Rowing against the tide

Passions, pains, and lessons from defending and developing GMO crops in agriculture and forestry

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Oregon State University

Roadmap

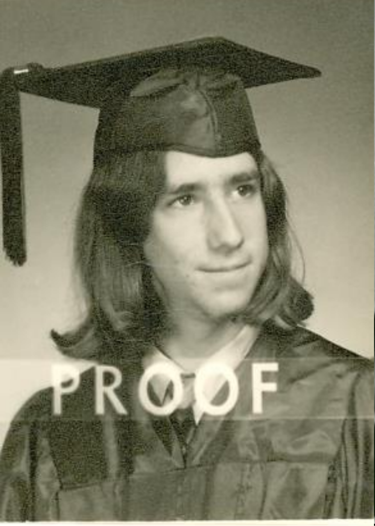
- Ancient background
- Early science at OSU
- Biotech buzz 1.0 – ag GMOs take form
- Making it real - Poplars and Oregon
- Getting drunk – Gene science and tech getting better and better
- Keeping your head – Science not hype
- Morning after – Society left the party early
- Fighting back – GMO science advocacy
- Lessons

Grew up in Brooklyn, NY

Tough

Cute

Member of 60-70s Eco-Culture



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Early science: Used DNA to understand tree evolution and diversity

Abundant Mitochondrial Genome Diversity, Population Differentiation and Convergent Evolution in Pines

Junyuan Wu, Konstantin V. Krutovskii[1] and Steven H. Strauss

Department of Forest Science, Oregon State University, Corvallis, Oregon 97331-7501

Manuscript received February 27, 1998
Accepted for publication August 19, 1998

ABSTRACT

We examined mitochondrial DNA polymorphisms via the analysis of restriction
phisms in three closely related species of pines from western North America:
Lemm.), Monterey (*P. radiata* D. Don), and bishop (*P. muricata* D. Don). A
from 13 populations were analyzed using 13 homologous mitochondrial gene p
species by polymerase chain reaction. Twenty-eight distinct mitochondrial DNA
and no common haplotypes were found among the species. All three species
within populations, but strong differentiation among populations. Based on hap
diversity within populations (H_S) averaged 0.22, and population differentiation
Analysis of molecular variance also revealed that >90% of the variation reside

Proc. Natl. Acad. Sci. USA
Vol. 85, pp. 3898–3902, June 1988
Evolution

Chloroplast genomes of two conifers lack a large inverted repeat and are extensively rearranged

(gymnosperms/evolution/chloroplast DNA/restriction maps/gene mapping)

Steven H. Strauss*†, Jeffrey D. Palmer‡, Glen T. Howe*, and Allan H. Doerksen*

*Department of Forest Science, Oregon State University, Corvallis, OR 97331; and ‡Department of Biology, University of Michigan, Ann Arbor, MI 48109

[*Pinus radiata* D. Don].
ucture to that of angio-
plast genomes of both
ture from the vast ma-
nospecific order (13) of
biloba. The two conifer
non to most land plants,
present in *Ginkgo* or

Evolution, 44(4), 1990, pp. 1081–1096

RESTRICTION FRAGMENT ANALYSIS OF PINE PHYLOGENY[1]

Steven H. Strauss and Allan H. Doerksen

Department of Forest Science, Peavy Hall 154, Oregon State University, Corvallis, OR 97331-5705

Abstract.—We used restriction fragment analysis of chloroplast, nuclear, and mitochondrial DNA to study phylogeny in the genus *Pinus*. Total genomic DNA of 18 to 19 pine species that spanned 14 of the 15 subsections in the genus was cut with 8 restriction enzymes, blotted, and then probed with up to 17 cloned DNA fragments—which were mostly from the chloroplast genome of Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco). A total of 116 shared characters, the majority repre-

Basic science continues, genomics style

New Phytologist

Research

The floral transcriptome of *Eucalyptus grandis*

Kelly J. Vining[1], Elisson Romanel[2], Rebecca C. Jones[3], Amy Klocko[1], Marcio Alves-Ferreira[4], Charles A. Hefer[5], Vindhya Amarasinghe[1,6], Palitha Dharmawardhana[6], Sushma Naithani[6], Martin Ranik[7], James Wesley-Smith[8], Luke Solomon[9], Pankaj Jaiswal[6], Alexander A. Myburg[6] and Steven H. Strauss[10]

[1]Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR 97... Paulo (EEL-USP), CP 116, 12602-810 São Paulo, Brazil; [3]School of Biological Sciences, Un... Molecular Vegetal (LGMV), Departamento de Genética, Universidade Federal do Rio de Jan... of Botany, University of British Columbia, 3529-6270 University Blvd, Vancouver, BC V6T... 97331, USA; [7]Department of Genetics, Forestry and Agricultural Biotechnology Institute (F... and Industrial Research, 1 Meiring Naude Rd, Pretoria, South Africa; [9]Seed Technology Pro... Ecosystems and Society, Oregon State University, Corvallis, OR 97331, USA

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Steven H. Strauss
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Email: steven.strauss@oregonstate.edu

Summary

- As a step toward fu... ment within the *Eucal*... mes of floral buds fr... transcriptomes of dive...

Research article — Highly accessed — Open Access

Genome-wide transcriptome analysis of the transition from primary to secondary stem development in *Populus trichocarpa*

Palitha Dharmawardhana[1], **Amy M Brunner**[2] and **Steven H Strauss**[1*]

* Corresponding author: Steven H Strauss
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1 Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR, 97331-5752, USA

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For all author emails, please log on.

BMC Genomics 2010, **11**:150 doi:10.1186/1471-2164-11-150

The electronic version of this article is the complete one and can be found online at: http://www.biomedcentral.com/1471-2164/11/150

Received: 24 November 2008
Accepted: 4 March 2010
Published: 4 March 2010

Abstract

Background

With its genome sequence and other experimental attributes, *Populus trichocarpa* has become the model species for genomic studies of wood development. Wood is derived from secondary growth of tree stems, and begins with the development of a ring of vascular cambium in the young developing stem. The terminal region of the developing shoot provides a steep developmental gradient from primary to secondary growth that facilitates identification of genes that play specialized functions during each of these phases of growth.

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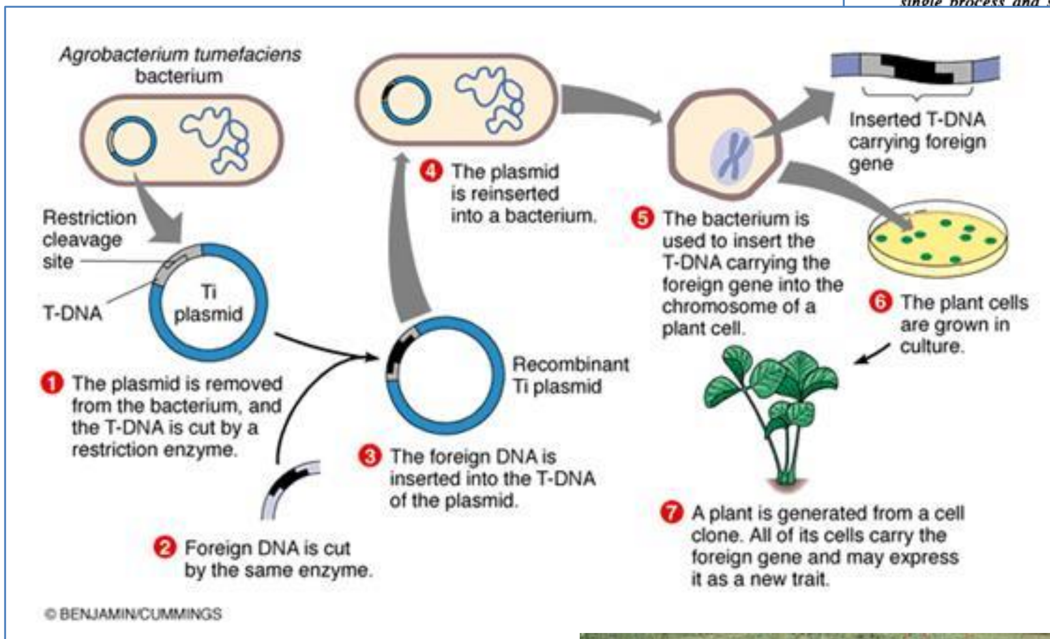
GMO biotech explodes in 80-90s

A Simple and General Method for Transferring Genes into Plants

Abstract. *Transformed petunia, tobacco, and tomato plants have been produced by means of a novel leaf disk transformation-regeneration method. Surface-sterilized leaf disks were inoculated with an* Agrobacterium tumefaciens *strain containing a modified tumor-inducing plasmid (in which the phytohormone biosynthetic genes from transferred DNA had been deleted and replaced with a chimeric gene for kanamycin resistance) and cultured for 2 days. The leaf disks were then transferred to selective medium containing kanamycin. Shoot regeneration occurred within 2 to 4 weeks, and transformants were confirmed by their ability to form roots in medium containing kanamycin. This method for producing transformed plants combines gene transfer, plant regeneration, and effective selection for transformants into a single process and should be applicable to plant species that can be infected by* … *egenerated from leaf explants.*



of an *A. tumefaciens* strain (GV3Ti11SE) containing a modified octopine Ti plasmid (pTiB6S3SE) in which all phytohormone biosynthetic genes and the T_L-DNA right border sequence have been deleted has been described (*2*). Formation of a cointegrate between pTiB6S3SE and the intermediate vectors pMON120 or pMON200 results in a functional, avirulent T-DNA (*2*, *7*). Plasmid pMON200 is a derivative of pMON120, which contains a translationally-improved chimeric NOS/NPTII/NOS gene for kanamycin resistance and confers a high degree of resistance to aminoglycoside antibiotics on transformed plant cells (*8*). The vectors also contain the nopaline synthase gene, which provides a second marker in the transformed plant cells (*1*).

Disks were punched from surface-sterilized leaves with a paper punch (6 mm in diameter) and submerged in a culture of *A. tumefaciens* grown overnight in luria broth at 28°C. After gentle shaking to ensure that all edges were infected, the disks were blotted dry and incubated upside-down on nurse culture plates prepared as described (*7*) containing medium that induces regeneration of shoots of the species being transformed. The age and titer of the bacterial inoculum had little influence on the effectiveness of the transformation; however, it was important to avoid excessive soaking of the internal tissues of the leaf disk by the bacterial culture. After 2 to 3 days, the disks were transferred to petri plates containing the same medium but without feeder cells or filter papers and containing carbenicillin (500 μg/ml) and kanamycin (300 μg/ml).

After 2 to 4 weeks, shoots that developed were excised from calli and transplanted to appropriate root-inducing medium containing carbenicillin (500 μg/ml) and kanamycin (100 μg/ml). Rooted plantlets were transplanted to soil as soon as possible after roots appeared. *Nicotiana tabacum* varieties Samson and Havana 425 (*9*) and a first-generation cross-fertilized (F_1) hybrid of *Petunia hybrida* (*10*) were easily transformed by this system. L2 tomato plants (*11*) responded better when the feeder plate medium was modified by reducing the amount of inorganic salts to one-tenth the usual concentration.

Uninoculated petunia leaf disks and those inoculated with *A. tumefaciens* strains containing pTiB6S3SE::pMON-120 (which lacks the chimeric gene for kanamycin resistance) did not produce calli or shoots on medium containing 300 μg of kanamycin per milliliter (Fig. 1). In contrast, leaf disks inoculated with *A.*

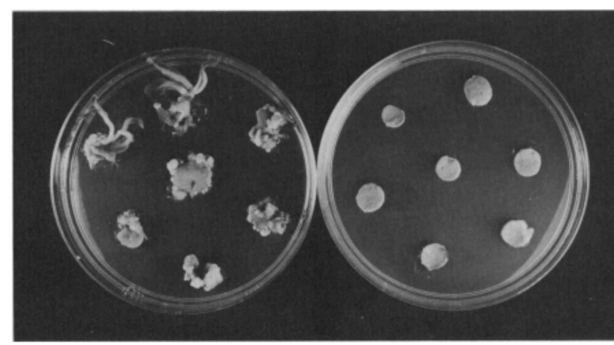
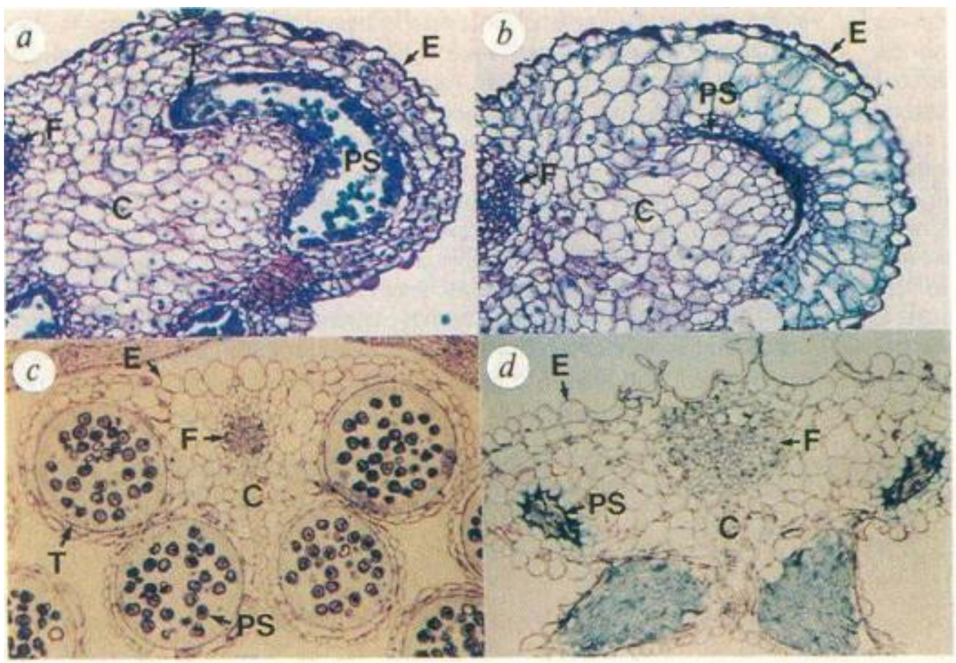


