Transforming trees and societies

Innovations and frustrations abounding

Steve Strauss
Oregon State University
Department of Forest Ecosystems and Society, College of Forestry

IUFRO Xmas Tree Conference/ Blowing Rock, NC / 10 June 2026

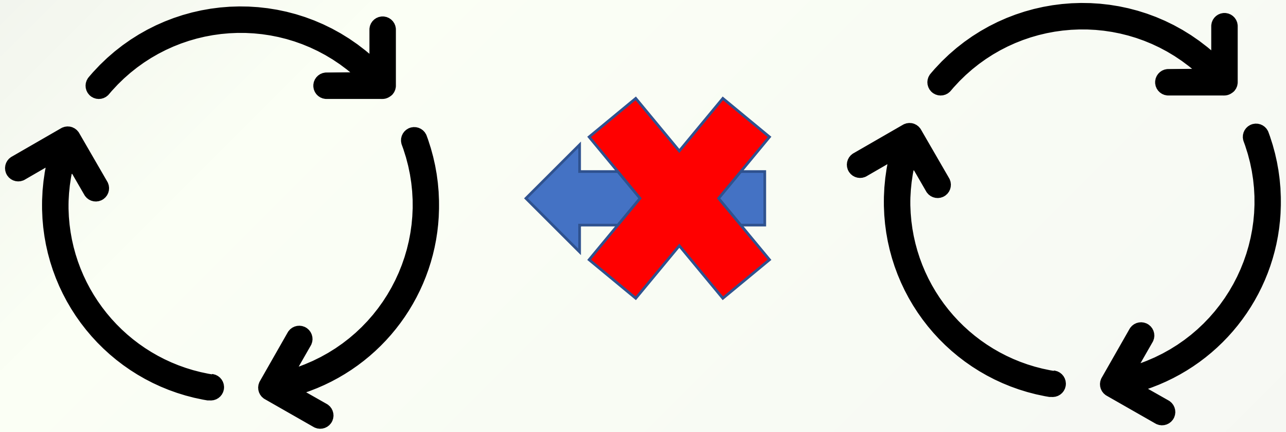
Agenda

- **The big picture – social and biological**
  - The improving but difficult road to regulatory and market rationalization
  - Science innovations and frustrations in plant transformation
- **An example of an innovation “abounding” – the RESET transformation system**
  - Background
  - The basic system
  - Some activities to improve it

Abstract: What can biotech do for trees

- When built upon high quality conventional and molecular breeding programs…..
- Recombinant biotechnologies such as CRISPR and transgenesis have the potential to enhance tree performance in diverse ornamental, forestry, and bioenergy applications
  - Enhanced morphological diversity
  - Accelerated breeding
  - Enhanced propagation and regeneration
  - Customized wood quality
  - Improved disease or stress tolerance

Relationship of breeding and biotech



Breeding populations

Biotech innovations

Polygenic:
Growth rate and adaptation

Oligogenic:
Specific modifications and novel traits

These need to be integrated in a way that does not slow down conventional breeding, with its growing power and urgency in a climate changed world

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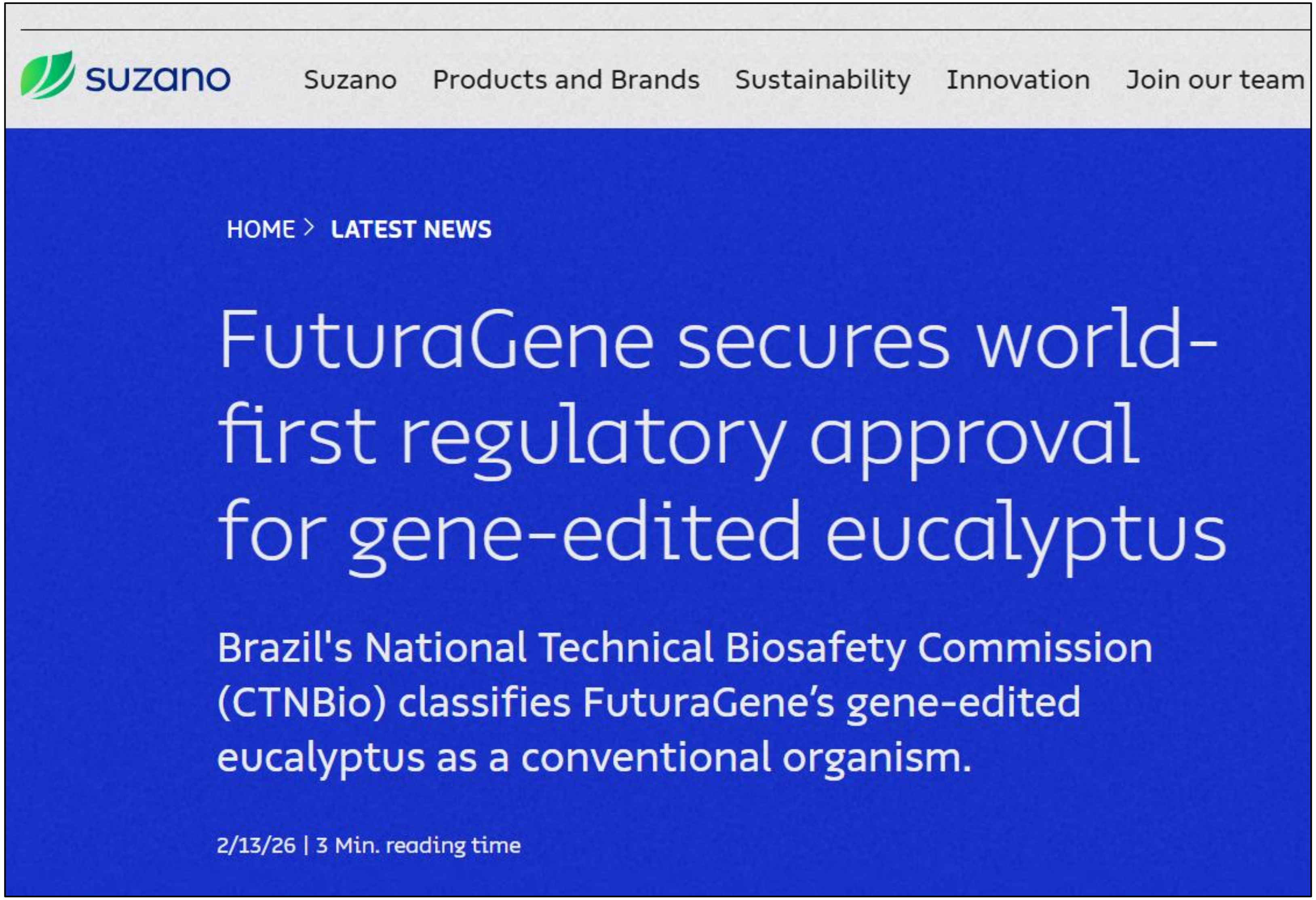
Suzano/Futuragene the exception for forestry

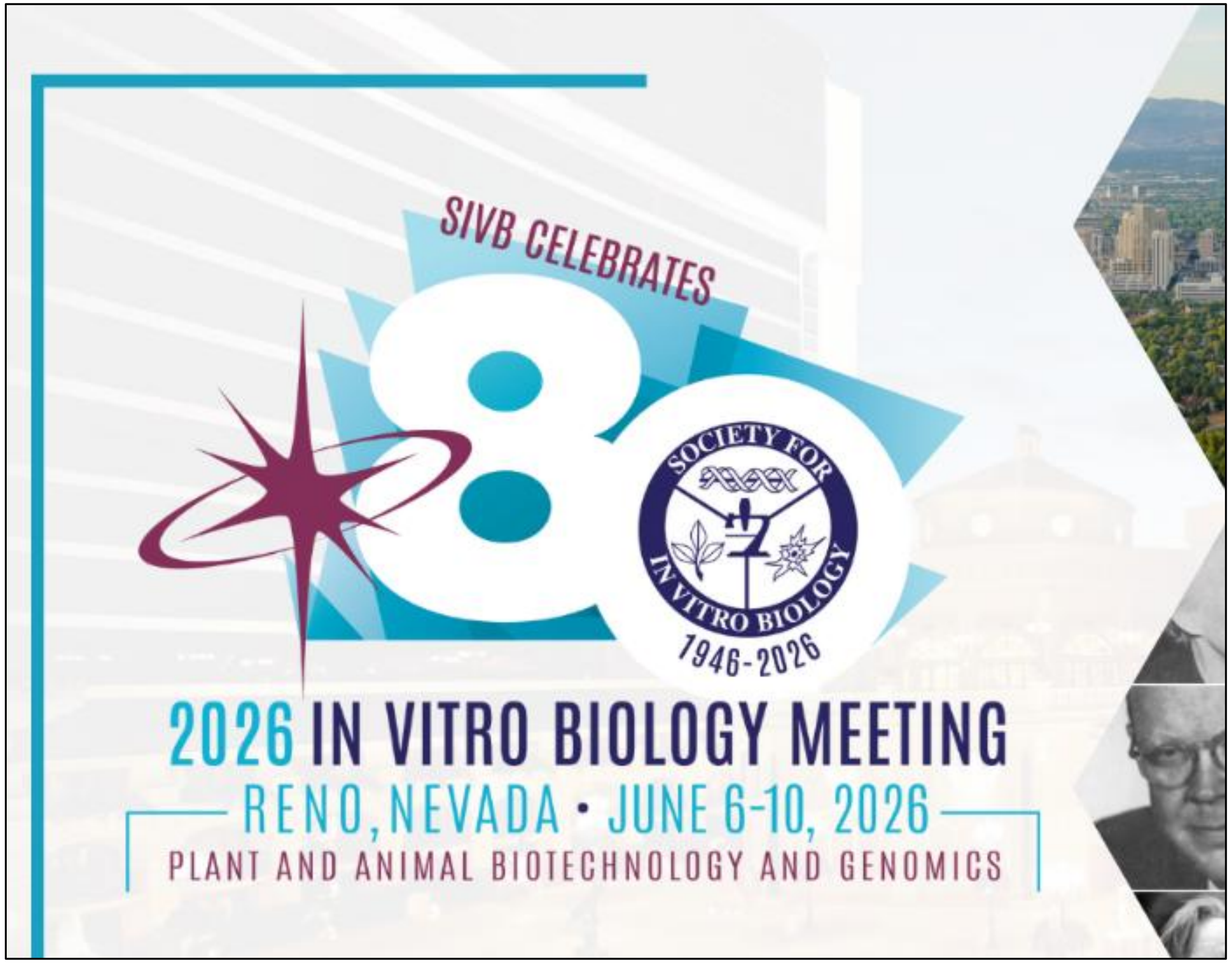


FutuRaGene secures world-first regulatory approval for gene-edited eucalyptus

Brazil's National Technical Biosafety Commission (CTNBio) classifies FuturaGene's gene-edited eucalyptus as a conventional organism.

