenic forestry may have detrimental impacts on biodiversity. Forest trees produce large amounts of seeds and pollen, and long-distance and transboundary movement of transgenes will be inevitable. Transgenes could be passed on to wild conspecific populations and to wild relatives, thereby triggering new invasions and causing changes in communities and ecosystems. Furthermore, escaping transgenes may threaten valuable genetic resources

by contaminating indigenous tree germplasm. Negative impacts on biodiversity may result also from non-target effects of transgenic tree plantations.

In addition to ecological impacts, transgenic plantations will also have social consequences (Mayer 2004, Baily et al. 2002a). The technological and economic power associated with transgenic forestry is likely to have consequences similar to those experienced in agriculture, where the number of producers typically declines and a few large corporations control the production system. Ownership of gene technology will provide forestry corporations with even greater decision-making powers than today. Furthermore, being heavily mechanised and centralised, transgenic plantations will offer little in terms of local employment and profit. Where commodities from natural forests and transgenic plantations compete, the latter could actively undermine wood prices and discourage incentives for natural forest management. As indigenous people are often the largest landowners of naturally managed forests, transgenic plantations could lead to a decline in the income of poor people. Moreover, given that the spread of transgenic seeds will be inevitable, the coexistence between transgenic tree plantations and less intensively managed public and private forestlands will pose new economic and liability problems, especially in landscapes made up of a mosaic of public forests, corporate timberlands, wildlife refuges and family timberlands.

Many questions about transgenic trees remain unanswered, in particular those related to their impact on biodiversity. Some of the ecological questions could be answered by laboratory and greenhouse experiments and by small-scale field tests. But, because of the long lifespan of forest trees, most of the questions relevant for an adequate risk assessment will remain unanswered. For example, the data necessary to determine genetic stability, the extent and rate of gene flow, and the persistence and invasiveness of transgenic trees would have to involve experiments lasting over several generations of the plant, conducted under different environmental conditions. The relevant timescale for appropriate risk research exceeds the life of individual scientists and regulators as well as the typical lifespan of the corporations involved in transgenic forestry.

The various ecological risks of transgenic forest trees are significant and are likely to prove unpredictable, unmanageable and irreversible. While potential benefits will accrue to some shareholders, the ecological and social risks of transgenic forest trees are likely to be shared by everyone.

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