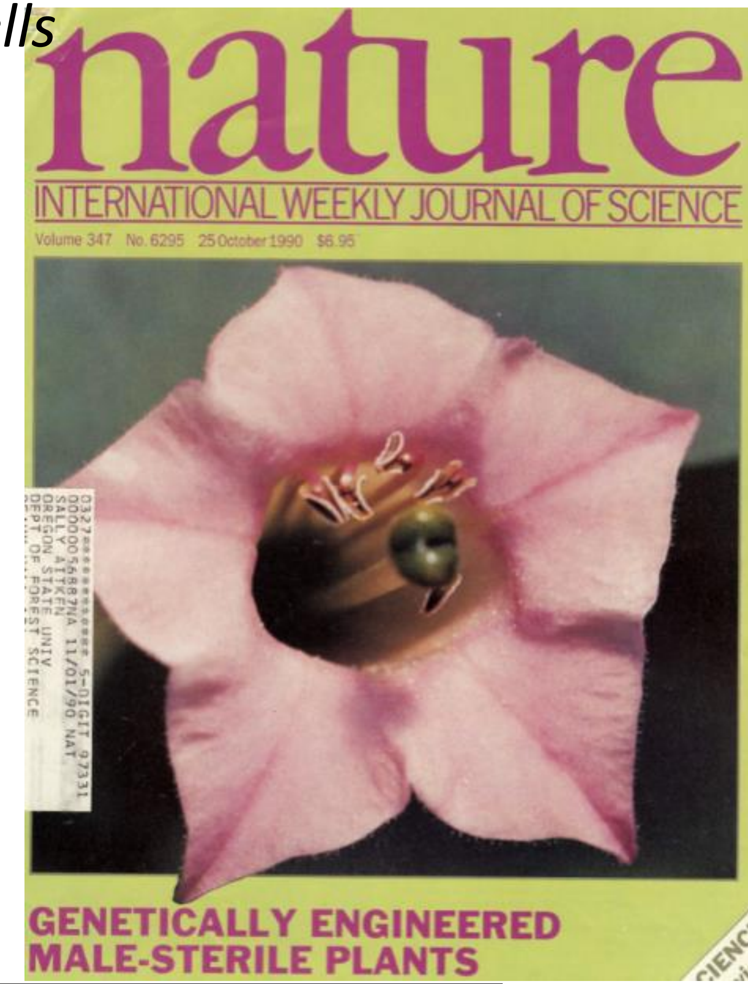
Fig. 1. Leaf disk transformation and selection of antibiotic-resistant cells. Leaf disks were punched from a surface-sterilized leaf of *Petunia hybrida* (Mitchell), inoculated with *Agrobacterium tumefaciens* strains, cultured on feeder plates, and transferred 2 days later to medium containing 300 μg of kanamycin per milliliter. The cultures were photographed 21 days after inoculation. Leaf disks transformed with pTiB6S3SE::pMON200 (which contains the chimeric gene for kanamycin resistance) are shown on the left, and disks transformed with pTiB6S3SE::pMON120 (which lacks the kanamycin-resistance gene) are shown on the right.

1229

First demonstration of transgenic male-sterility -- via “ablation” method

Cell-disrupting genes turned on in floral cells
Anther promoter::RNAse

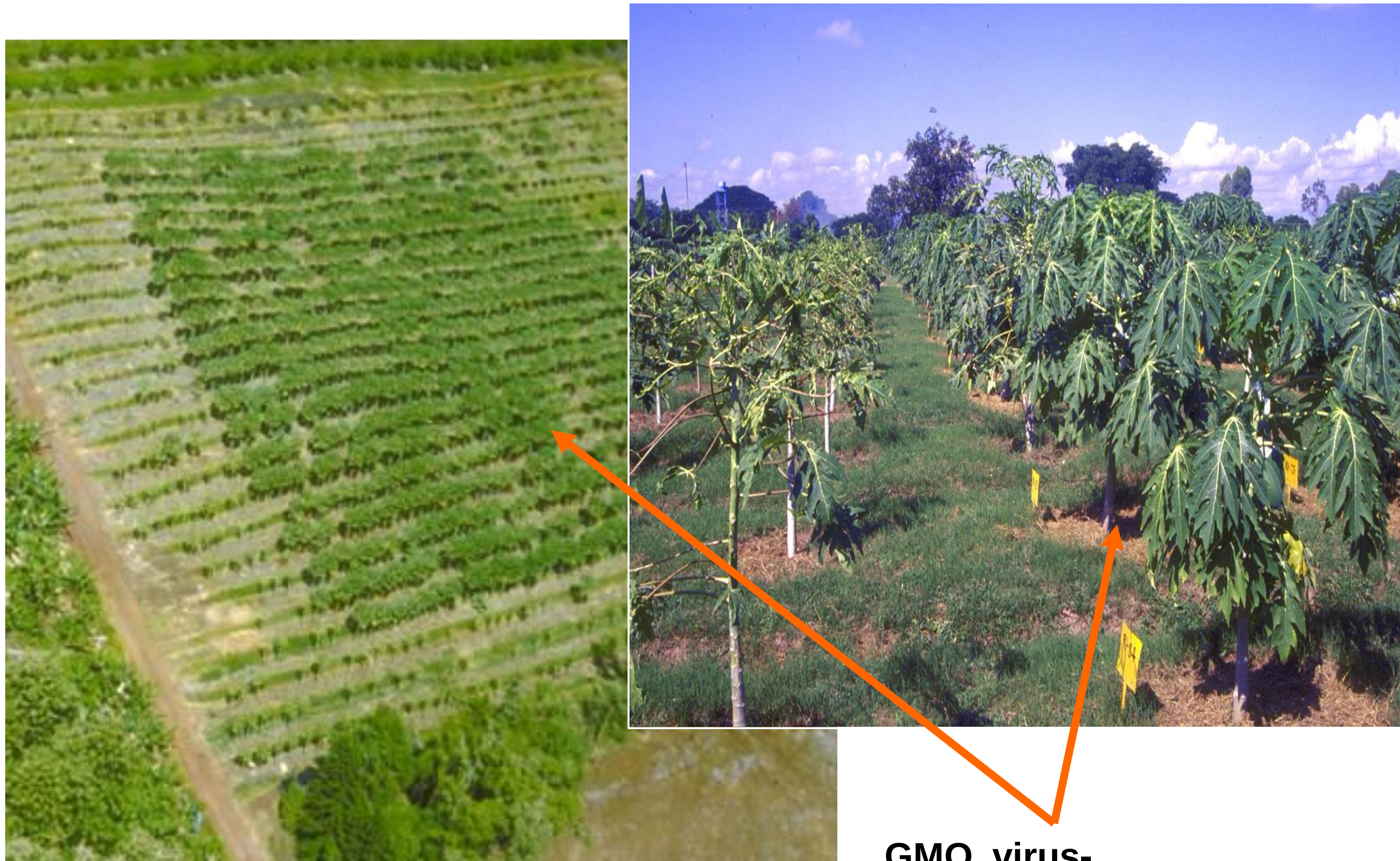




Induction of male sterility in plants by a chimaeric ribonuclease gene
Celestina Mariani*, Marc De Beuckeleer*, Jessie Truettner†,
Jan Leemans* & Robert B. Goldberg†‡

Virus-resistant papaya saved the Hawaiian industry in the mid-1990s / ~80% of papaya today

- Nobel prize winning "immunization" in plants – **stimulates natural defenses**
- Great humanitarian potential in developing world



GMO, virus-resistant trees

Courtesy of Denis Gonsalves, formerly of Cornell University

Healthier soy oils: Science underlying high oleic acid and high omega-3

The New York Times

Business Day

In a Bean, a Boon to Biotech

DuPont Pioneer

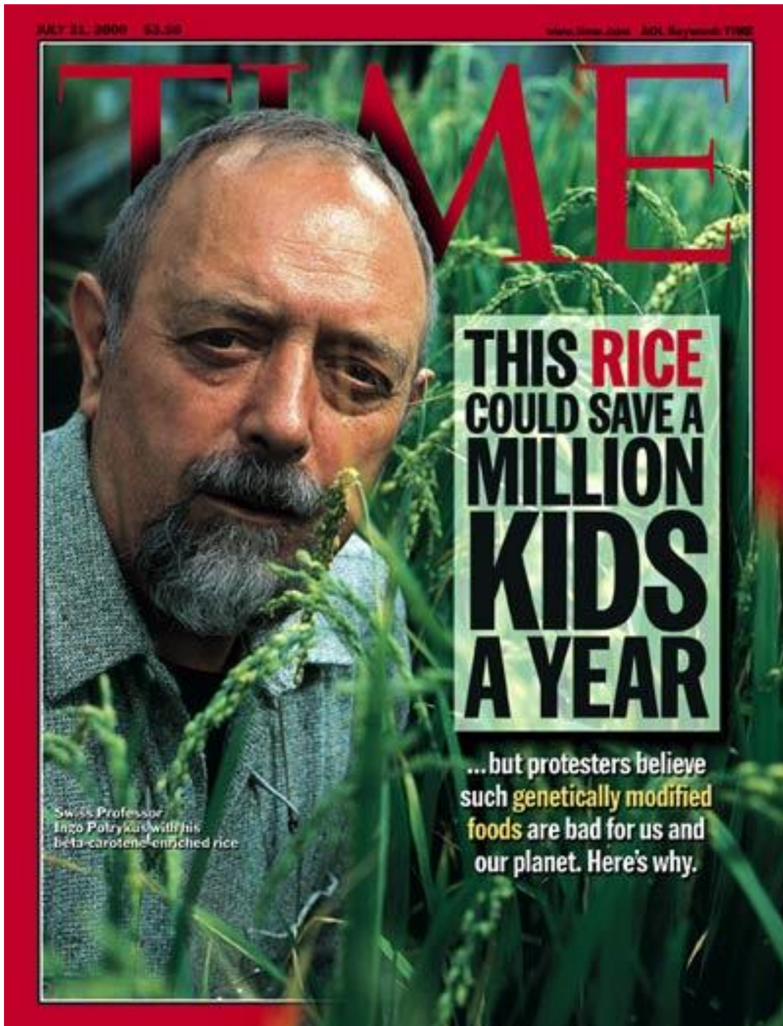
DuPont Pioneer's oil compared with soybean oils with partly hydrogenated oils, the source of trans fats.

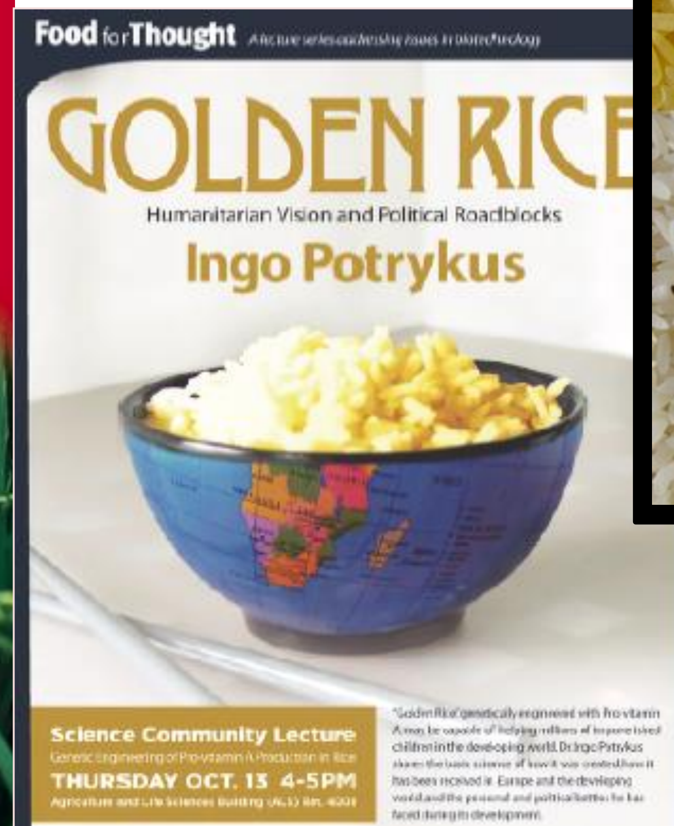
By ANDREW POLLACK
Published: November 15, 2013

A new federal push to purge artery-clogging trans fats from foods could be just what the doctor ordered — not only for public health but for the unpopular biotechnology industry, specifically, two developers of genetically modified crops.

"It almost mirrors olive oil in terms of the composition of fatty acids."

Biofortification - Golden Rice and many others since to help the billions of malnourished