2/13/26 | 3 Min. reading time

SIVB showcased extraordinary progress and innovation, including for horticulture, mostly enabled by relaxation of gene editing regulations



SIVB CELEBRATES 80

SOCIETY FOR IN VITRO BIOLOGY

1946-2026

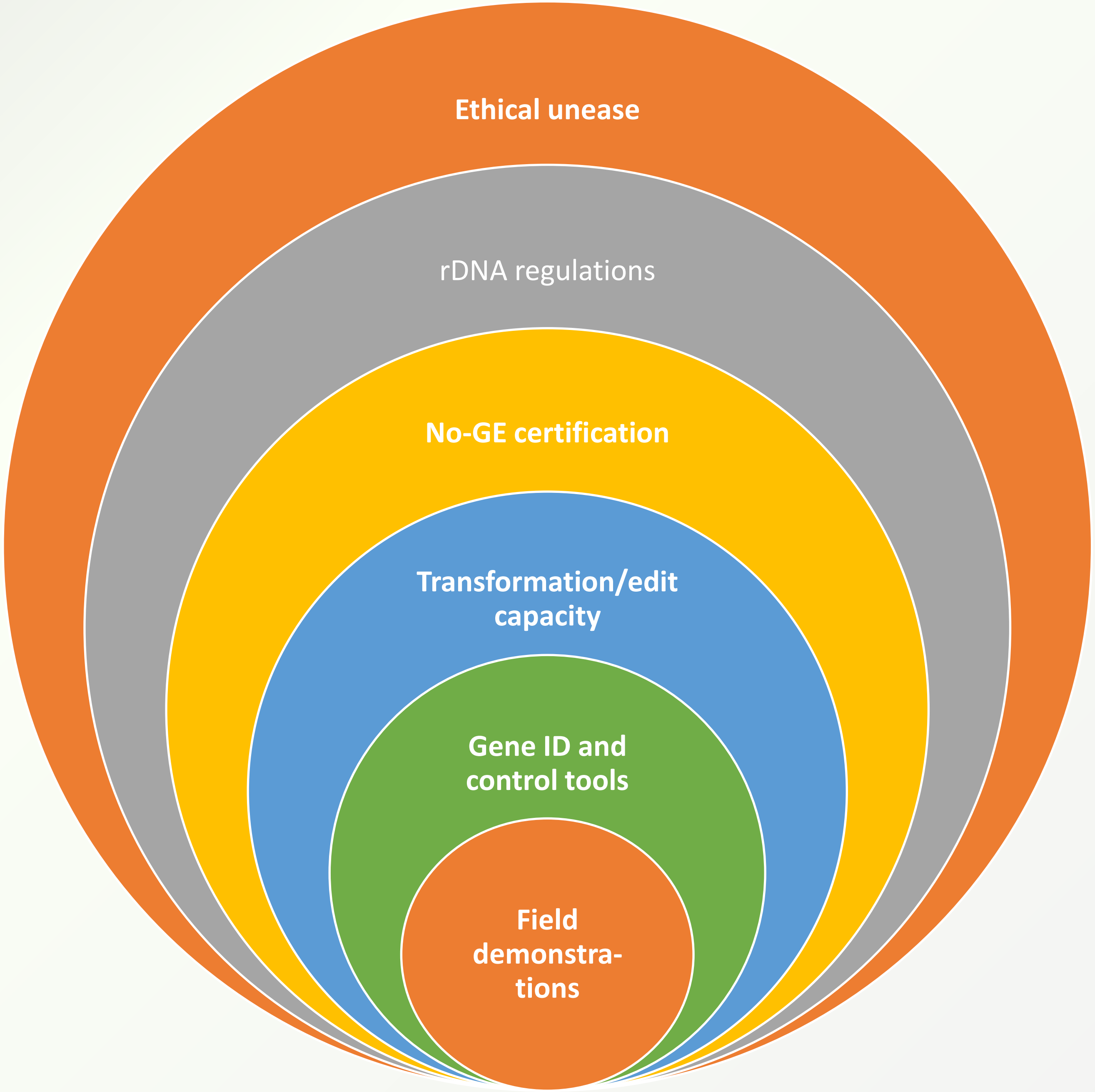
2026 IN VITRO BIOLOGY MEETING

RENO, NEVADA • JUNE 6-10, 2026

PLANT AND ANIMAL BIOTECHNOLOGY AND GENOMICS

Why is forest biotech under-performing?

It’s a nexus of problems constraining progress



Ethical unease

rDNA regulations

No-GE certification

Transformation/edit capacity

Gene ID and control tools

Field demonstrations

Nexus of problems, explained

- **Ethical unease:** Corporations, patents, transparency, plantation monocultures, GMOitis, gene flow
- **rDNA regulations:** rDNA-based presumption of guilt and impairment of effective research and integration with breeding
- **No-GE certification:** Disinvestment, prevention of significant use in research, breeding, or products on certified lands
- **Transformation/edit capacity**: Inability to effectively address a diversity of species and genotypes in breeding programs in reliable, cost-effective manner
- **Gene ID/control tools:** Target genes, reliable systems for control of gene expression, excision, editing, and stability when in routine use or for synthetic biology innovations
- **Field demonstrations:** Public evidence that biotech modifications add significant value and do not compromise sustainability, or breeding progress & productivity, in field environments

I have been active working on these issues for a while….
International forest biotech scientists, after meeting in Oxford in 1999, speak out about the need for case-by-case approach, and workable regulations to enable field trials (amidst hysteria and ecovandalism!)

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COMMENTARY

GENETICALLY MODIFIED ORGANISMS

Forest biotechnology makes its position known

Steven Strauss, Wout Boerjan, John Cairney, Malcolm Campbell, Jeffrey Dean, David Ellis, Lise Jouanin, and Björn Sundberg

Last July, the world's largest group of scientists studying molecular biology and biotechnology of forest trees met at the University of Oxford, England*. To the surprise of the attendees, the meeting, organized by the International Union of Forestry Research Organizations (IUFRO, Vienna, Austria), was the subject of a protest by an antibiotechnology group called GEFF (Genetic Engineering Free Forests, London, UK). During the meeting, GEFF staged a protest outside the meeting hall (the vener-

the environment was an important rationale for the study. Its ultimate goal was to produce trees that require the use of fewer chemicals in paper and pulp production, and thus creating less environmental pollution.

During the session on the deployment of GM trees, and at the business meeting, IUFRO scientists debated a draft position statement on the benefits and risks of GM crops and plantations. Based on comments from the group, the statement was revised and put to a vote via the Internet. It was ratified by 99% of those who

quences or it can produce substantially modified organisms. The large-scale use of transgenic crops in some countries show that transgenic traits can be highly stable after normal field screening of genotypes during breeding. The credible issues center on which genes can be effectively used to modify which traits for which environments.

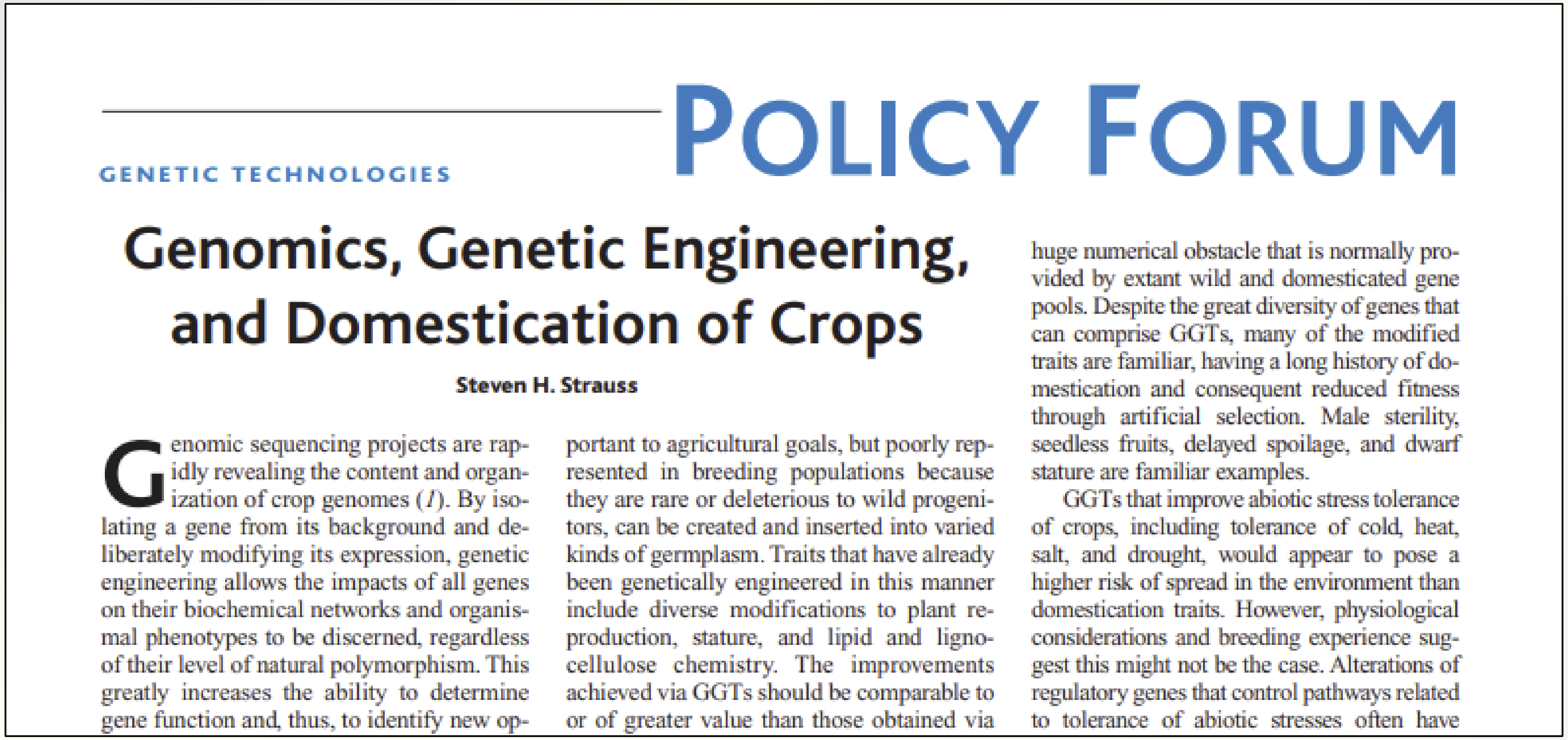
While transgenic traits pose some risks for plantations and associated ecosystems, many options exist to mitigate their impacts. Priority

Ecovandals destroy the only GE tree field trial in the UK to “honor” IUFRO conference attendees

FRANKENSTEIN’S FOREST

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.

My early attempt to help guide the creation of a trait- vs. method-based system



GENETIC TECHNOLOGIES

POLICY FORUM

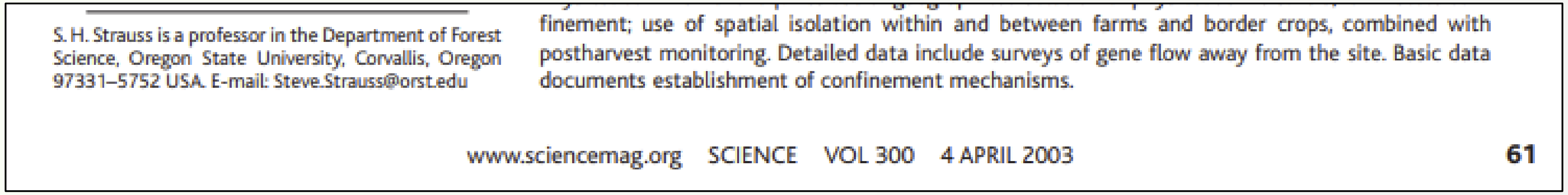
Genomics, Genetic Engineering, and Domestication of Crops

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 op- portant to agricultural goals, but poorly represented in breeding populations because they are rare or deleterious to wild progenitors, can be created and inserted into varied kinds of germplasm. Traits that have already been genetically engineered in this manner include diverse modifications to plant reproduction, stature, and lipid and lignocellulose chemistry. The improvements achieved via GGTs should be comparable to or of greater value than those obtained via

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 of crops, including tolerance of cold, heat, salt, and drought, would appear to pose a higher risk of spread in the environment than domestication traits. However, physiological considerations and breeding experience suggest this might not be the case. Alterations of regulatory genes that control pathways related to tolerance of abiotic stresses often have



S. H. Strauss is a professor in the Department of Forest Science, Oregon State University, Corvallis, Oregon 97331–5752 USA. E-mail: Steve.Strauss@orst.edu

finement; use of spatial isolation within and between farms and border crops, combined with postharvest monitoring. Detailed data include surveys of gene flow away from the site. Basic data documents establishment of confinement mechanisms.

An attempt to address regulation and no-GMO forest certification 12 years later based on climate/forest health threats

Traces of the emerald ash borer on the trunk of a dead ash tree in Michigan, USA. This non-native invasive insect from Asia threatens to kill most North American ash trees.

BIOTECHNOLOGY

Genetically engineered trees: Paralysis from good intentions

Forest crises demand regulation and certification reform

By **Steven H. Strauss**[1*], **Adam Costanza**[2], **Armand Séguin**[3]

Intensive genetic modification is a longstanding practice in agriculture, and, for some species, in woody plant horticulture and forestry (*1*). Current regulatory systems for genetically engineered

recently initiated an update of the Coordinated Framework for the Regulation of Biotechnology (*2*), now is an opportune time to consider foundational changes.

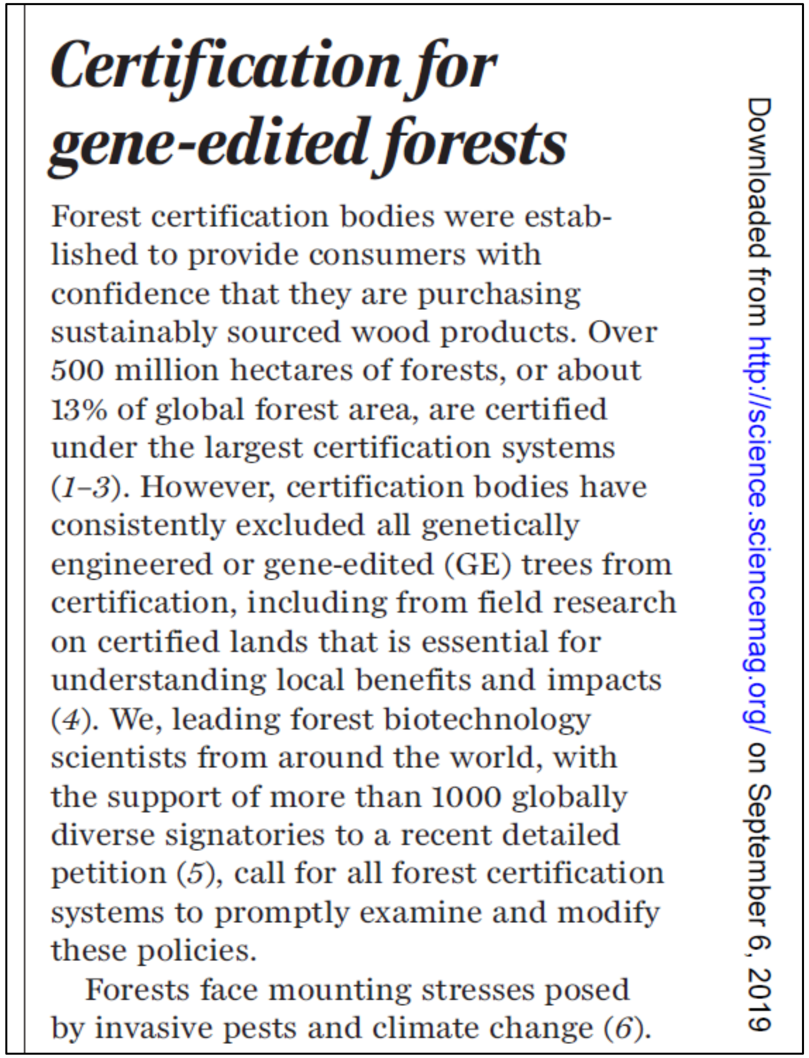
Difficulties of conventional tree breeding make genetic engineering (GE) methods relatively more advantageous for forest trees than for annual crops (*3*). Obstacles

Although only a few forest tree species might be subject to GE in the foreseeable future, regulatory and market obstacles prevent most of these from even being subjects of translational laboratory research. There is also little commercial activity: Only two types of pest-resistant poplars are authorized for commercial use in small areas in China and two types of eucalypts, one approved in Brazil and another under lengthy review in the USA (*5*).

METHOD-FOCUSED AND MISGUIDED. Many high-level science reports state that the GE method is no more risky than conventional breeding, but regulations around the world essentially presume that GE is hazardous and requires strict containment

Downloaded from www.sciencemag.org on August 21, 2015

Letter published in Science about certification obstacle to GE trees (September 2019)



Certification for gene-edited forests

Forest certification bodies were established to provide consumers with confidence that they are purchasing sustainably sourced wood products. Over 500 million hectares of forests, or about 13% of global forest area, are certified under the largest certification systems (*1–3*). However, certification bodies have consistently excluded all genetically engineered or gene-edited (GE) trees from certification, including from field research on certified lands that is essential for understanding local benefits and impacts (*4*). We, leading forest biotechnology scientists from around the world, with the support of more than 1000 globally diverse signatories to a recent detailed petition (*5*), call for all forest certification systems to promptly examine and modify these policies.

Forests face mounting stresses posed by invasive pests and climate change (*6*).

Downloaded from http://science.sciencemag.org/ on September 6, 2019

Engineering, and Medicine recently completed an in-depth study on forest health and biotechnology, concluding that the potential benefits are numerous and rapidly increasing (*12*). Our forests are in dire need of assistance, and GE trees hold tremendous potential as a safe and powerful tool for promoting forest resilience and sustainability.

Steven H. Strauss[1]*, Wout Boerjan[2], Vincent Chiang[3], Adam Costanza[4], Heather Coleman[5], John M. Davis[6], Meng-Zhu Lu[7], Shawn D. Mansfield[8], Scott Merkle[9], Alexander Myburg[10], Ove Nilsson[11], Gilles Pilate[12], William Powell[13], Armand Seguin[14], Sofia Valenzuela[15]

[1]Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331, USA. [2]Department of Plant Biotechnology and Bioinformatics, Ghent University and Center for Plant Systems Biology, VIB, 9052 Ghent, Belgium. [3]Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC 27695, USA. [4]Chapel Hill, NC 27517, USA. [5]Department of Biology, Syracuse University, Syracuse, NY 13244, USA. [6]School of Forest Resources and Conservation, University of Florida, Gainesville, FL 32611, USA. [7]State Key Laboratory of Subtropical Silviculture, School of Forestry and Biotechnology, Zhejiang A&F University, Hangzhou 311300, China. [8]Forest Sciences Centre, University

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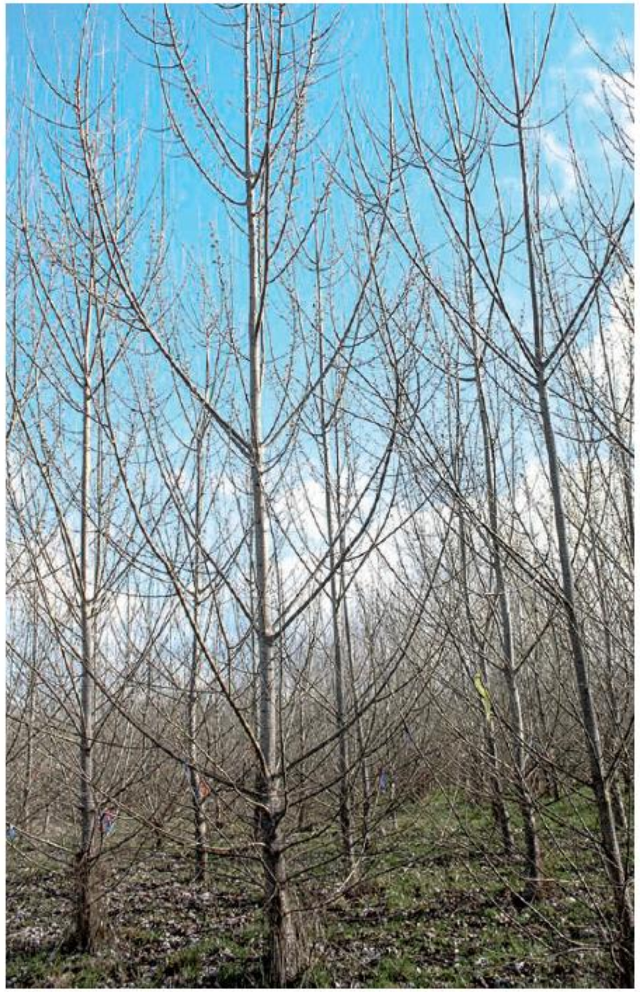
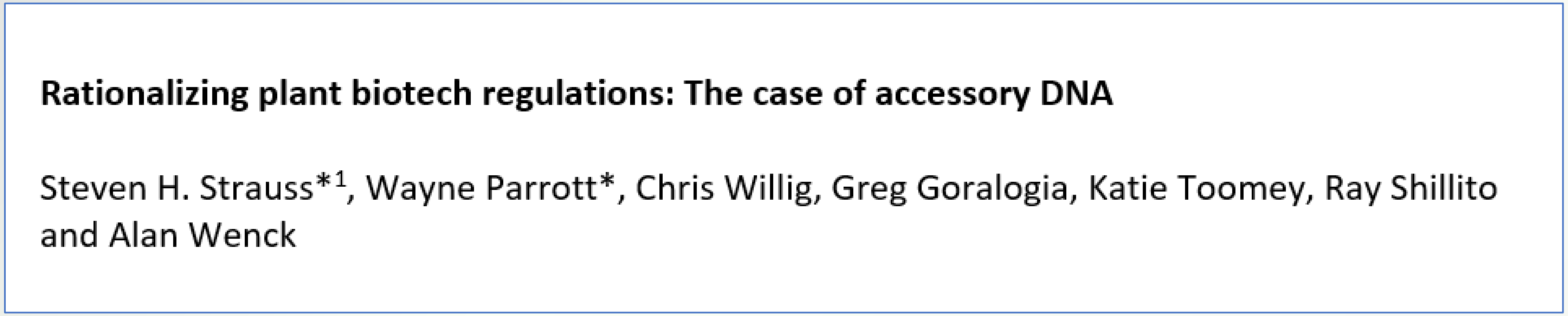


Gene-edited and genetically engineered trees, such as these poplars, should be allowed in certified forests.

Still trying…..