β-carotene makes the rice look golden

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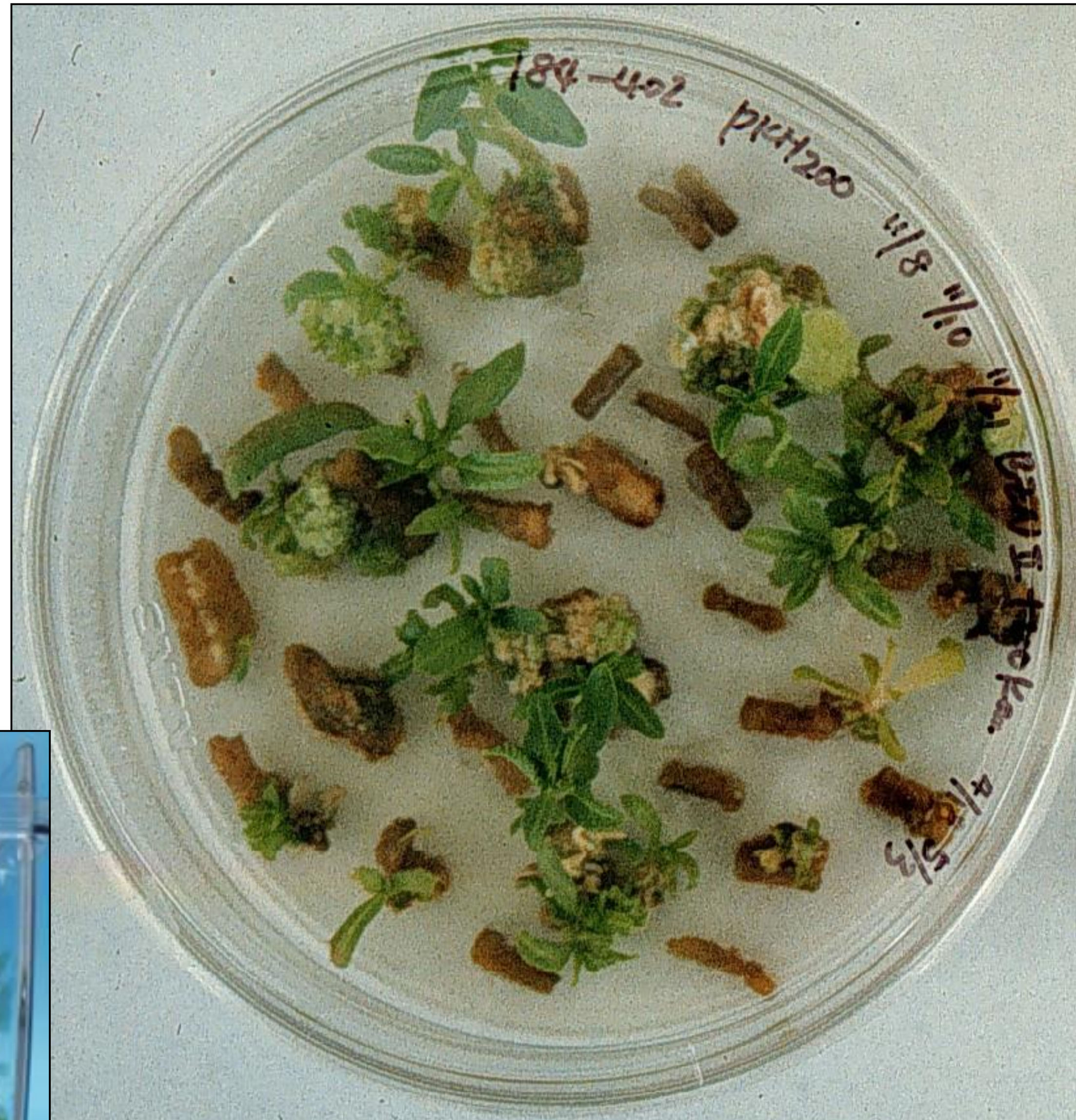
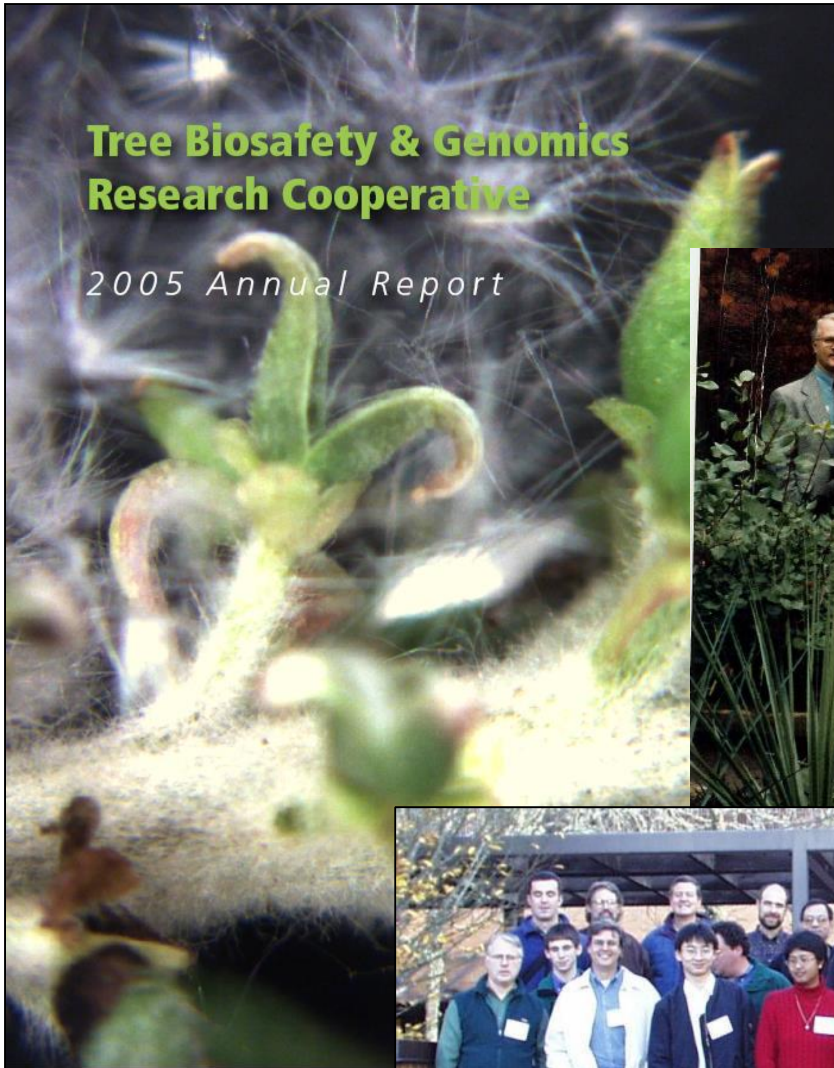
Poplars adopted as wood, pulp, and bioenergy crop in northwest USA

Poplars first genetically transformed shortly thereafter, in 1987



Formed industry consortium in 1994



Insect resistant Bt-cottonwoods in eastern Oregon field trial

Growth rate benefits substantial for Bt-poplars (cry3a) – >>10-20%

28

NRC Research Press

ARTICLE

Bt-Cry3Aa transgene expression reduces insect damage and improves growth in field-grown hybrid poplar

Amy L. Klocko, Richard Meilan, Rosalind R. James, Venkatesh Viswanath, Cathleen Ma, Peggy Payne, Lawrence Miller, Jeffrey S. Skinner, Brenda Oppert, Guy A. Cardineau, and Steven H. Strauss

Abstract: The stability and value of transgenic pest resistance for promoting tree growth are poorly understood. These data are essential for determining if such trees could be beneficial to commercial growers in the face of substantial regulatory and marketing costs. We investigated growth and insect resistance in hybrid poplar expressing the *cry3Aa* transgene in two field trials. An initial screening of 502 trees comprising 51 transgenic gene insertion events in four clonal backgrounds (*Populus trichocarpa* × *Populus deltoides*, clones 24-305, 50-197, and 198-434; and *P. deltoides* × *Populus nigra*, clone OP-367) resulted in transgenic trees with greatly reduced insect damage. A large-scale study of 402 trees from nine insertion events in clone OP-367, conducted over two growing seasons, demonstrated reduced tree damage and significantly increased volume growth (mean 14%). Quantification of Cry3Aa protein indicated high levels of expression, which continued after 14 years of annual or biannual coppice in a clone bank. With integrated management, the *cry3Aa* gene appears to be a highly effective tool for protecting against leaf beetle damage and improving yields from poplar plantations.

Résumé : La stabilité et la valeur de la résistance transgénique aux ravageurs pour favoriser la croissance des arbres ne sont pas bien connues. Ces données sont essentielles si l'on veut déterminer dans quelle mesure de tels arbres transgéniques pourraient être profitables pour des producteurs commerciaux considérant les coûts substantiels reliés à la réglementation et la mise en marché de tels arbres. Les auteurs ont étudié la croissance et la résistance aux insectes de peupliers hybrides exprimant le

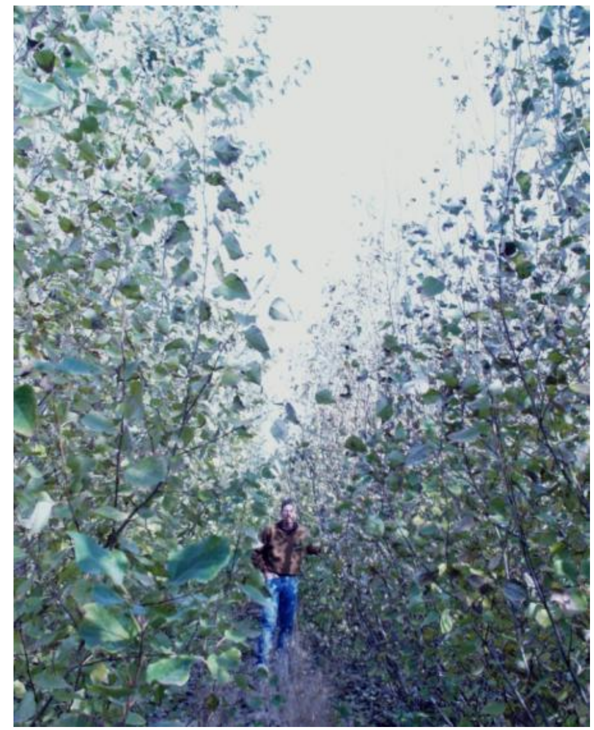
Can. J. For. Res. 44: 28–35 (2014) dx.doi.org/10.1139/cjfr-2013-0270

Published at www.nrcresearchpress.com/cjfr on 28 October 2013.

Striking and stable herbicide resistance in the field – 20% growth improvement

Screen of primary transformants

2 yr-old field trial



Wild type controls

Stable male-sterility

Tree Genetics & Genomes (2014) 10:1583–1593
DOI 10.1007/s11295-014-0781-6

ORIGINAL PAPER

A tapetal ablation transgene induces stable male sterility and slows field growth in *Populus*

Estefania Elorriaga · Richard Meilan · Cathleen Ma · Jeffrey S. Skinner · Elizabeth Etherington · Amy Brunner · Steven H. Strauss

Received: 20 March 2014 / Revised: 18 July 2014 / Accepted: 18 July 2014 / Published online: 13 August 2014

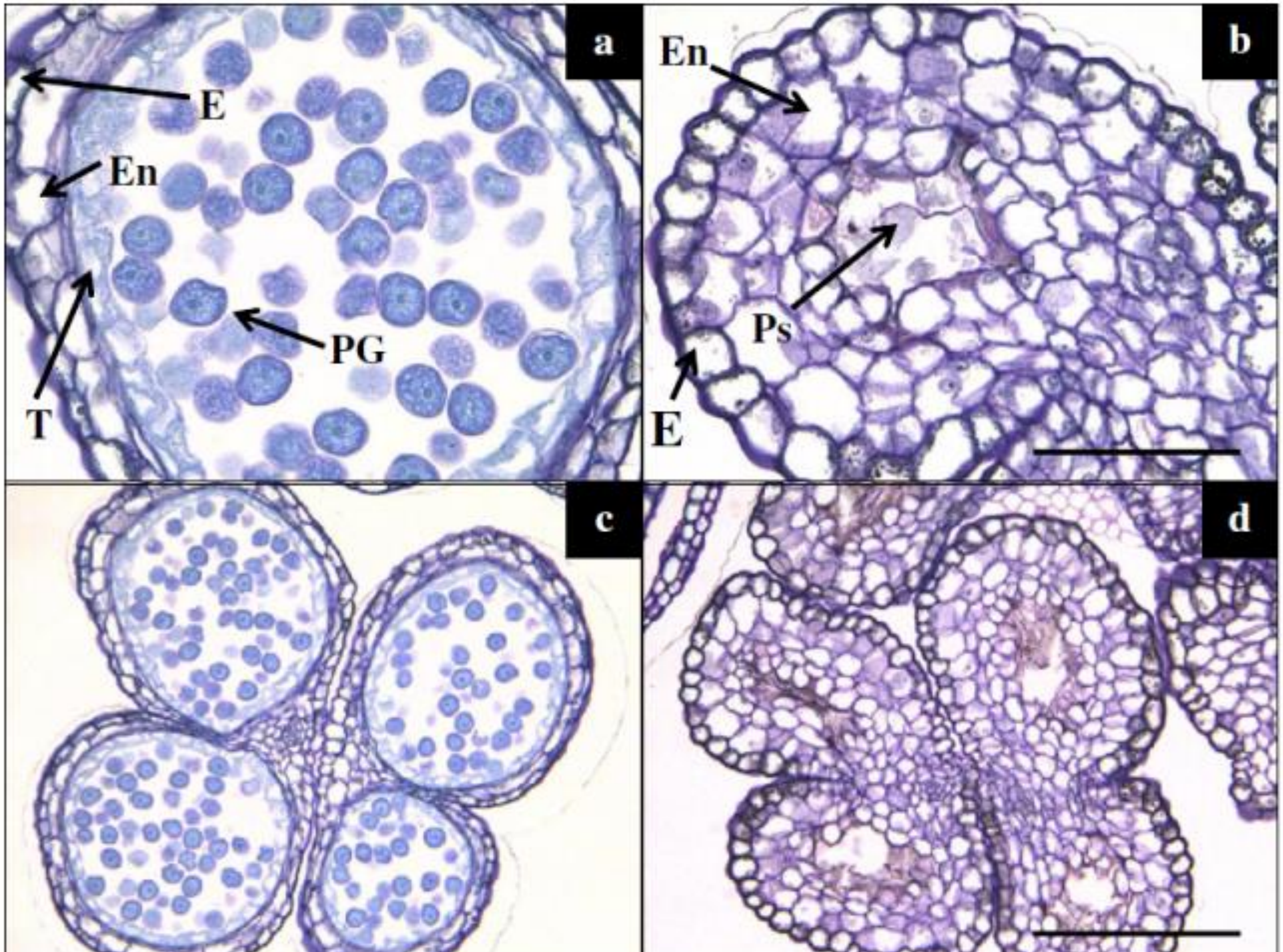
Abstract The field performance of genetic containment technologies–considered important for certain uses of transgenic trees in forestry–is poorly known. We tested the efficiency of a barnase gene driven by the *TA29* tapetum-dominant promoter for influencing growth rate and inducing male sterility in a field trial of transgenic hybrid poplar (*Populus tremula* × *Populus tremuloides*). When the growth of 18 transgenic

transgenic event grew significantly more slowly than the control. In contrast, when we compared the growth of transgenic trees containing four kinds of *β-glucuronidase* (GUS) reporter gene constructs to non-transgenic trees—all of which had been produced using the same transformation method and poplar clone and grown at the same field site—there were no statistically significant differences in growth after three grow-