A proposal to ease gene editing regulation where non-expressed GMO DNA remains -- a worldwide problem with many flavors (EU, trade, diverse and funky US rules) – manuscript being finalized



Rationalizing plant biotech regulations: The case of accessory DNA

Steven H. Strauss*[1], Wayne Parrott*, Chris Willig, Greg Goralogia, Katie Toomey, Ray Shillito and Alan Wenck

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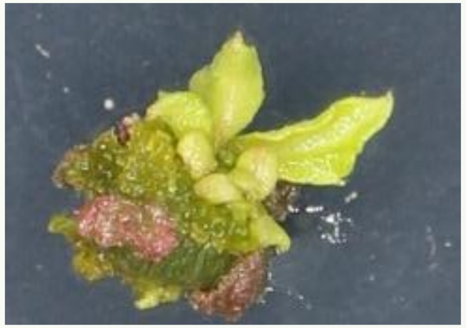
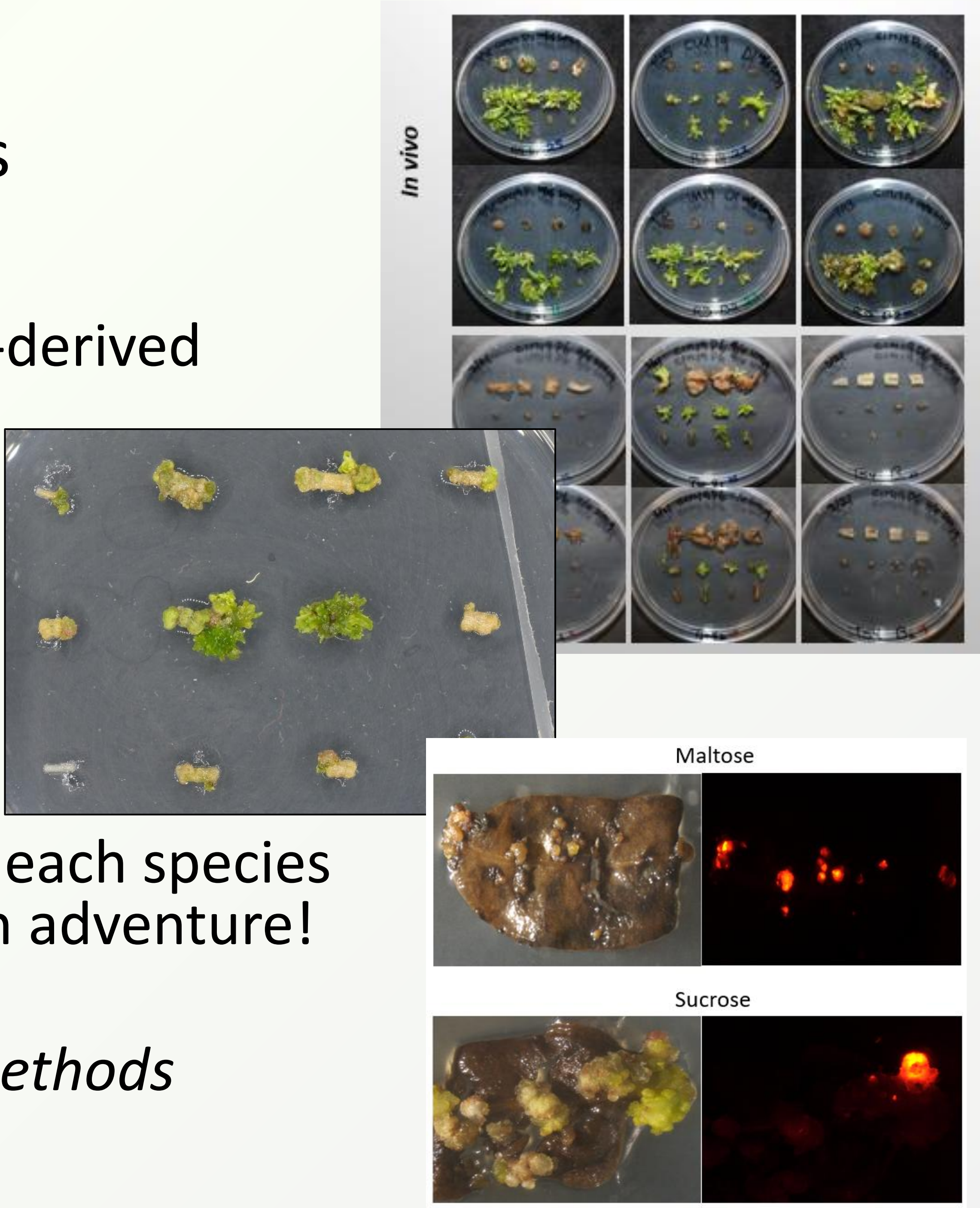
Regeneration & transformation continue to be major limiting factors for gene editing & engineering in plants



- Species and genotypic differences often dramatic
- Minor and woody crop species perhaps most problematic
  - Tough biology, research investment limited
- Slow, costly, complex customization efforts usually needed
- On top of often large social/regulatory constraints,
  often a “deal breaker”

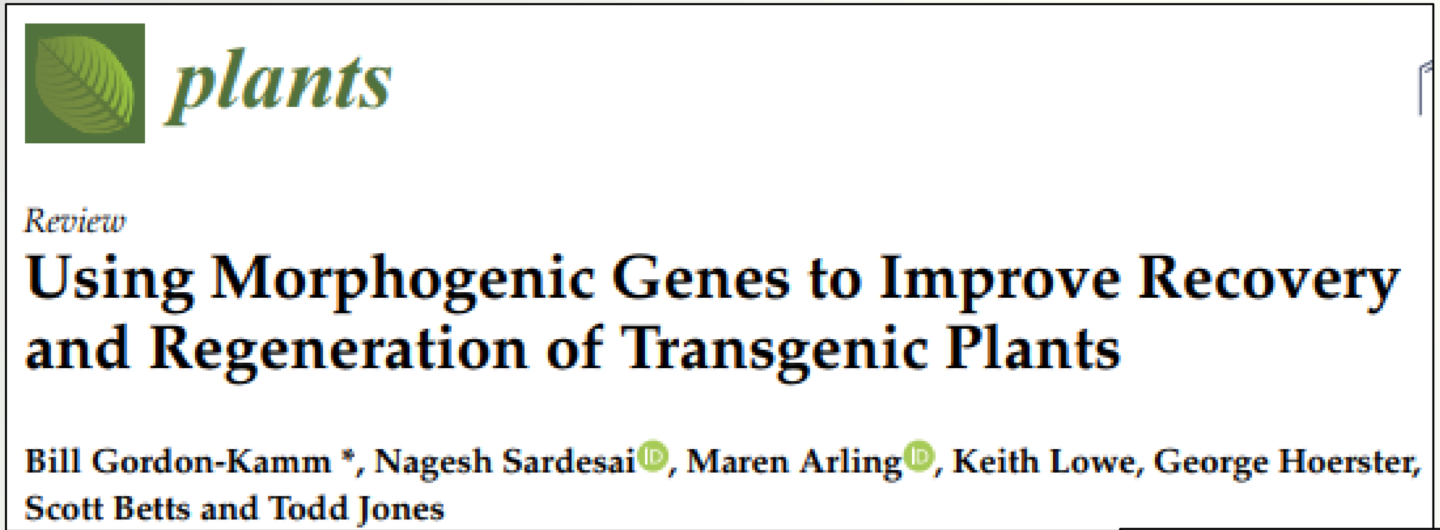
Woody experimental system challenges

- Elite clones, mature propagules, not seed-derived
- High physiological diversity
  - Growth environment, age, explant type and source
- Great tissue sample heterogeneity in response
- Common necrotic responses
- Very high genetic diversity of forest trees, each species and genotype a new regen-transformation adventure!
- Large interactions among all of the above and more – *leading to low generality of methods and low reproducibility*



Science to the rescue!

Molecular biology is now giving us lots of tools to help in regen-transformation technology: MORPHOGENIC REGULATOR (MR) GENES

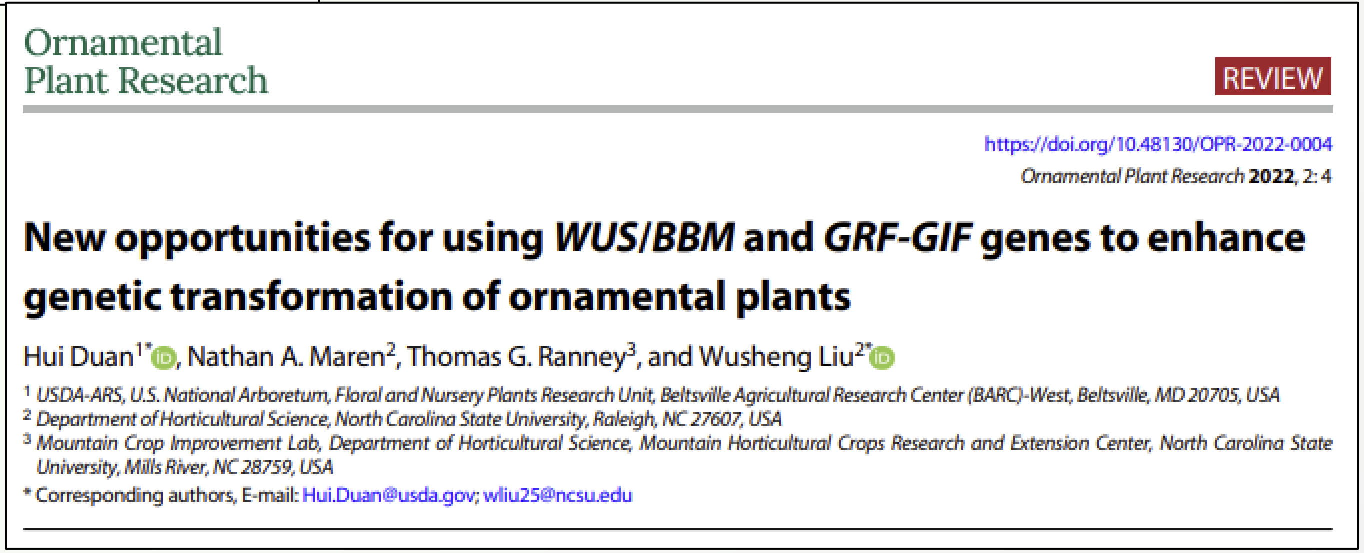


plants

Review

Using Morphogenic Genes to Improve Recovery and Regeneration of Transgenic Plants

Bill Gordon-Kamm *, Nagesh Sardesai, Maren Arling, Keith Lowe, George Hoerster, Scott Betts and Todd Jones



Ornamental
Plant Research

REVIEW

https://doi.org/10.48130/OPR-2022-0004
Ornamental Plant Research **2022**, 2: 4

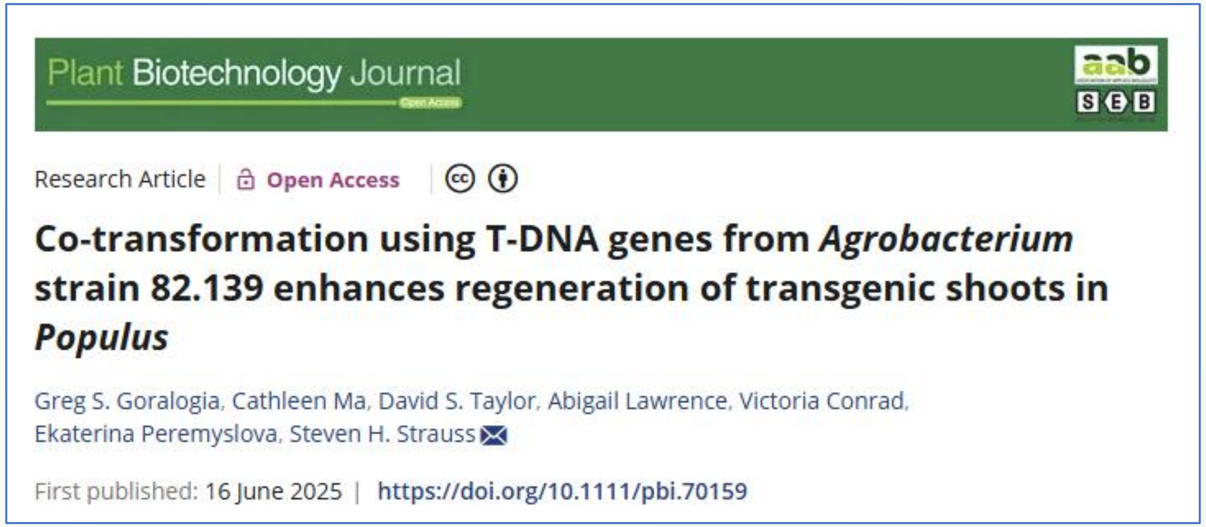
New opportunities for using *WUS/BBM* and *GRF-GIF* genes to enhance genetic transformation of ornamental plants

Hui Duan[1*], Nathan A. Maren[2], Thomas G. Ranney[3], and Wusheng Liu[2*]

[1] *USDA-ARS, U.S. National Arboretum, Floral and Nursery Plants Research Unit, Beltsville Agricultural Research Center (BARC)-West, Beltsville, MD 20705, USA*
[2] *Department of Horticultural Science, North Carolina State University, Raleigh, NC 27607, USA*
[3] *Mountain Crop Improvement Lab, Department of Horticultural Science, Mountain Horticultural Crops Research and Extension Center, North Carolina State University, Mills River, NC 28759, USA*
* Corresponding authors, E-mail: Hui.Duan@usda.gov; wliu25@ncsu.edu