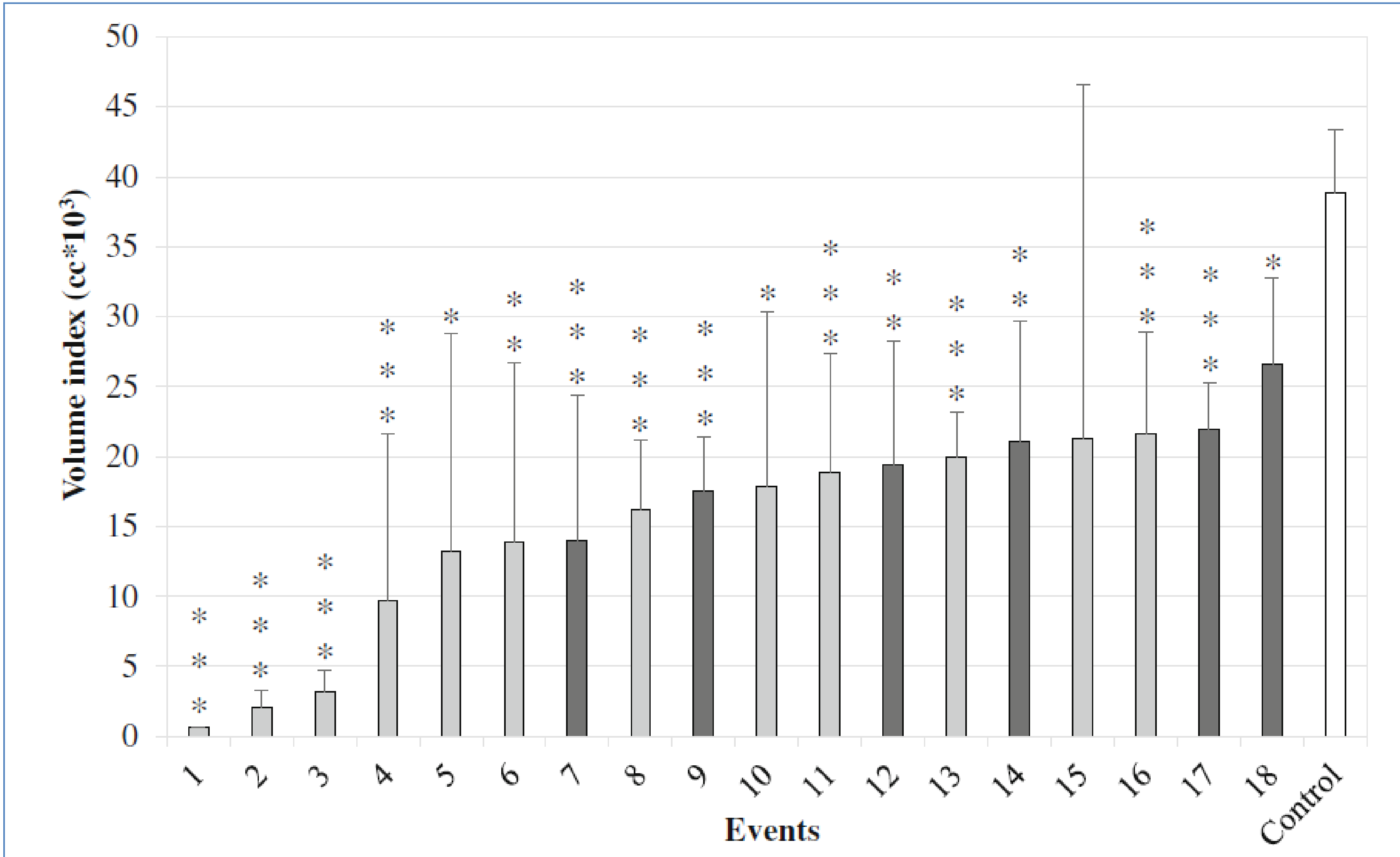
It takes years…then harvesting the flowers up there…

Pollen-less catkins in 8 yr-old male poplars in Oregon with same sterility gene

Tapetal collapse



Pleiotropy: Deleterious effects of barnase on tree growth



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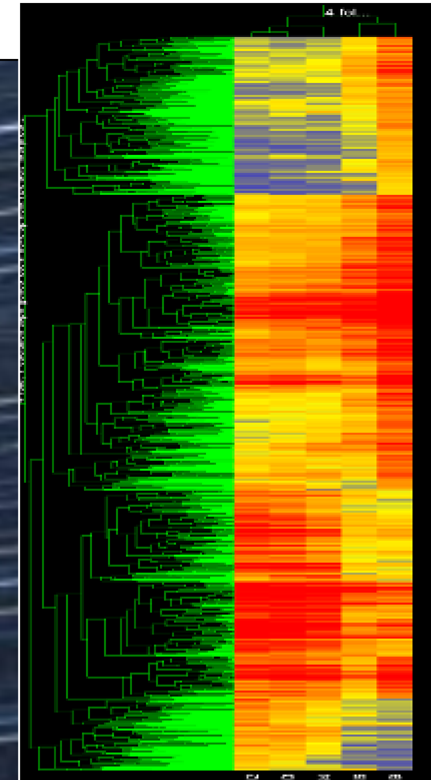
Poplar genome sequence – 3rd plant sequenced!



15 SEPTEMBER 2006 VOL 313 **SCIENCE** www.sciencemag.org

Gene suppression takes off - RNAi

RNAi gene suppression accelerates flowering in poplar

the plant journal

SEB SOCIETY FOR EXPERIMENTAL BIOLOGY

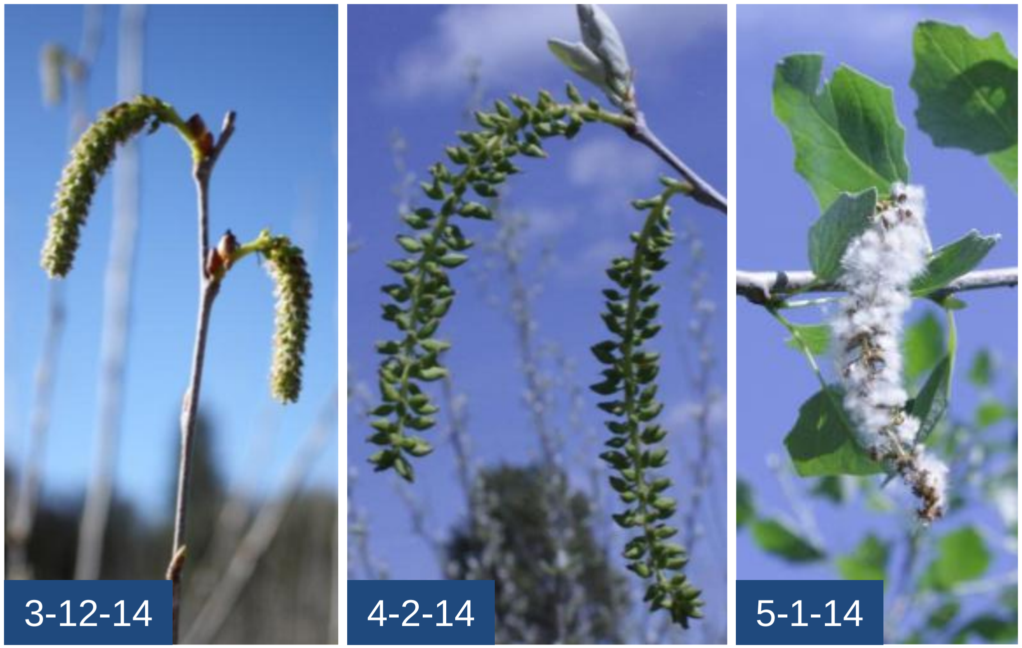
The Plant Journal (2010) doi: 10.1111/j.1365-313X.2010.04185.x

Populus CEN/TFL1 regulates first onset of flowering, axillary meristem identity and dormancy release in *Populus*

Rozi Mohamed[1,†,‡], Chieh-Ting Wang[2,†,§], Cathleen Ma[1], Olga Shevchenko[1], Sarah J. Dye[1], Joshua R. Puzey[2
Elizabeth Etherington[1], Xiaoyan Sheng[2], Richard Meilan[3], Steven H. Strauss[1] and Amy M. Brunner[2,*]

[1]*Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331-5752, USA,*
[2]*Department of Forest Resources and Environmental Conservation, Virginia Polytechnic Institute and State U*
Blacksburg, VA 24061-0324, USA, and
[3]*Department of Forestry and Natural Resources, Purdue University, West Lafayette, IN 47907-2061, USA*

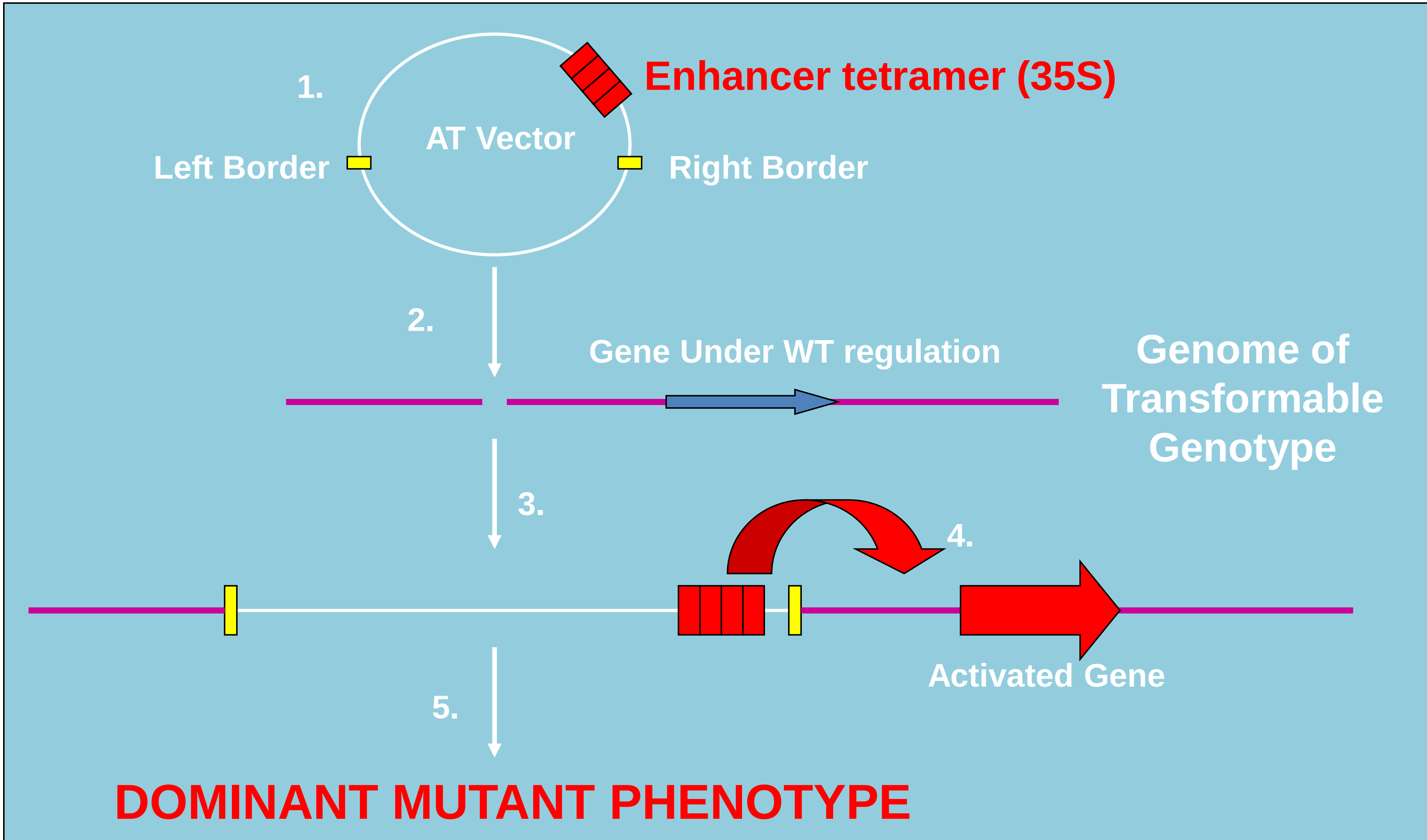
RNAi:*LFY* catkins do not produce seeds or cotton



Control

RNAi-LFY

Activation tagging: An effective mutagenesis tool for trees



Field mutagenesis screens

Tree Genetics & Genomes (2011) 7:91–101
DOI 10.1007/s11295-010-0317-7

ORIGINAL PAPER

Activation tagging is an effective gene tagging system in *Populus*

Victor Busov • Yordan Yordanov • Jiqing Gou • Richard Meilan • Cathleen Ma • Sharon Regan • Steven Strauss

Received: 23 March 2010 / Revised: 24 May 2010 / Accepted: 8 June 2010 / Published online: 8 July 2010

Abstract Knowledge of the functional relationship between genes and organismal phenotypes in perennial plants is extremely limited. Using a population of 627 independent events, we assessed the feasibility of activation tagging as a forward genetics tool for *Populus*. Mutant identification after 2 years of field testing was nearly sevenfold morphological and physiological traits, including leaf size and morphology, crown architecture, stature, vegetative dormancy, and tropic responses. Characterization of the insertion in more than 100 events with and without mutant phenotypes showed that tags predominantly (70%) inserted in a 13-Kbp region up- and downstream of the genes'

Examples of mutants observed

Two pairs of trees planted per event

Big leaf

South oriented growth

Early bud flush

Delayed senescence

PNAS

EARLY BUD-BREAK 1 (*EBB1*) is a regulator of release from seasonal dormancy in poplar trees

Yordan S. Yordanov[a], Cathleen Ma[b], Steven H. Strauss[b], and Victor B. Busov[a,1]

[a]School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931; and [b]Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331-5752

Edited by Ronald R. Sederoff, North Carolina State University, Raleigh, NC, and approved May 16, 2014 (received for review March 27, 2014)

Trees from temperate latitudes transition between growth and dormancy to survive dehydration and freezing stress during winter months. We used activation tagging to isolate a dominant mutation affecting release from dormancy and identified the corresponding gene *EARLY BUD-BREAK 1* (*EBB1*). We demonstrate through positioning of the tag, expression analysis, and retransformation experiments that *EBB1* encodes a putative APETALA2/Ethylene responsive factor transcription factor. Transgenic up-regulation of the gene caused early bud-flush, whereas down-regulation delayed bud-break. Native *EBB1* expression was highest in actively growing apices, undetectable during the dormancy period, but rapidly increased before bud-break. The *EBB1* transcript was localized in the L1/L2 layers of the shoot meristem and leaf primordia. *EBB1*-overexpressing transgenic plants displayed enlarged shoot meristems, open and poorly differentiated buds, and a higher rate of cell division in the apex. Transcriptome analyses of the *EBB1* transgenics identified 971 differentially expressed genes whose expression correlated with the *EBB1* expression changes in the transgenic plants. Promoter analysis among the differentially expressed genes for the presence of a canonical EBB1-binding site identified 65 putative target genes, indicative of a broad regulatory context of EBB1 function. Our results suggest that EBB1 has a major and integrative role in reactivation of meristem activity after winter dormancy.

adaptation | phenology | regeneration | climate change

Temporal modifications in plant growth and reproduction in conjunction with cyclical changes in climate are essential for adaptation to variable environments (1). The annual alterations of growth and dormancy in forest trees from boreal and temperate regions in response to changing temperature and/or moisture regimes are well-known examples of such cyclical changes. The molecular mechanisms governing these cycles remain poorly understood (2).

By definition, dormancy is the absence of visible growth in any plant structure containing a meristem (3). The transition from active growth to dormancy in poplar is initiated in the fall by the short-day photoperiod, causing initial cessation of shoot elongation (4). This event is followed by transformation of the apex into a bud (5) and establishment of poorly known physiological changes collectively known as endodormancy, an inability of the meristem and the youngest leaf primordia to respond to growth-promoting signals. Resumption of bud growth, known as bud-break, occurs after meeting a chilling requirement (exposure for several months to low temperatures, with variable species-specific duration) and is controlled almost exclusively by high temperatures (6). The timing of entry and release from dormancy is CONSTANS (FT/CO) module (10, 11) and via regulatory proteins controlling circadian rhythms (12, 13). In *Arabidopsis*, the ability of FT and other floral integrators to respond to inductive signals is controlled by a suite of MADS (MCM1, AGAMOUS, DEFICIENS, SRF) box genes like SHORT VEGETATIVE PHASE (SVP) and FLOWERING LOCUS C (FLC) (14). Similar MADS box genes, known as DORMANCY-ASSOCIATED MADS (DAM) genes (15), appear to be involved in regulation of bud dormancy in several woody perennial species (6). Involvement of ethylene and abscisic acid signaling in bud formation has also been suggested (16, 17). Modulation of auxin response was also found to be important for the transition to dormancy in poplar (18).

Even less is known about control of endodormancy and reinitiation of bud growth. Studies in *Picea*, *Vitis*, and *Populus* have used transcription profiling to study gene expression during endodormancy and/or resumption of growth (19–21). Homologies to vernalization have been invoked, but critical differences exist because the vernalization-associated epigenetic mechanism requires sustained division, whereas bud dormancy can be imposed and reset in the same meristem cells (2). Recently, it has been shown that the plasmodesmata connections to the meristem are plugged during dormancy and need to be reopened before growth-promoting signals like FT can reach their target's tissues in the apex (22). Expression of cell-cycle marker genes indicates that after endodormancy establishment, cambium meristem cells are arrested in the G1/S transition and unable to respond to growth-permissive conditions (23). Studies in *Arabidopsis* have identified many of the regulators of cell proliferation in the shoot apical meristem (SAM) (24), and expression of poplar homologs of these genes correlates with arrest of cell proliferation during dormancy (25). However, functional characterization of

Significance

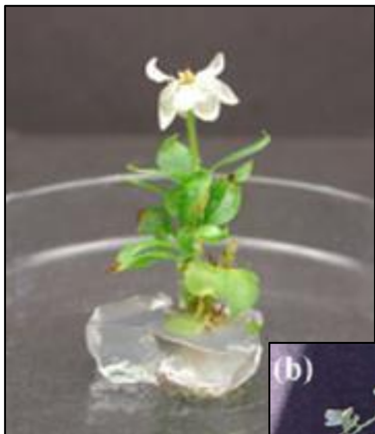
Timing of vegetative bud dormancy is an environmentally and economically important trait whose importance will grow due to rapid climate changes. However, the underpinning regulatory mechanisms are still poorly understood. We report the identification and characterization of the *Early Bud-Break 1* (*EBB1*) gene in poplar that regulates the timing of bud-break. EBB1 plays a major and integrative role in the reactivation of the shoot apical meristem after winter dormancy. The knowledge about EBB1 function can enable novel approaches for population management, molecular breeding, and genetic engineering of dormancy-associated traits.

Author contributions: Y.S.Y., S.H.S., and V.B.B. designed research; Y.S.Y., C.M., and V.B.B.

An answer to speed research

Overexpression of endogenous flowering genes induces early flowering

Apple



Orange

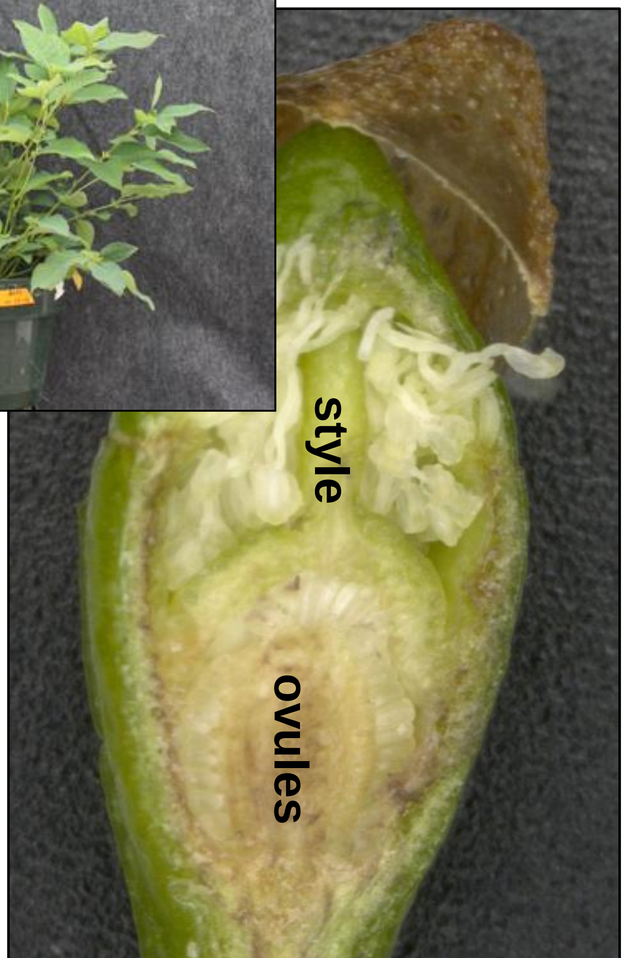
Plum

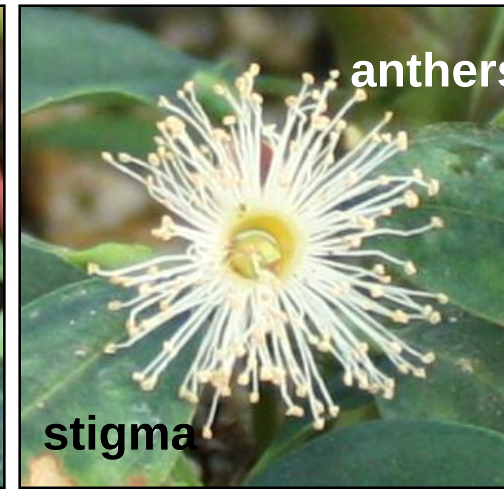
Poplar

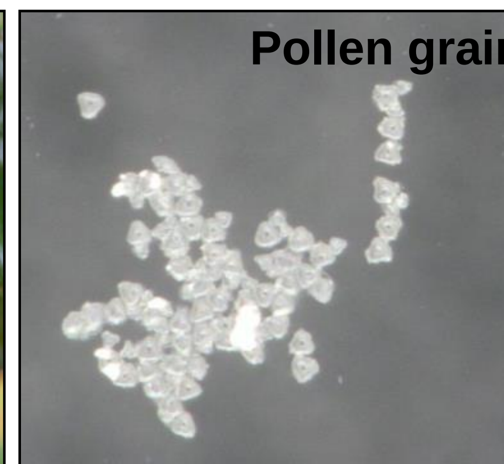
Flowering locus T (FT) to accelerate flowering in poplar – Heat induced by heat-shock promoter

LB	NOSp::NPTII::NOSt	GmHsp	FT sequence	35St	RB

Early flowering effective in eucalypts too....







Roadmap

- Ancient background
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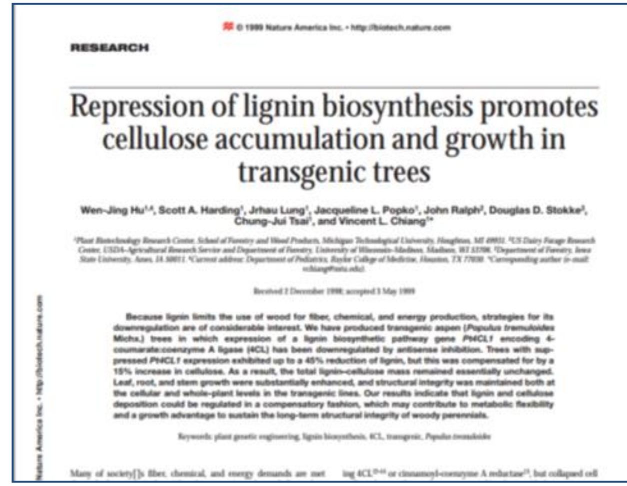
- Fighting back – GMO science advocacy
- Lessons

Do lignin-reduced trees really have magical growth and wood?



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RESEARCH

Repression of lignin biosynthesis promotes cellulose accumulation and growth in transgenic trees

Wen-Jing Hu[1,4], Scott A. Harding[1], Jrhau Lung[1], Jacqueline L. Popko[1], John Ralph[2], Douglas D. Stokke[3], Chung-Jui Tsai[1], and Vincent L. Chiang[1*]

Received 2 December 1998; accepted 3 May 1999

Because lignin limits the use of wood for fiber, chemical, and energy production, strategies for its downregulation are of considerable interest. We have produced transgenic aspen (*Populus tremuloides* Michx.) trees in which expression of a lignin biosynthetic pathway gene *Pt4CL1* encoding 4-coumarate:coenzyme A ligase (4CL) has been downregulated by antisense inhibition. Trees with suppressed *Pt4CL1* expression exhibited up to a 45% reduction of lignin, but this was compensated for by a 15% increase in cellulose. As a result, the total lignin-cellulose mass remained essentially unchanged. Leaf, root, and stem growth were substantially enhanced, and structural integrity was maintained both at the cellular and whole-plant levels in the transgenic lines. Our results indicate that lignin and cellulose deposition could be regulated in a compensatory fashion, which may contribute to metabolic flexibility and a growth advantage to sustain the long-term structural integrity of woody perennials.

Keywords: plant genetic engineering, lignin biosynthesis, 4CL, transgenic, *Populus tremuloides*

- Nature Biotechnology 1999 – antisense *4CL* genes generated much excitement
- Increase of growth rate, halving of lignin content, no obvious ill effects in greenhouse

Its different in the field

Antisense Down-Regulation of *4CL* Expression Alters Lignification, Tree Growth, and Saccharification Potential of Field-Grown Poplar[1[W][OA]]

Steven L. Voelker, Barbara Lachenbruch, Frederick C. Meinzer, Michael Jourdes, Chanyoung Ki, Ann M. Patten, Laurence B. Davin, Norman G. Lewis, Gerald A. Tuskan, Lee Gunter, Stephen R. Decker, Michael J. Selig, Robert Sykes, Michael E. Himmel, Peter Kitin, Olga Shevchenko, and Steven H. Strauss*

Department of Wood Science and Engineering (S.L.V., B.L.) and Department of Forest Ecosystems and Society (O.S., S.H.S.), Oregon State University, Corvallis, Oregon 97331; United States Department of Agriculture Forest Service, Pacific Northwest Research Station, Corvallis, Oregon 97331 (F.C.M.); Washington State University, Institute of Biological Chemistry, Pullman, Washington 99164–6340 (M.J., C.K., A.M.P., L.B.D., N.G.L.); BioEnergy Science Center, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831–6422 (G.A.T., L.G., S.R.D., M.J.S., R.S., M.E.H.); National Renewable Energy Laboratory, Golden, Colorado 80401 (G.A.T., L.G., S.R.D., M.J.S., R.S., M.E.H.); and Laboratory for Wood Biology and Xylarium, Royal Museum for Central Africa, B–3080 Tervuren, Belgium (P.K.)

Plant Physiology, October 2010

Research

New Phytologist

Reduced wood stiffness and strength, and altered stem form, in young antisense *4CL* transgenic poplars with reduced lignin contents

Steven L. Voelker[1], Barbara Lachenbruch[1], Frederick C. Meinzer[2] and Steven H. Strauss[3]

[1]Department of Wood Science & Engineering, Oregon State University, Corvallis, OR 97330, USA; [2]USDA Forest Service, Pacific Northwest Research Station, 3200 Jefferson Way, Corvallis, OR 97330, USA; [3]Department of Forest Ecosystems and Socie

Plant, Cell & Environment

PC&E

Plant, Cell and Environment (2011)

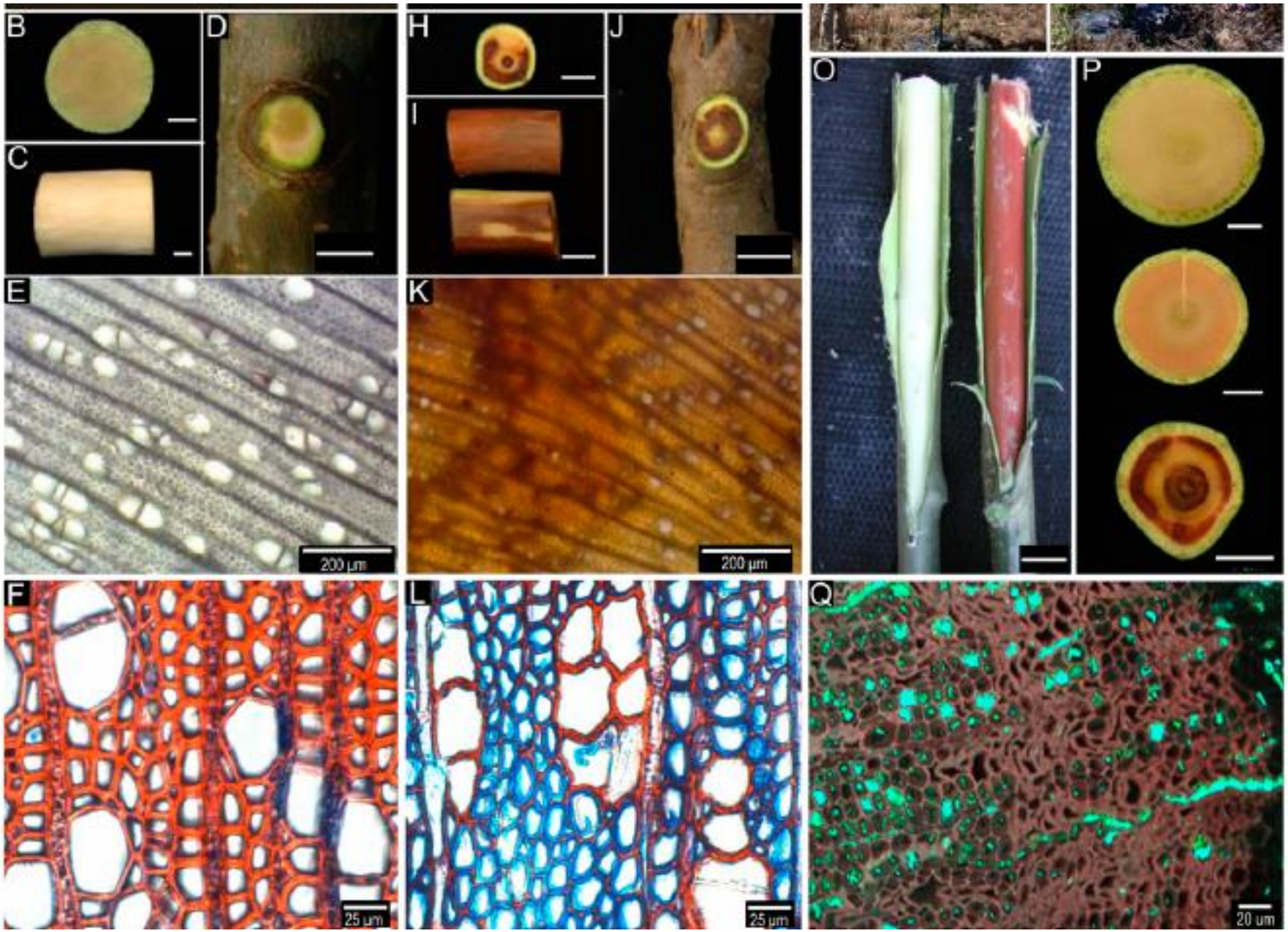
doi: 10.1111/j.1365-3040.2010.02270.x

Transgenic poplars with reduced lignin show impaired xylem conductivity, growth efficiency and survival

STEVEN L. VOELKER[1], BARBARA LACHENBRUCH[1], FREDERICK C. MEINZER[2], PETER KITIN[3] & STEVEN H. STRAUSS[4]

[1]Department of Wood Science and Engineering and [4]Department of Forest Ecosystems and Society, Oregon State University, [2]U.S.D.A. Forest Service, Forest Sciences Laboratory, 3200 Jefferson Way, Corvallis, OR 97330, USA and [3]Laboratory for Wood Biology and Xylarium, Royal Museum for Central Africa, B-3080, Tervuren, Belgium

Brown wood, disturbed xylem development in the field



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PERSPECTIVES

SCIENCE AND SOCIETY

Opposition to transgenic technologies: ideology, interests and collective action frames

Ronald J. Herring

Abstract | Genetic engineering has enabled significant, accepted innovations in medicine and other fields. In agriculture, however, a global cognitive divide around 'genetically modified organisms' (GMOs) has limited the diffusion and scope of this technology. The framing of agricultural products of recombinant DNA technology as GMOs lacks biological coherence, but has proved to be a powerful frame for opposition. Disaggregating the concept of the 'GMO' is a necessary condition for confronting misconceptions that constrain the use of biotechnology in addressing imperatives of development and escalating challenges from nature, especially in less-industrialized nations.