We have tested many types of MR genes in poplars or eucalypts – many both *in vitro* and *in planta*

- LEC 1, 2 – LEAFY COTYLEDON
- EBB1 - EARLY BUD BREAK 1 (ESR family)
- BBM – BABY BOOM
- WOX 5, 11 -- WUSCHEL RELATED HOMEOBOX
- WUS – WUSCHEL
- GRF-GIF – GROWTH REGULATOR FACTOR 4 and GRF INTERACTING FACTOR 1
- **But mostly disappointing, still genotype-specific responses!**



Plant Biotechnology Journal

Research Article | Open Access

Co-transformation using T-DNA genes from *Agrobacterium* strain 82.139 enhances regeneration of transgenic shoots in *Populus*

Greg S. Goralogia, Cathleen Ma, David S. Taylor, Abigail Lawrence, Victoria Conrad, Ekaterina Peremyslova, Steven H. Strauss

First published: 16 June 2025 | https://doi.org/10.1111/pbi.70159

- *Agrobacterium* tumefaciens also inserts MR genes – our recent focus

- **rol – hairy root-inducing genes from *Agrobacterium rhizogenes* – the foundation of the RESET transformation system**

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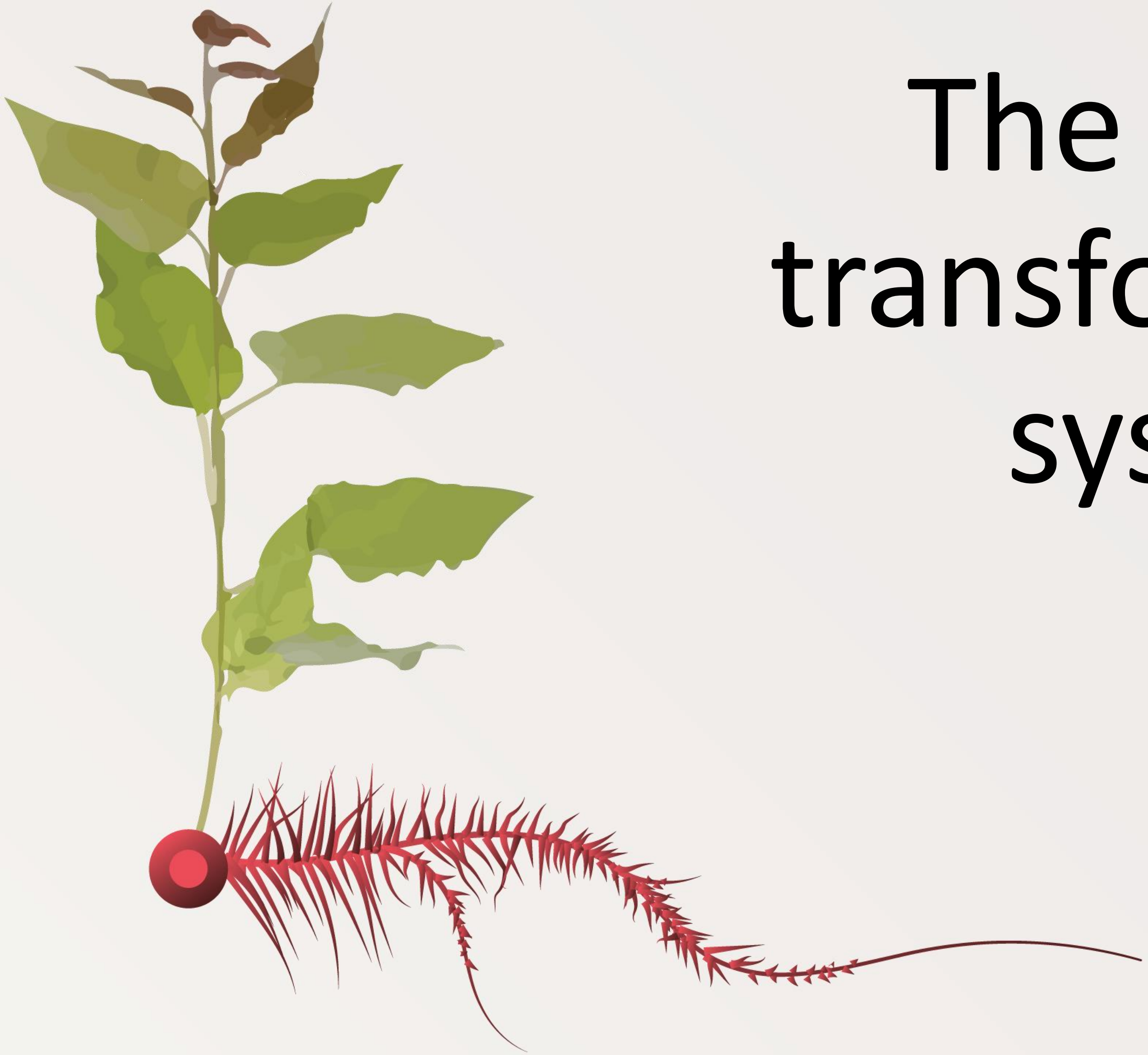


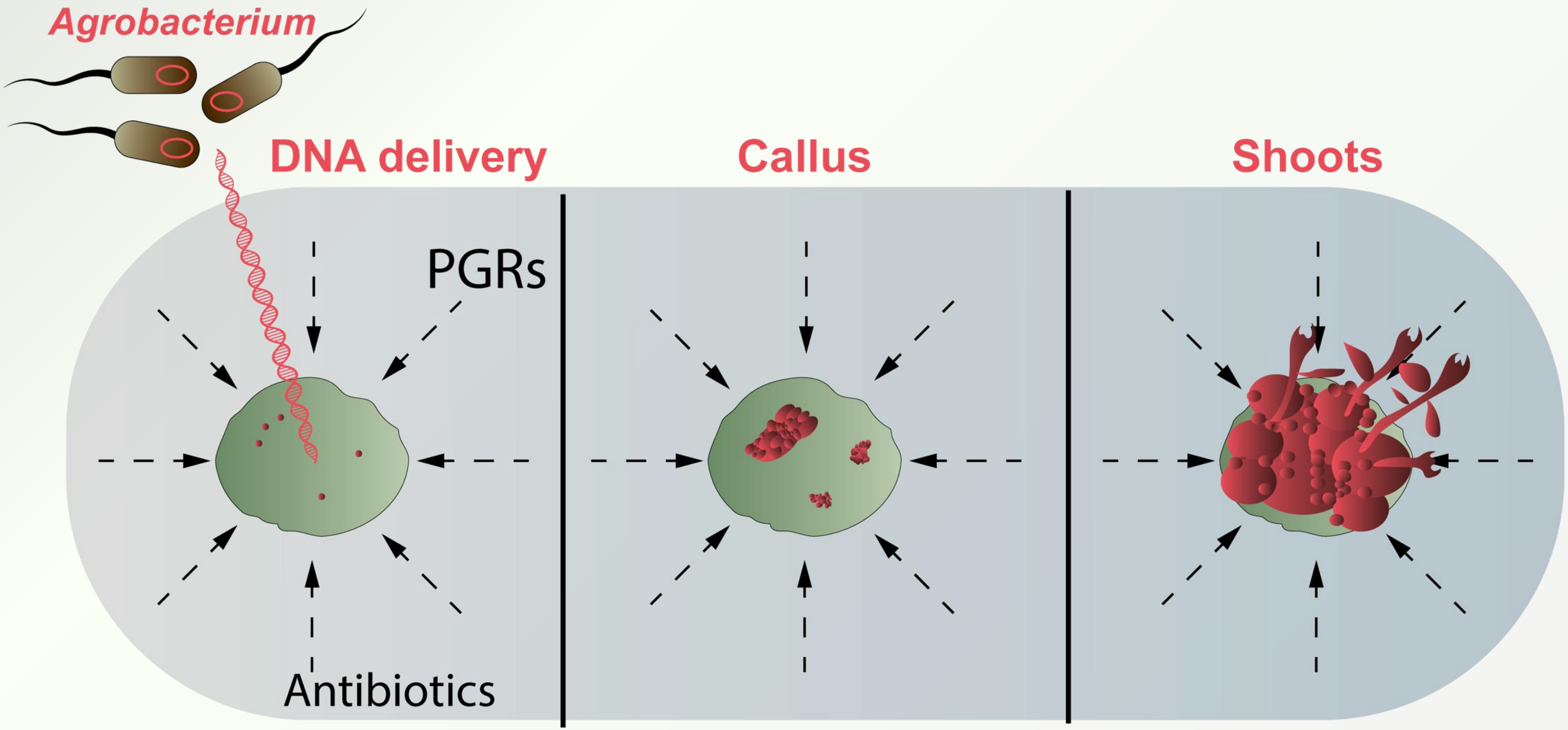
The RESET transformation system

Greg Goralogia, postdoc

RESET elements

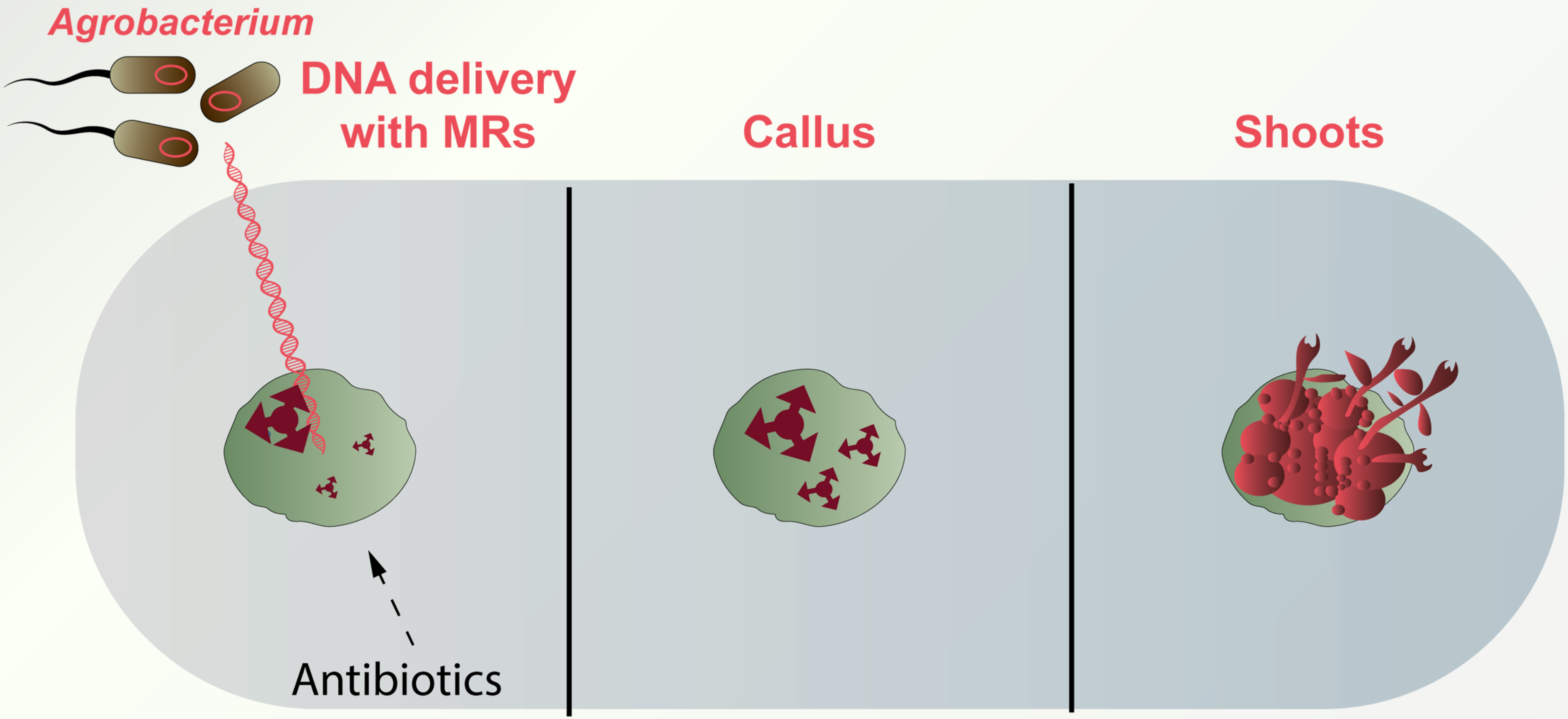
- Transformation background
- The basic RESET system
- Activities to improve it

Conventional transformation methods rely on exogenous phytohormones supplied in the culture medium



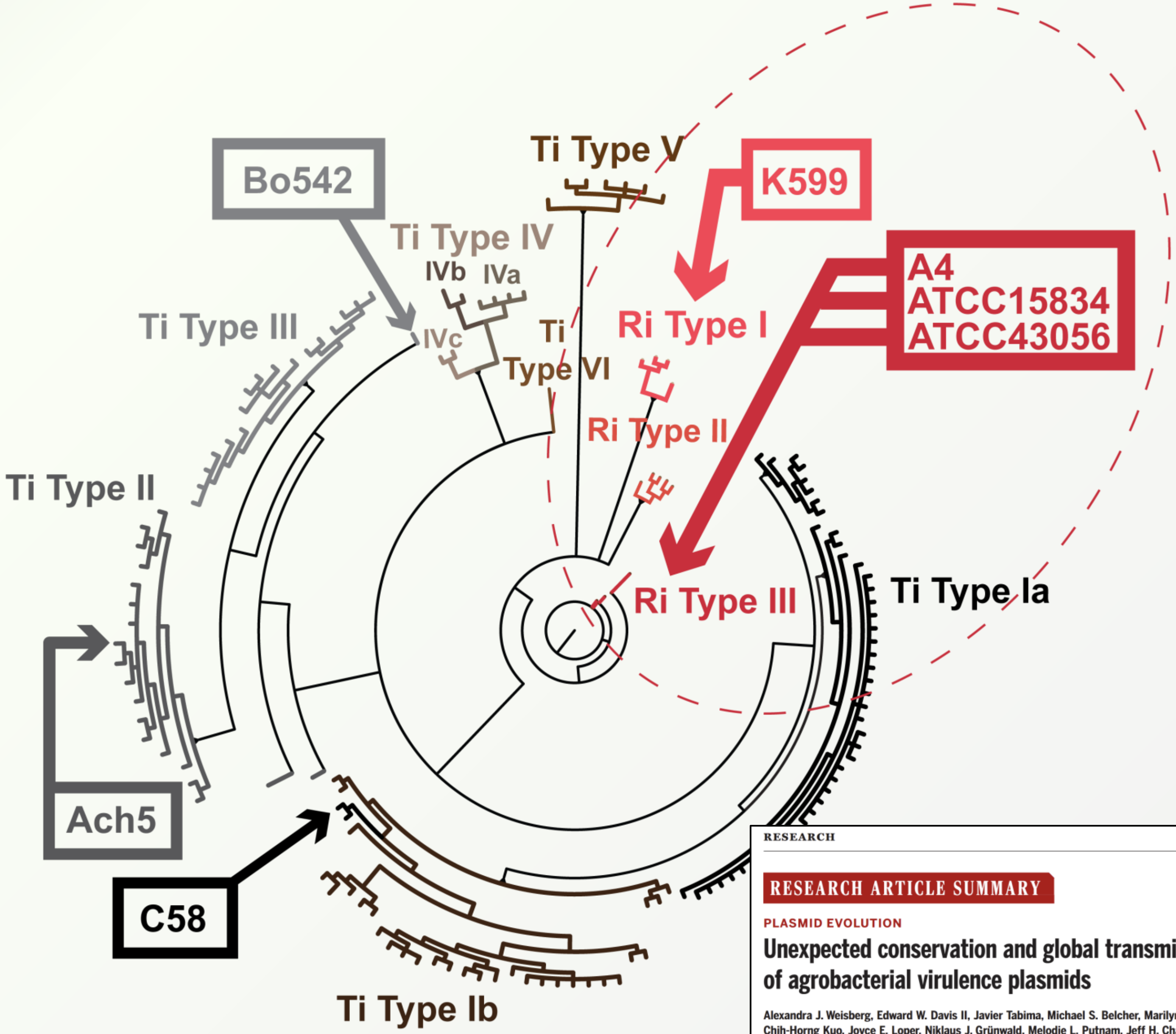
PGRs = Plant growth regulators, hormones

Morphogenic regulators spur developmental reprogramming via delivered DNA – sometimes in the absence of exogenous PGRs



Hairy root disease is caused by unique T-DNA genes contained in Ri plasmids

Hairy roots in hydroponically grown tomato



RESEARCH

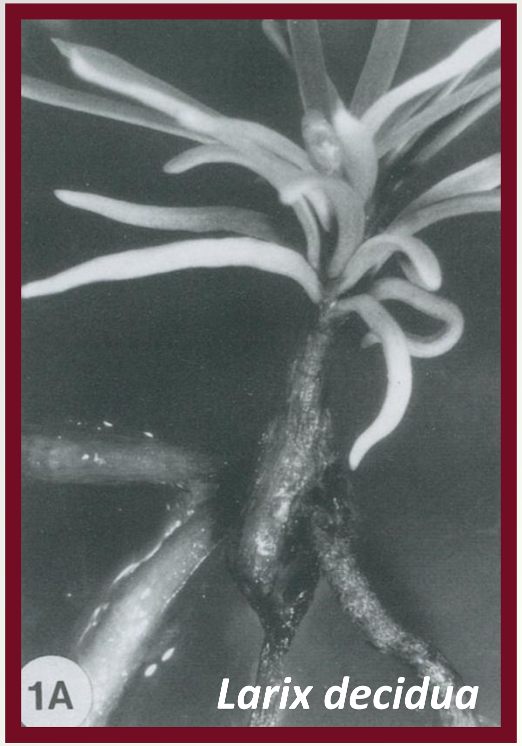
RESEARCH ARTICLE SUMMARY

PLASMID EVOLUTION

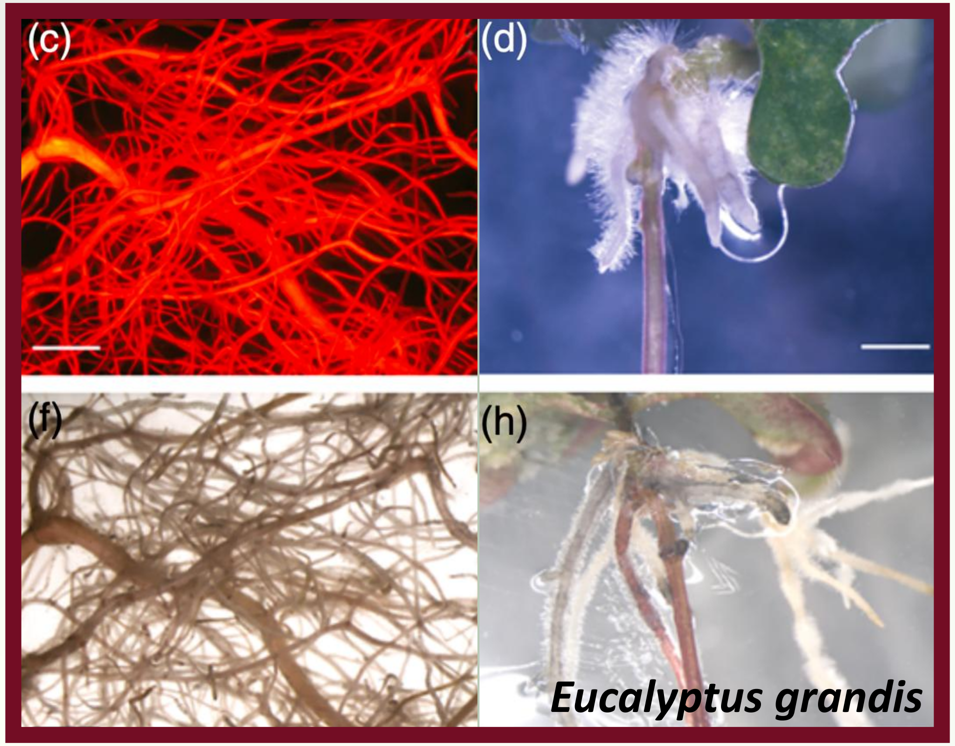
Unexpected conservation and global transmission of agrobacterial virulence plasmids

Alexandra J. Weisberg, Edward W. Davis II, Javier Tabima, Michael S. Belcher, Marilyn Miller, Chih-Horng Kuo, Joyce E. Loper, Niklaus J. Grünwald, Melodie L. Putnam, Jeff H. Chang*

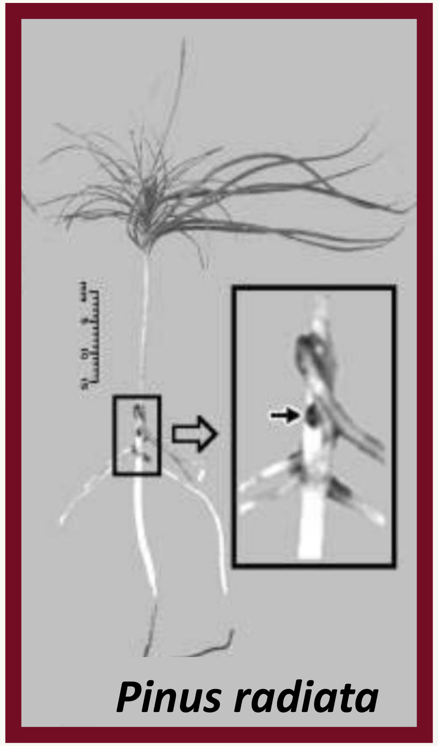
Hairy root *rol* genes are an effective way to generate transgenic tissues across diverse tree species – including conifers



Larix decidua



Eucalyptus grandis



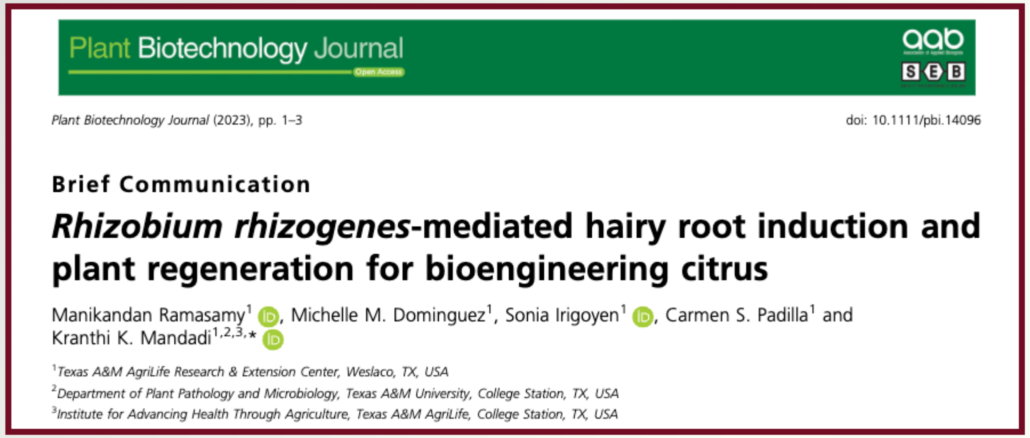
Pinus radiata

Ginkgo biloba

Salix purpea

Huang et al. 1991 *IVCDB-Plant*, Placencia et al. 2016. *Plant Biotech J.*, Li et al. 2003 *EJ Biotech,* Gomes et al. 2019 *FIPS,* Du et al. 2025 *PNAS*.