Much of the current public discourse on genetic engineering targets 'Luddism' or 'anti-science' as obstacles to taking more advantage of the genomics revolution. However, this view fails to appreciate the complex network of interests and ideas surrounding genetic engineering. After outlining global patterns of diffusion of agricultural biotechnology, this article explores the reasons for, and the results of, successful opposition. It concludes with implications for future applications of the genomics revolution in biology, particularly in the less industrialized world.

Diffusion of agricultural biotechnology

In the most recent data, for 2007, 23 countries have officially-approved transgenic crops growing in fields. Despite the political rhetoric of north versus south, more than half of these countries do not fall into the category of 'high-income economies'. In descending order of acreage

Nature Reviews | Genetics | June 2008 | 459

Money: Advocacy targeting food & agriculture is large and growing

- Agbiotech Info Net
- Agribusiness Examiner
- ACGA
- American Pasturage
- APH
- Anim
- Beyo
- NCRI
- Cent
- Cent
- Cent
- CSPI
- Chef
- Chilc
- Common Dreams
- Consumer Federation of America
- Consumers Union
- Crop Choice
- David Suzuki Foundation
- Dawn Watch
- Deep Ecology
- Eco-Trust
- Economic Democracy
- Earth Spirit
- Earth First
- Environmental Defense
- Environmental Media Services
- FAIR
- Family Farm Defenders

- Farm Animal Reform Movement
- Farm Aid
- Farm Sanctuary
- Friends of the Earth
- Local Harvest
- NFFC
- Nishoren
- No Spray coalition
- NWARN
- Organic Consumers Association
- PANNA
- PETA
- PCRM
- PIRG
- Public Citizen
- Purdey Fund
- Sierra Club
- SEAC
- Water Keeper Alliance

More than 500 activist organizations in North America are spending in excess of $2 billion annually engaging in food-related campaigns targeting biotech and many other elements

Institute for Ecology

NRDC

Organic Consumers Association

TIDES

PeTA

Jay Byrne, 2012, V-fluence

Tree Biotechnology Conference at Oxford in 1999 - Vandalism against lignin modified trees to "welcome" conferees, Euro-press attacks

FRANKENSTEIN'S FOREST

The tree-top protesters, who confounded the Government's road-building programme by camping in the path of bulldozers, are now poised to target the very trees they might once have called home.

Whilst public attention has been focused on the threat of 'Frankenstein Foods', the same corporations who are forcing us to ingest genetically modified (GM) meals have been quietly perpetrating yet another crime against the environment.

The biotech industry has been understandably tight-lipped about its latest phase of the genetic revolution. But it is currently preparing to take over the world's forests – or what's

ment. Campaigners fear that GM trees will sap up water, nutrients and light, leaving indigenous trees to die out along with the host of insects, plants and fungi which rely upon them. In turn, birds and animals would lose many of their natural prey. Those surviving creatures would fall victim to herbicide weed-killer, liberally applied once the GM trees become resistant. The result, opponents fear, will be a sanitised, silent forest, cleansed of natural life.

This month, activists are targetting the Forest Biotechnology '99 conference, hosted by Oxford Forestry Institute from July 11 - 16. It will bring together some of the world's top

1997. The trees, engineered by the University of Derby, to be disease- and insect-resistant were destroyed by removing the bark. A growing spate of raids on food crops caused AstraZeneca to make a statement to the press before a GenetiX Snowball action earlier this year, fearing damage to their GM poplars.

In April, Monsanto teamed up with two of the world's biggest forest and paper corporations, International Paper and Westvaco. They also got New Zealand company, Fletcher Challenge, in on the deal as they own the all-important patents on newly developed genes which will give the consortium the monopoly on GM trees that they're after. Having sunk

vention, which governs global emissions of greenhouse gases, came into force after the 1997 Kyoto conference, industrialised countries have been forced to clean up. However, the corporations argue that by planting more trees, they should be awarded 'carbon credits', because trees absorb carbon dioxide.

Recently, naturally rich native forests have fallen to the chainsaw, only to be replaced by invasive foreign plantation species such as eucalyptus. To the undiscerning eye, one forest is indistinguishable from another, allowing corporations to boast about how well they are managing their operations. Look behind the greenwash and companies such as Shell are

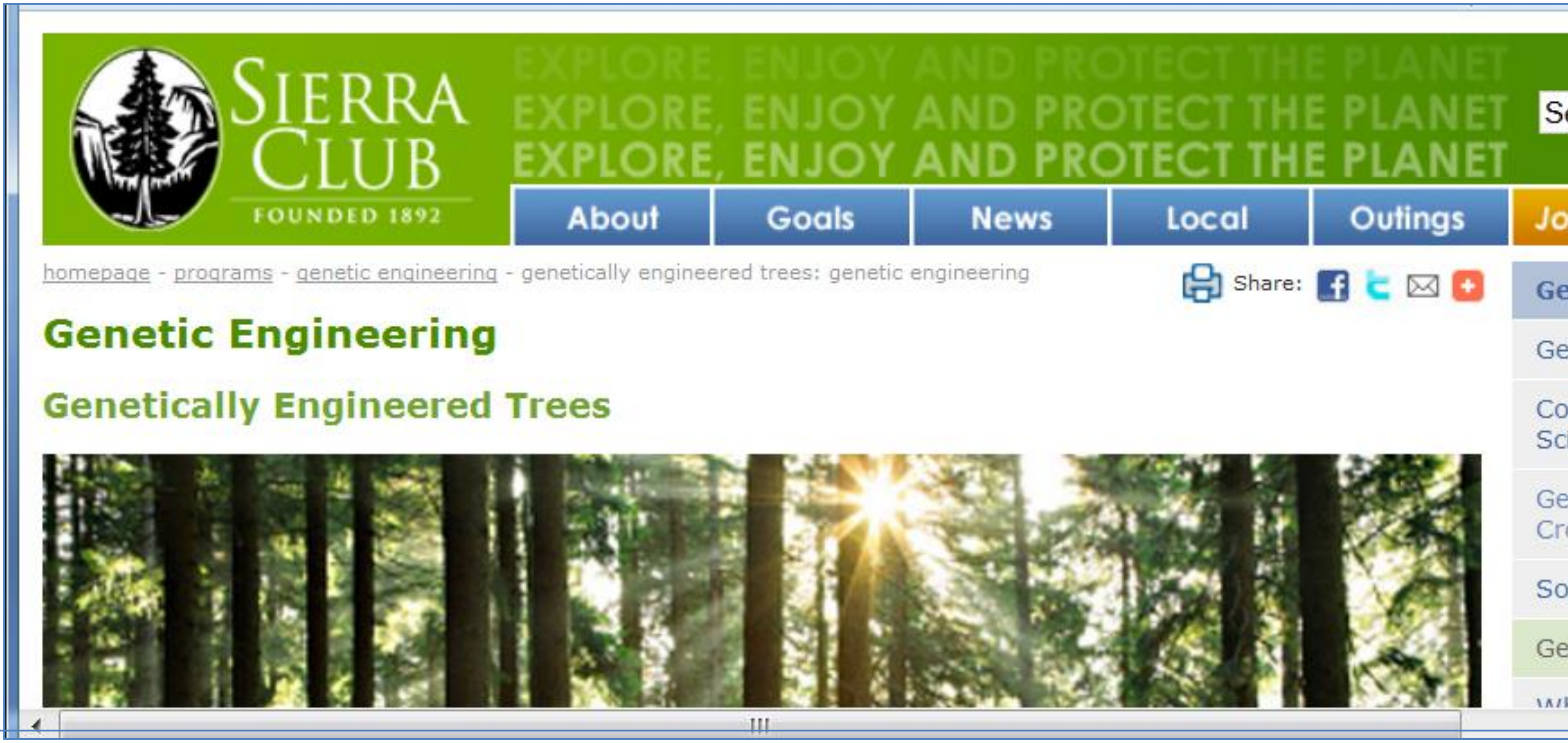
Whilst public attention has been focused on the threat of 'Frankenstein Foods', the same corporations who are forcing us to ingest genetically modified (GM) meals have been quietly perpetrating yet another crime against the environment.

Bradshaw (UW) and Strauss (OSU) "eco"vandalism - 2001

U Wash

Oregon State

Some of the major environmental groups are powerful opponents



"The possibility that the new genes spliced into GE trees will interfere with natural forests isn't a hypothetical risk but a certainty. …genetic engineering may do as much damage to forests and wildlife habitat as chain saws and sprawl." (11/10/13)

Greenpeace the world anti-GMO leader – trees and ag

International treaties push for ever more stringent regulations of GE trees

Strangled at birth? Forest biotech and the Convention on Biological Diversity

Steven H Strauss, Huimin Tan, Wout Boerjan & Roger Sedjo

Against the Cartagena Protocol and widespread scientific support for a case-by-case approach to regulation, the Convention on Biological Diversity has become a platform for imposing broad restrictions on research and development of all types of transgenic trees.

The Convention on Biological Diversity (CBD) has become a major focus of activist groups that wish to ban field research and commercial development of all types of genetically modified (GM) trees. Recent efforts to influence CBD recommendations by such groups has led to the adoption of recommendations for increased regulatory stringency that are inconsistent with the views of most scientists and most of the major environmental organizations. We suggest that the increasingly stringent recommendations adopted by the CBD in recent years are impeding, and in many places may foreclose, much of the field research needed to develop useful and safe applications of

A convention co-opted

Negotiated under the United Nations (UN) Environment Program, CBD was adopted in June 1992 and subsequently entered into force in December 1993. The CBD has been signed by 191 of the 192 members of the UN, making it one of the largest international treaties. The aim of the CBD is to promote the conservation and sustainable use of biodiversity, and the fair and equitable sharing of benefits from the use of genetic resources. Because transgenic organisms have the potential to affect biodiversity, special provisions of the CBD cover the use and trade in living modified organisms (LMOs, also known as genetically modified organisms; GMOs).

In 2000, the Cartagena Protocol on Biosafety

mandate in the CBD

NATURE BIOTECHNOLOGY VOLUME 27 NUMBER 6 JUNE 2009

ECO

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VOLUME 21, ISSUE 4
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6. Agenda Regional de La Araucania, Chile
7. Agrupación ambientalista Koyam Newen, Chile
8. Agrupación de jóvenes profesionales mapuche Konapewman, Chile
9. Alianza por una Mejor Calidad de Vida (RAP-Chile), Chile
10. Amigos de la Tierra España – Friends of the Earth Spain, Spain
11. AOPA - Associação para o Desenvolvimento da Agroecologia, Brazil
12. Argonautas Ambientalistas da Amazônia, Brazil
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14. Associação de Programas em Tecnologias Alternativas-APTA, Brazil

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25. CAxTIERRA (Comisión de Apoyo X Tierra), Uruguay
26. Centro de Agricultura Alternativa do Norte de Minas - CAA NM, Brazil
27. Centro de Defesa dos Direitos Humanos – CDDH, Brazil
28. Centro de Estudos Ambientais (CEA), Brazil
29. CENTRO ECOLOGICO BORDE RIO, Chile
30. Centro Federal de Educação Tecnológica de Rio Pomba (CEFET-Rio Pomba), Brazil
31. CLOC (Coordinadoria LatinoAmericana de las Organizaciones del Campo), Republica Dominicana

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33. COATI - Centro de Orientação Ambiental Terra Integrada - Jundiaí, Brazil
34. CODEFF / Amigos de la Tierra, Chile
35. Comissão Pastoral da Terra - Diocese Itabuna/Bahia, Brazil
36. Coorporación Unión Araucana "XAPELEAI TAIÑ KIMVN", Padre Las Casas, Chile
37. Crescente Fértil, Brazil
38. Cumberland Countians for Peace & Justice, USA
39. Development Fund, Norway
40. Dogwood alliance, USA
41. Down to Earth - the International Campaign for Ecological Justice in IndonesiaUnited Kingdom
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47. Federação de Órgãos Para

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74. Greenpeace, International
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76. Grupo Mamangava, Brazil
77. GT Ambiente / AGB-Rio e AGB-Niteroi, Brazil
78. IDESA (Instituto de Desenvolvimento Social e Ambiental), Brazil
79. Indiana Forest Alliance, USA
80. Indigenous Environmental Network (IEN), USA/Canada
81. Institute for Responsible Technology, USA
82. Institute for Social Ecology, USA
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110. Rede de Educadores Ambientais da Baixada de Jacarepaguá, Rio de Janeiro, Brazil
111. Rede de Integração Verde, Brazil
112. Rettet den Regenwald, Germany
113. Rising Tide North America, USA
114. Robin Wood, Germany
115. Safe Alternatives for our Forest Environment (SAFE)USA
116. Sierra Club, USA
117. Sindicato dos Trabalhadores de Rio Pardo de Minas - MG, Brazil
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135. Worldforests, Scotland
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GE Tree Statement

Below is a brief description of the statement and letter signed by 137 groups.

Statement signatories begin by stating that their *"concern is based on the fact that the genetic manipulation being undertaken is aimed at consolidating and further expanding a model of monoculture tree plantations that has already proven to result in serious social and environmental impacts in many of our countries."*

The statement then provides a number of examples on how current research would impact on the environment, given that trees are being genetically manipulated for.

The signatories remind country delegates that "the last Conference of the Parties to the Convention on Biological Diversity (COP-8) adopted decision VIII/19", which *"recommends Parties to take a precautionary approach when addressing the issue of genetically modified trees"* and urge them *"to definitely ban GE trees - including fields trials – because of the serious risks they pose on the Planet's biological diversity."*

Full letter and signatories available at: http://www.wrm.org.uy/actors/BDC/SBSTT

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“Green” certification creates a severe barrier to research and investment

Plantation Certification & Genetic Engineering

FSC’s Ban on Research Is Counterproductive

Steven H. Strauss, Malcolm M. Campbell, Simon N. Pryor, Peter Coventry, and Jeff Burley

ABSTRACT

Genetic engineering, also called genetic modification (GM), is the isolation, recombinant modification, and asexual transfer of genes. It has been banned in forest plantations certified by the Forest Stewardship Council (FSC) regardless of the source of genes, traits imparted, or whether for research or commercial use. We review the methods and goals of tree genetic engineering research and argue that FSC’s ban on research is counterproductive because it makes it difficult for certified companies to participate in the field research needed to assess the value and biosafety of GM trees. Genetic modification could be important for translating new discoveries about tree genomes into improved growth, quality, sustainability, and pest resistance.

Keywords: biotechnology; entomology and pathology; ethics; genetics; silviculture

Genetic engineering, commonly called genetic modification (GM) in much of the world, is the use of recombinant DNA and asexual gene transfer methods to breed more productive or pest-resistant crops. It has been the subject of considerable controversy, with concerns raised from biological, socioeconomic, political, and ethical perspectives. Some of the issues are similar to those raised by the use of molecular biology and genetic engineering in medicine, which we see in the news headlines daily. However, genetic modification in agriculture and forestry raises environmental issues as well.

GM crops, mainly herbicide- and pest-resistant varieties of soybeans, maize, or cotton, have been vigorously adopted by farmers in North America because they are easy to manage and they improve yields, reduce costs, or reduce pesticide ecotoxicity (Carpenter and Gianessi 2001). However, the controversy, primarily embodied in regulatory barriers to trade of GM crops with Europe and Japan, has slowed their adoption considerably in recent years.

If GM trees are used in forestry in the near future, they are likely to occur primarily in intensively managed environments, such as urban forests or plantations. In urban forestry, genetic modification is expected to help trees adapt to the stresses and special demands of human-dominated systems. Examples would be trees that are more tolerant of heavy metals or other pollutants, resist urban pests or diseases, grow slower, or do not produce fruits when these create hazards in street environments (Brunner et al. 1998).

Plantations, although very different from natural forests in structure and function, are considered part of the spectrum of methods in sustainable forest management (Romm 1994). Plantations can relieve pressure on natural forests for exploitation and can be of great social value by supplying community and industrial wood needs and fueling economic development. The environmental role of plantations is recognized by the Forest Stewardship Council (FSC), an international body for certification of sustainably managed forests. FSC Principle 10 states that plantations should “complement the management of, reduce pressures on, and promote the restoration and conservation of natural forests” (FSC 2001).

FSC has certified some of the most intensively managed plantations in the world, including poplar plantations and the intensive pine and eucalypt plantations of the Southern Hemisphere. Although many environmental mitigations are built into these certified plantation systems, within the areas dedicated to wood production they function as tree farms. Such intensive plantation systems often use highly bred genotypes, possibly including exotic species, hybrids, and clones, as well as many other forms of intensive silvicultural management. It is in the context of these biointensive systems that the additional expense of GM trees is likely to be worthwhile.

However, FSC currently prohibits all uses of GM trees, and is the only certification system to have done so

FSC

Forest Stewardship Council

“…genetically modified trees are prohibited…”

No research exemptions

Regulatory confusion, obstacles at national and international levels

Feature

The Phantom Forest: Research on Gene-Altered Trees Leaps Ahead, into a Regulatory Limbo

STEVE NASH

At an industrial park in Walnut Creek, California, technicians and robots are sorting through the 550 million base pairs of genetic code in poplar DNA to sequence a tree genome for the first time. They are poised to unlock a fine, full toolbox for the work of genetic engineering in trees.

In Vermont, a group called Action for Social and Ecological Justice has just kicked off a national campaign to pressure companies to ban research on genetically engineered (GE) trees. The Sierra Club, the World Wildlife Fund, and the American Lands Alliance, among others, have called for a moratorium on commercialization of GE trees.

In Wa
key resp
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response

More than 200 notices of field trials have been filed with federal regulators for lab-engineered fruit, nut, and forest trees—also known as genetically modified, biotech, or transgenic trees. But aside from a virus-resistant, bushlike papaya tree grown in Hawaii, no one has yet sought regulatory approval for commercial use of a gene-altered tree.

Westvaco Corporation, and two New Zealand firms. Arborgen estimates that, if tests go very well, the product could be ready for the market in a decade.

Cloned cathedrals

Tinkering with tree DNA presents some issues for research and for public policy, however. Casting an uncertain light over

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Regulation of field research is problematic for many crops and trees

- Regulations around the world generally target the GMO method, not the trait or its novelty – assuming hazard until proven otherwise
- Regulations for research field trials thus require containment (do not assess ecological risks or benefits of particular genes or traits)
- Beyond a boutique trial, 100% containment in the field is very hard to accomplish, especially for trees

Unexpected summer flowering of GA-gene modified, semi-dwarf transgenic poplar in field trial

The upright summer “catkins” and veg-catkin transition structures

Confusion as regulatory system evolved

- The field trial had been appended to a larger APHIS permit that permitted flowering in this location and with this genotype (incompatible with wild relatives, female tree)
- But APHIS was unsure if this meant the appended trial also could flower legally

What to do?

- Being a good soldier, we faithfully and immediately reported this unexpected occurrence (as the permit requires)
- Then discussed what to do about it with APHIS regulatory science contacts for several days
- We wanted to leave the catkins for study, as they were scientifically interesting, risk seemed to be zero, and would be difficult to remove

What to do?

- I pointed out the layers of safety from the genes (dwarf thus fitness reduced) and biology (lack of pollen or receptive females in summer, no seed dormancy) to APHIS
- The APHIS scientists agreed about safety but they felt, legally, they must report it to the **compliance branch** as a permit violation/release….


802
© AP Photo/Rogelio V. Solis

Take action!

- A science colleague at APHIS had alerted me that the report to Compliance had occurred prior to a visit and action
- Rather than risk arrest, fines, and who knows what else by federal agents…..Including what would be sure to be highly publicized as major disregard for the rules and the environment
- All students in our lab were dispatched to manually remove every “catkin” … and the same in spring and beyond…

Students removing catkins from transgenic trees

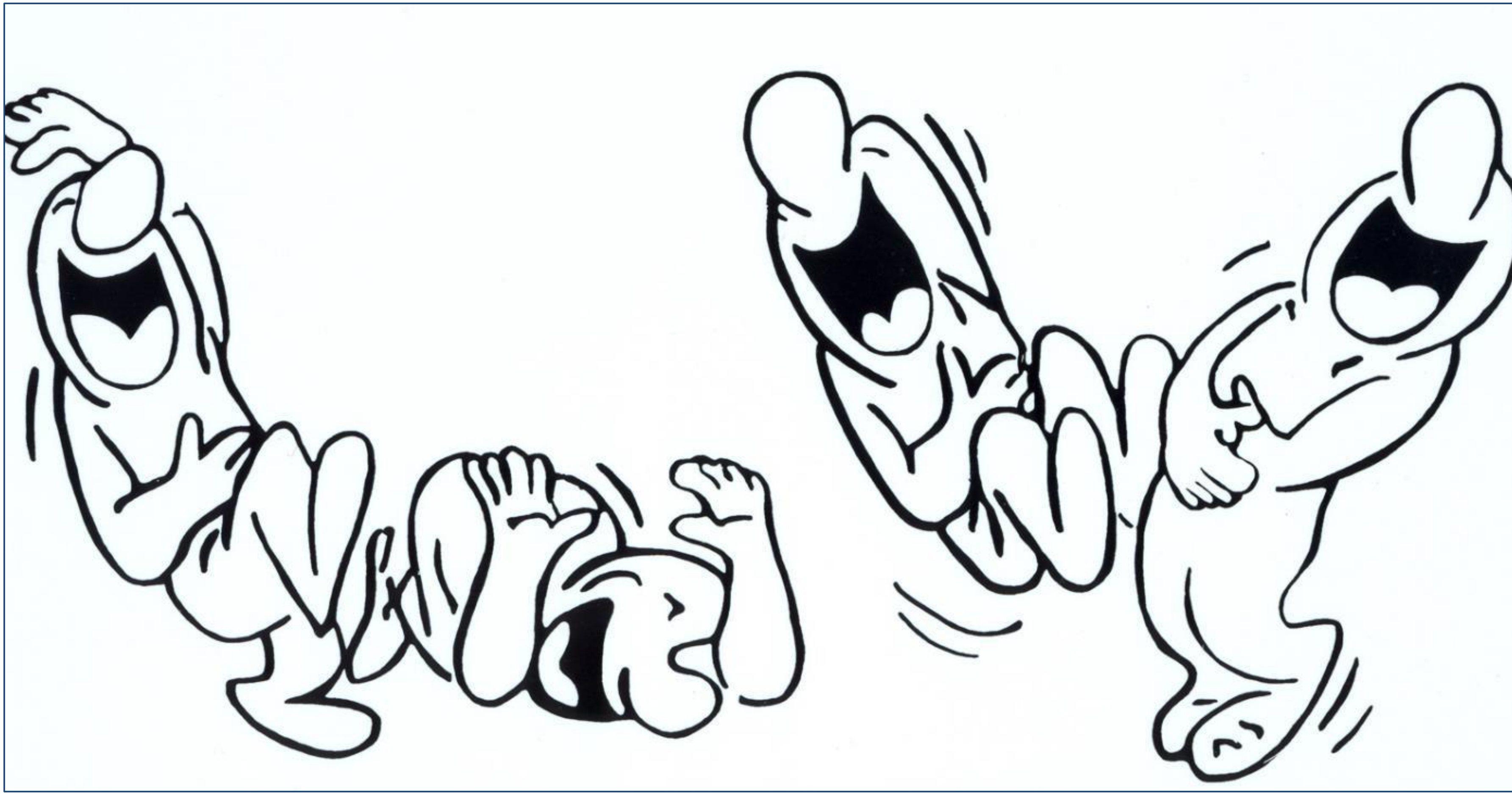
We documented for APHIS that “All removed flowers were collected and brought back to the lab, then autoclaved”

A powerful lesson

- It’s the letter of the law
  - GE methods are considered dangerous until proven otherwise, period
- Biology, safety, gene function, and benefit are irrelevant
  - Parallel case with wheat “contamination” in Oregon
- How to advance studies given importance of field studies, and difficulty of full containment, during flowering stage?
  - Critical issue for all ag: How to do field research and development for most crops?
  - Critical for forest applications, and studies of containment-sterility

One answer is to deregulate putatively sterile trees for science

- Containment of every pollen grain and seed during field research would not be required if containment not 100%
- So I visited APHIS and suggested this given the increased safety of the trait and benefits of improved knowledge



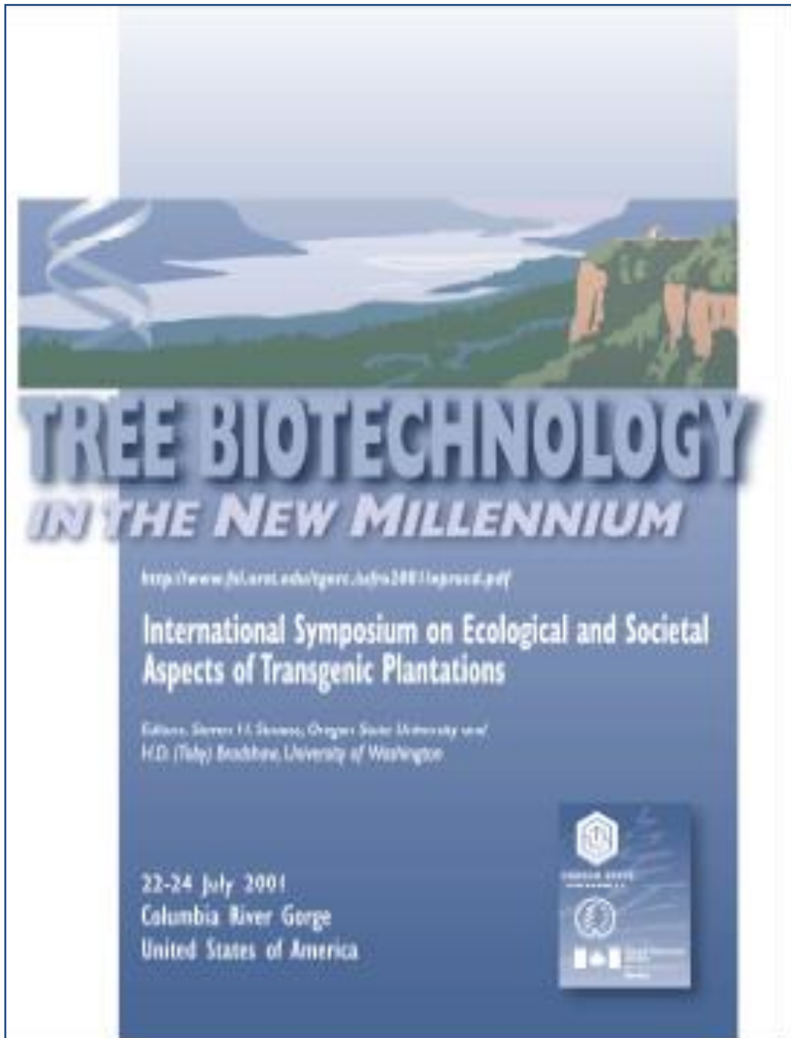
No way!