Hairy root transformation is becoming popular for genotype-independent generation of "mostly" normal looking transgenic plants



Plant Biotechnology Journal

Plant Biotechnology Journal (2023), pp. 1–3

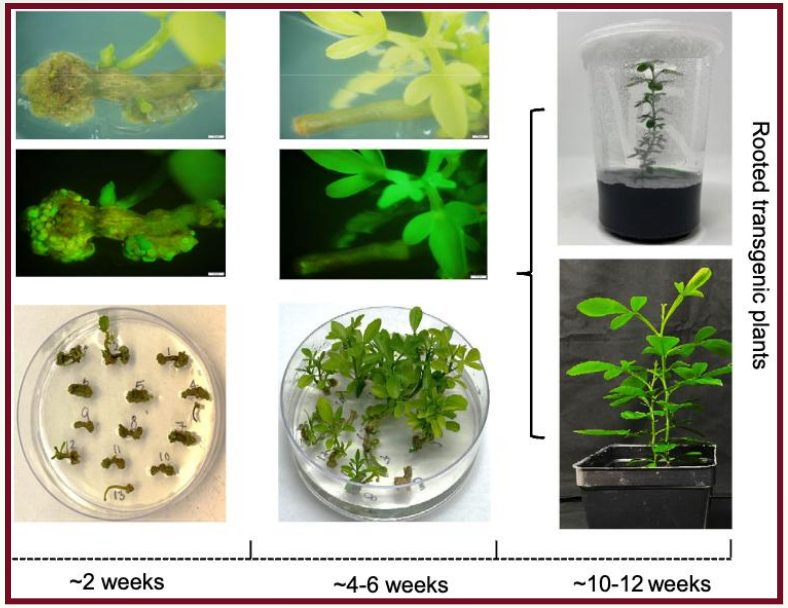
doi: 10.1111/pbi.14096

Brief Communication

***Rhizobium rhizogenes*-mediated hairy root induction and plant regeneration for bioengineering citrus**

Manikandan Ramasamy[1], Michelle M. Dominguez[1], Sonia Irigoyen[1], Carmen S. Padilla[1] and Kranthi K. Mandadi[1,2,3,*]

[1]Texas A&M AgriLife Research & Extension Center, Weslaco, TX, USA
[2]Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX, USA
[3]Institute for Advancing Health Through Agriculture, Texas A&M AgriLife, College Station, TX, USA

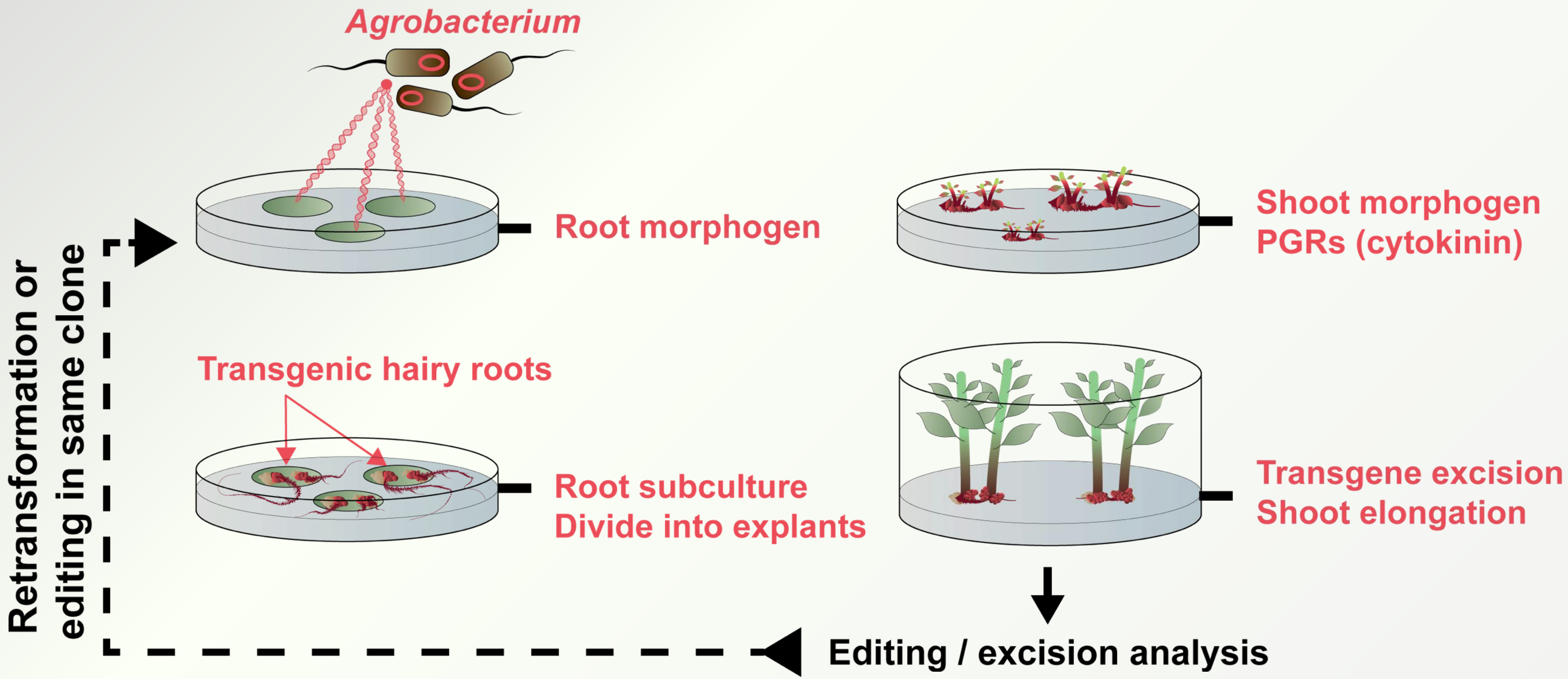


Osteospermum fruticosum (cape daisy)

rol transgenics often show dwarfism and changed floral timing and architecture

Desmet et al. 2021 *Plant Cell Rep.*

A concept for Root Excision System for Efficient Transformation



Root to shoot regeneration, followed by excision, is an elaboration of older ideas

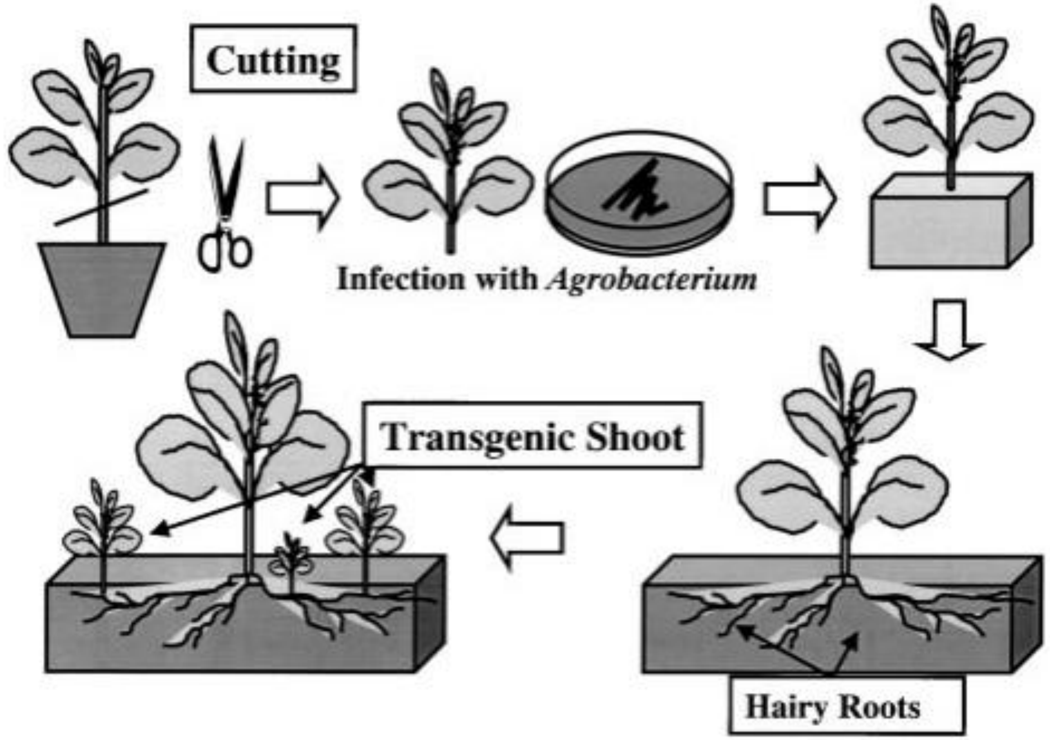
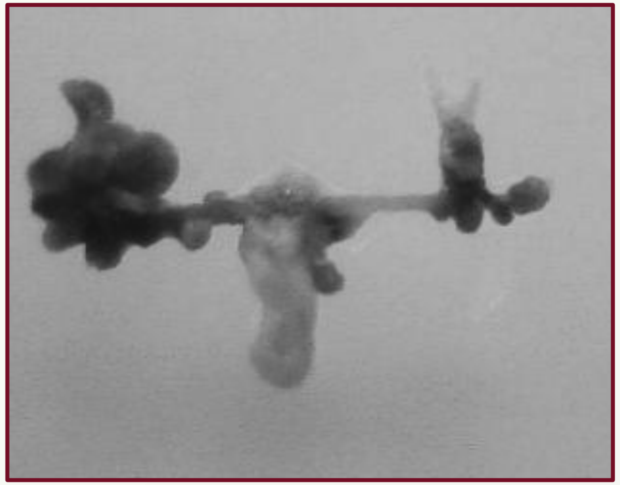
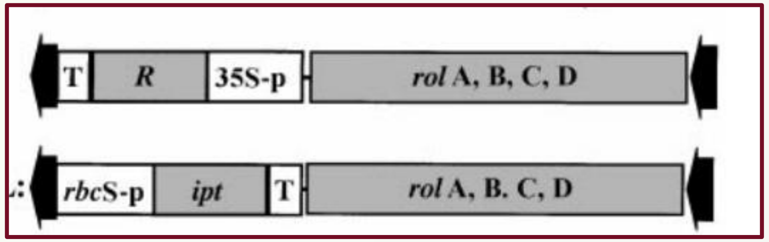


FIG. 8. Outline of *in vivo* transformation using cuttings. Cuttings are infected with *Agrobacterium* containing the *rol*-type MAT vector. After their rooting, marker-free transgenic shoots are induced from hairy roots by the light.