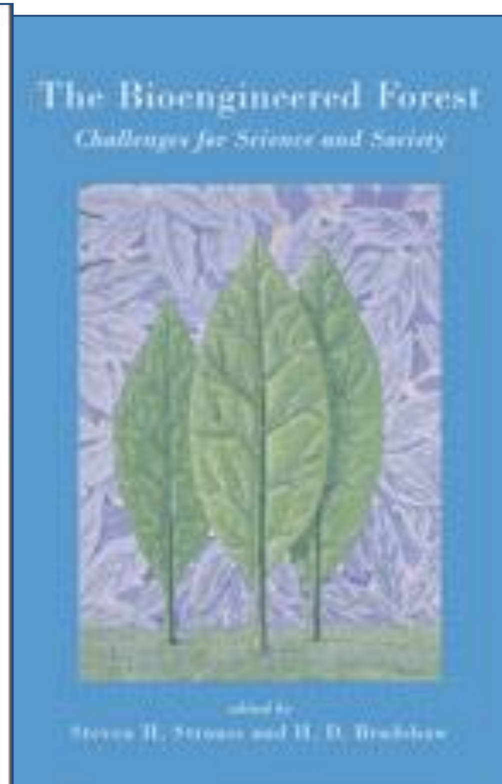
- They discussed how each gene insertion event needs a pile of data, and now certainly an EIS (environmental impact statement), to withstand lawsuits
- Getting this data requires the years of research (that is what we are trying to find a way to obtain!)

Roadmap

- Ancient background
- Early science at OSU
- Biotech buzz 1.0 – ag GMOs take form
- Making it real - Poplars and Oregon
- Getting drunk – Gene science and tech getting better and better
- Keeping your head – Science not hype
- Morning after – Society left the party early
- **Fighting back – GMO science advocacy**
- Lessons

Engaged diverse scientists and stakeholders – 2001 international conference and associated book





Proposed regulatory solutions

POLICY FORUM

GENETIC TECHNOLOGIES

Genomics, Genetic Engineering, and Domestication of Crops

Steven H. Strauss

Genomic sequencing projects are rapidly revealing the content and organization of crop genomes (*1*). By isolating a gene from its background and deliberately modifying its expression, genetic engineering allows the impacts of all genes on their biochemical networks and organismal phenotypes to be discerned, regardless of their level of natural polymorphism. This greatly increases the ability to determine gene function and, thus, to identify new options for crop domestication (*2*). The organismal functions of the large majority of genes in genomic databases are unknown.

portant to agricultural goals, but poorly represented in breeding populations because they are rare or deleterious to wild progeni-

huge numerical obstacle that is normally provided by extant wild and domesticated gene pools. Despite the great diversity of genes that can comprise GGTs, many of the modified traits are familiar, having a long history of domestication and consequent reduced fitness through artificial selection. Male sterility, seedless fruits, delayed spoilage, and dwarf stature are familiar examples.

GGTs that improve abiotic stress tolerance

Confinement level	Type 1 field trials (exploratory)	Type 2 field trials (precommercial)	Examples
High	Biological and physical confinement—detailed data		Highly toxic or allergenic pharmaceuticals and proteins
Medium	FSC, basic data	FSC, detailed data	Novel pest-management genes, low toxicity pharmaceuticals and proteins
Low: Stress tolerance	FSC, basic data	FSC, detailed data	Genomics-guided transgenes
Low: Domesticating	Petition for exemption?	FSC, basic data	Genomics-guided transgenes

Categories of confinement and monitoring for small- and large-scale transgenic field trials. Biological confinement includes genetic mechanisms to preclude spread and/or reproduction. Physical confinement requires use of geographical isolation or physical barriers. FSC, farm-scale confinement; use of spatial isolation within and between farms and border crops, combined with …oring. Detailed data include surveys of gene flow away from the site. Basic data …hment of confinement mechanisms.

PERSPECTIVE

nature biotechnology

Regulating transgenic crops sensibly: lessons from plant breeding, biotechnology and genomics

Kent J Bradford[1], Allen Van Deynze[1], Neal Gutterson[2], Wayne Parrott[3] & Steven H Strauss[4]

The costs of meeting regulatory requirements and market restrictions guided by regulatory criteria are substantial impediments to the commercialization of transgenic crops. Although a cautious approach may have been prudent initially, we argue that some regulatory requirements can now be modified to reduce costs and uncertainty without compromising safety. Long-accepted plant breeding methods for incorporating new diversity into crop varieties, experience from two decades

Regulatory costs also play a role in the growing disparity between the expanding global adoption of the large-market transgenic maize, soybean, cotton and canola crops[1] and the so-called 'small-market' or 'specialty' crops, for which field trials and commercial releases of transgenic food crops have all but stopped[3]. In 2003, fruits, vegetables, landscape plants and ornamental crops accounted for more than $50 billion in value in the United States, representing 47% of the total US farm crop income[9]. Of this, the only transgenic commodities currently mar-

Sound the alarm! Analysis of the legal implications of regulations for research & breeding

Articles

Far-reaching Deleterious Impacts of Regulations on Research and Environmental Studies of Recombinant DNA-modified Perennial Biofuel Crops in the United States

STEVEN H. STRAUSS, DREW L. KERSHEN, JOE H. BOUTON, THOMAS P. REDICK, HUIMIN TAN, AND ROGER A. SEDJO

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Get active around the globe

Strangled at birth? Forest biotech and the Convention on Biological Diversity

Steven H Strauss, Huimin Tan, Wout Boerjan & Roger Sedjo

Against the Cartagena Protocol and widespread scientific support for a case-by-case approach to regulation, the Convention on Biological Diversity has become a platform for imposing broad restrictions on research and development of all types of transgenic trees.

The Convention on Biological Diversity (CBD) has become a major focus of activist groups that wish to ban field research and commercial development of all types of genetically modified (GM) trees. Recent efforts to influence CBD recommendations by such groups has led to the adoption of recommendations for increased regulatory stringency that are inconsistent with the views of most scientists and most of the major environmental organizations. We suggest that the increasingly stringent recommendations adopted by the CBD in recent years are impeding, and in many places may foreclose, much of the field research needed

A convention co-opted

Negotiated under the United Nations (UN) Environment Program, CBD was adopted in June 1992 and subsequently entered into force in December 1993. The CBD has been signed by 191 of the 192 members of the UN, making it one of the largest international treaties. The aim of the CBD is to promote the conservation and sustainable use of biodiversity, and the fair and equitable sharing of benefits from the use of genetic resources. Because transgenic organisms have the potential to affect biodiversity, special provisions of the CBD cover the use and trade in living modified organisms (LMOs, also known as genetically modified organisms; GMOs).

...col on Biosafety

...date in the CBD

NATURE BIOTECHNOLOGY VOLUME 27 NUMBER 6 JUNE 2009

Help to define constraints and research priorities – work with think-tank “Resources for the Future” in Washington DC

Forest Scientist Views of Regulatory Obstacles to Research and Development of Transgenic Forest Biotechnology

Steve H. Strauss, Mikaela Schmitt, and Roger Sedjo

ABSTRACT

Despite many dozens of research projects, hundreds of field trials, and a long commercialized fruit tree, virus-resistant papaya, there continues to be very little public or private sector activity in the United States that is directed toward development of transgenic forest trees. We therefore undertook a survey of scientists knowledgeable in forest biotechnologies, breeding, ecology, and regulation to assess if they believed that the regulatory regime in the United States presents a significant obstacle to research or commercial development. Conducted in 2007, there were a total of 90 respondents (60% response rate) from throughout the United States. The large majority believed that regulations, in particular containment requirements during field evaluation, posed significant obstacles to development. Top priorities for research included development of gene containment methods and field studies of wood and abiotic stress modification. Priorities for regulatory reform included development of a tiered system and provisional authorizations to enable long-term field research.

Keywords: genetic engineering, genetic modification, tree biotechnology, genomics, survey

Genetic engineering (GE), commonly called genetic modification (GM), and the resulting organisms (GEOs, GMOs, and transgenics), are defined in science and regulation by the process used to produce them (Irwin and Jones 2006). They contain genes that have been inserted or modified via an asexual rather than a sexual process, and the sources of genes can be from the modified organisms, similar organisms, or from distant organisms. Typically, the genes have undergone some form of human-directed modification using recombinant DNA methods before insertion. GE methods are routine throughout all genetic biology and have been used to produce large numbers of pharmaceuticals, industrial enzymes, and several forms of GE crops that are now widely grown throughout the world (International Service for the Acquisition of Agri-biotech Applications 2008).

The only trees that have been authorized for commercial purposes are a virus-resistant papaya in Hawaii and insect-tolerant poplars in China. A virus-resistant plum has recently been deregulated by the USDA, but awaits decisions from the Environmental Protection Agency (EPA) and the USDA (Scorza et al. 2008). In the United States, the extent of field research in GE trees—a good indicator of applied, developmental research—has become highly restricted, being limited to a few academic laboratories and companies (Information Systems for Biotechnology 2008). There had been numerous confined field studies with the large majority in the USA; as of January 2008, *Populus* led all other genera with 189 authorized field tests. The traits studied included herbicide tolerance, insect resistance, disease resistance, improved growth, modified form, reduced fertility, heightened stress tolerance, and enhanced phytoremediation. In addition to the traits with direct environ-

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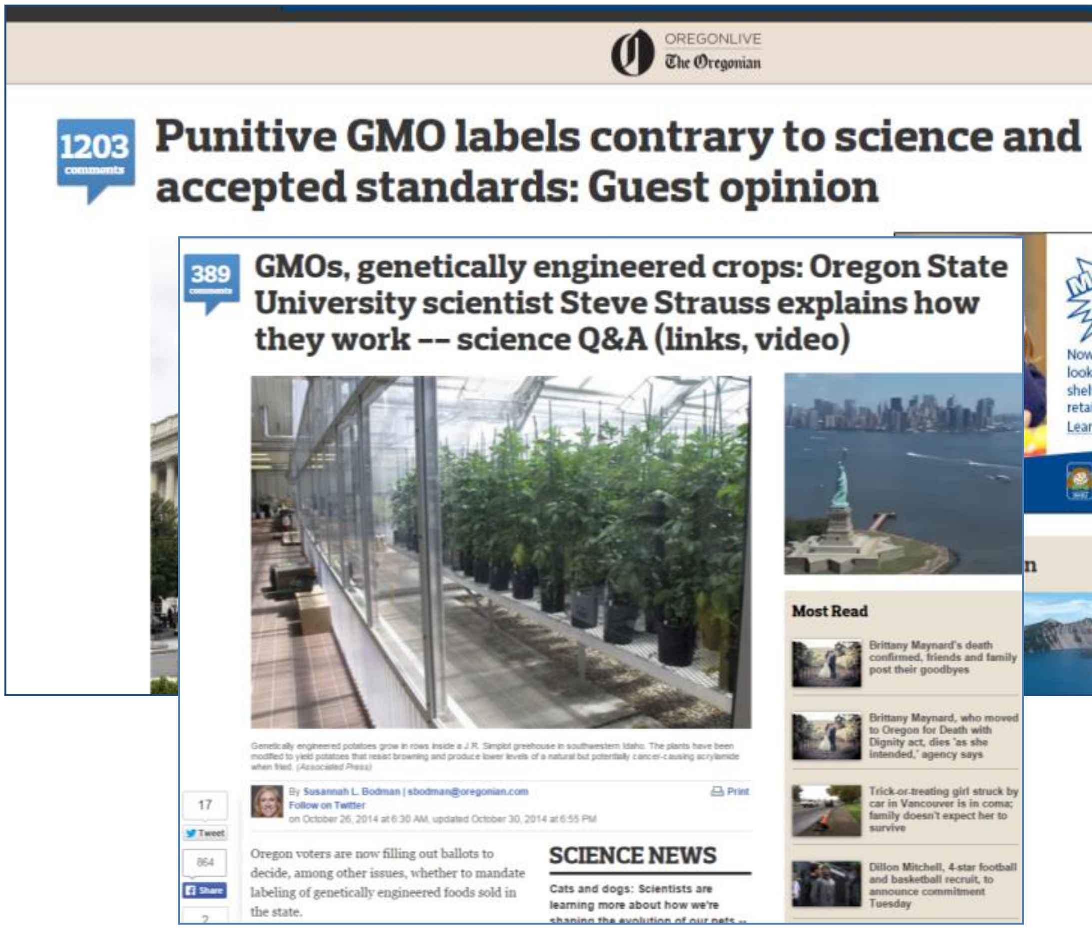
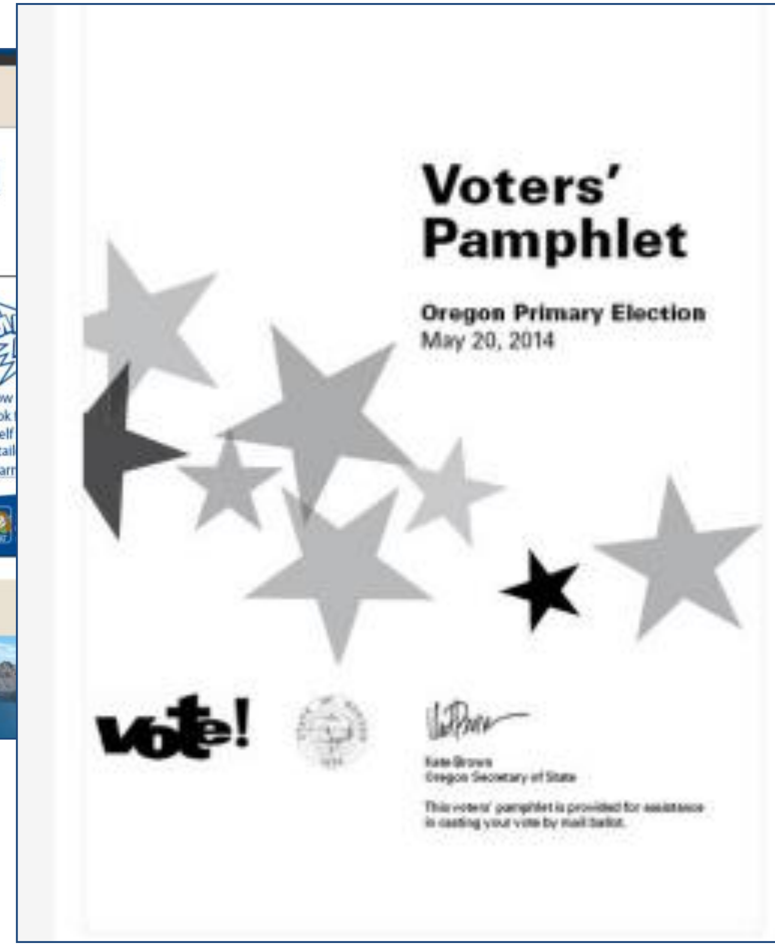
Educate and exchange views broadly

Biotech outreach and lecture series at Oregon State – 40 speakers, 8 years

Engage and advocate for science in your state and city





Lessons in summary

- Follow the science – small and large
  - Get out of the lab, train broadly, be ethical
  - Listen to and collaborate with good people
- Be aware of politics, ideology, money, and tribalism from all sides
  - The good guys can be the bad guys and visa versa
- Demand a lot of yourself and others, while showing kindness and care
- Act with courage, wisdom, and precaution
  - Don’t be reckless and arrogant
  - Use all tools to help manage a very scary future

Thanks to so many great students, employees, and friends