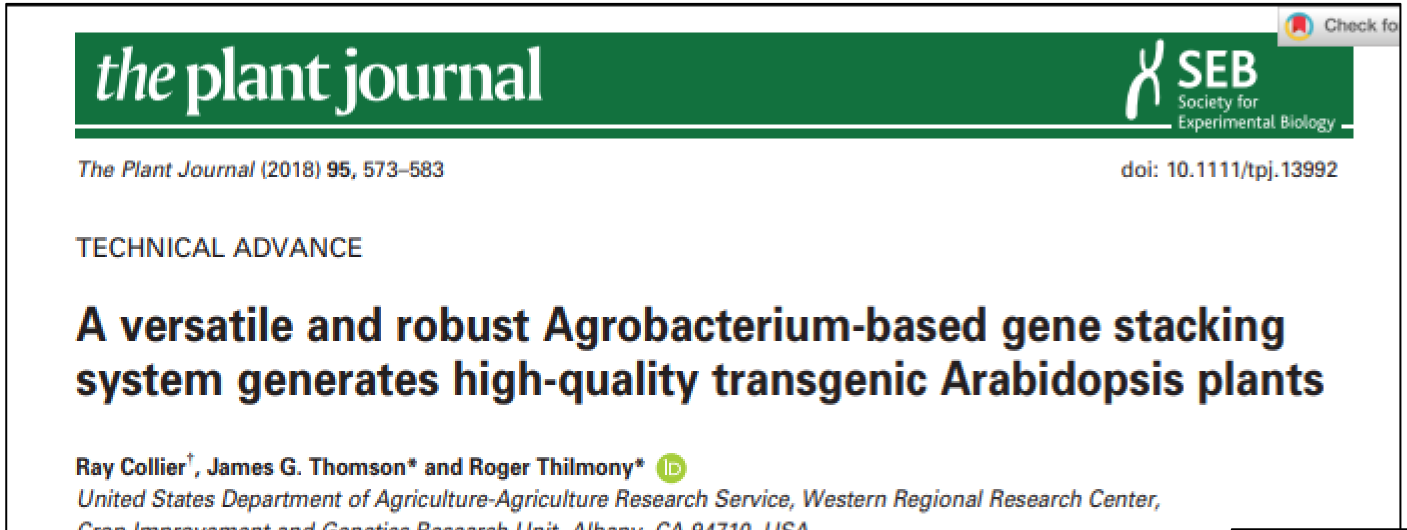


from Ebinuma and Komamine,
2001 In vitro cell and developmental biology -Plant

Hiroyasu Ebinuma
(Shinsu U. em,
Nippon Paper Co.)

GA*A*NTRY system has enabled ambitious T-DNA design

(Gene Assembly in Agrobacterium by Nucleic acid Transfer using Recombinase technology)



the plant journal SEB Society for Experimental Biology

The Plant Journal (2018) **95**, 573–583 doi: 10.1111/tpj.13992

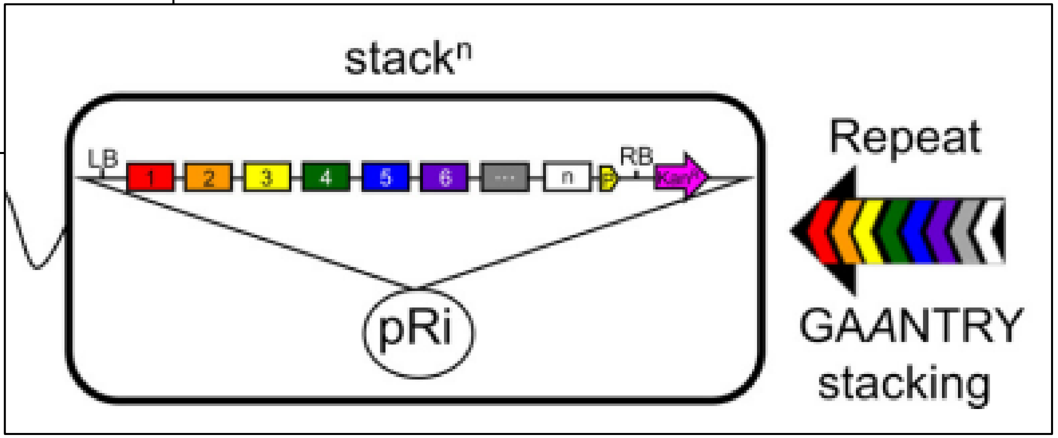
TECHNICAL ADVANCE

A versatile and robust Agrobacterium-based gene stacking system generates high-quality transgenic Arabidopsis plants

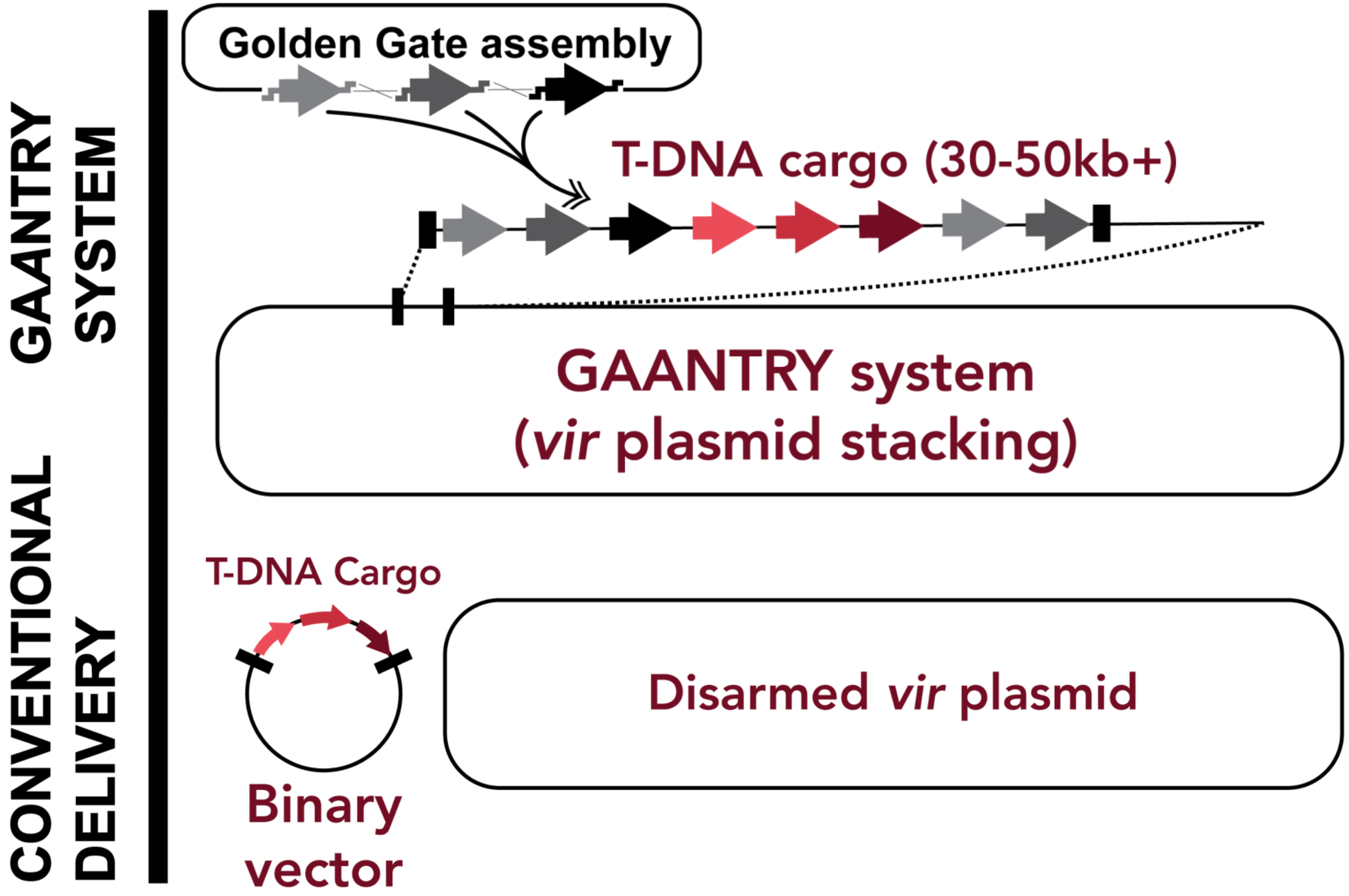
Ray Collier[†], **James G. Thomson*** and **Roger Thilmony***
United States Department of Agriculture-Agriculture Research Service, Western Regional Research Center,
Crop Improvement and Genetics Research Unit, Albany, CA 94710, USA

Received 9 April 2018; revised 15 May 2018; accepted 18 May 2018; published online 14 June 2018.

*For correspondence (e-mails Roger.Thilmony@ars.usda.gov or James.Thomson@ars.usda.gov).
[†]Present address: Wisconsin Crop Innovation Center, University of Wisconsin-Madison, 8520 University Green, Middleton, WI 53562, USA.



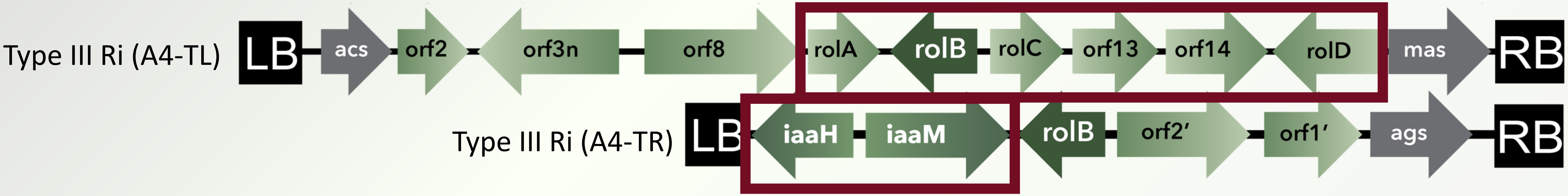
Assembly of our constructs would be next to impossible without GA*A*NTRY



RESET elements

- Background
- **The basic RESET system**
- Activities to improve it

We selected a set of six *rol* genes from strain A4, a Type III Ri plasmid which is known to work in tree species

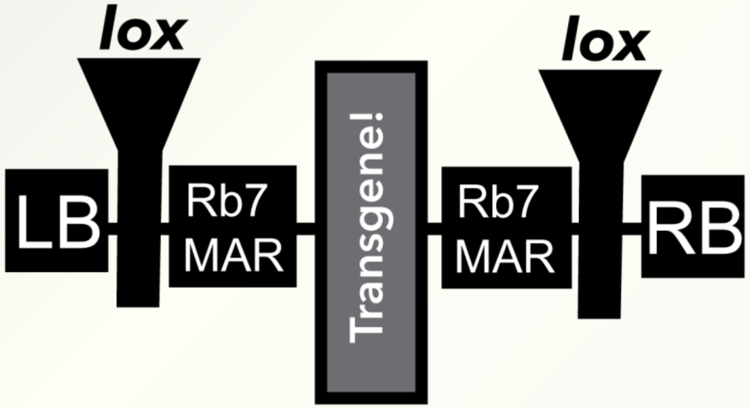


Two Ti plasmids in A4, we used genes from both

rolB is required for hairy root formation -- Others including *rolA,B,C,D, orf13* and *orf14* quantitatively increase hairy root formation in many species

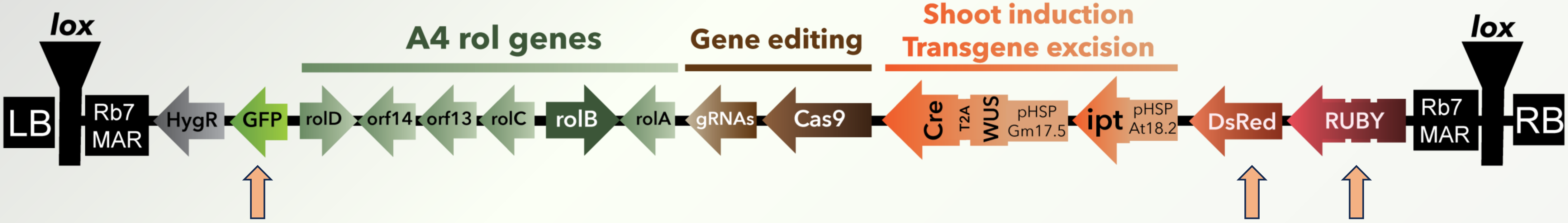
Iaa genes encode genes for auxin biosynthesis

We selected ***WUSCHEL*** and ***ipt*** as shoot morphogens, **Cre-lox** for excision, and chose heat shock for induction of both



- *WUS* shown to induce shoot trans-differentiation from roots in plants
- *ipt*, an *Agrobacterium* T-DNA gene which produces cytokinins and has been known to work in poplar and most plant species for decades
- Heat shock induction is known to be effective but leaky in poplar and many plant species
- Cre recombinase used to induce transgene excision between lox sites, widely used in poplar and other plants
- Rb7 MAR elements known to reduce DNA – methylation dependent transgene silencing in poplar and other plants

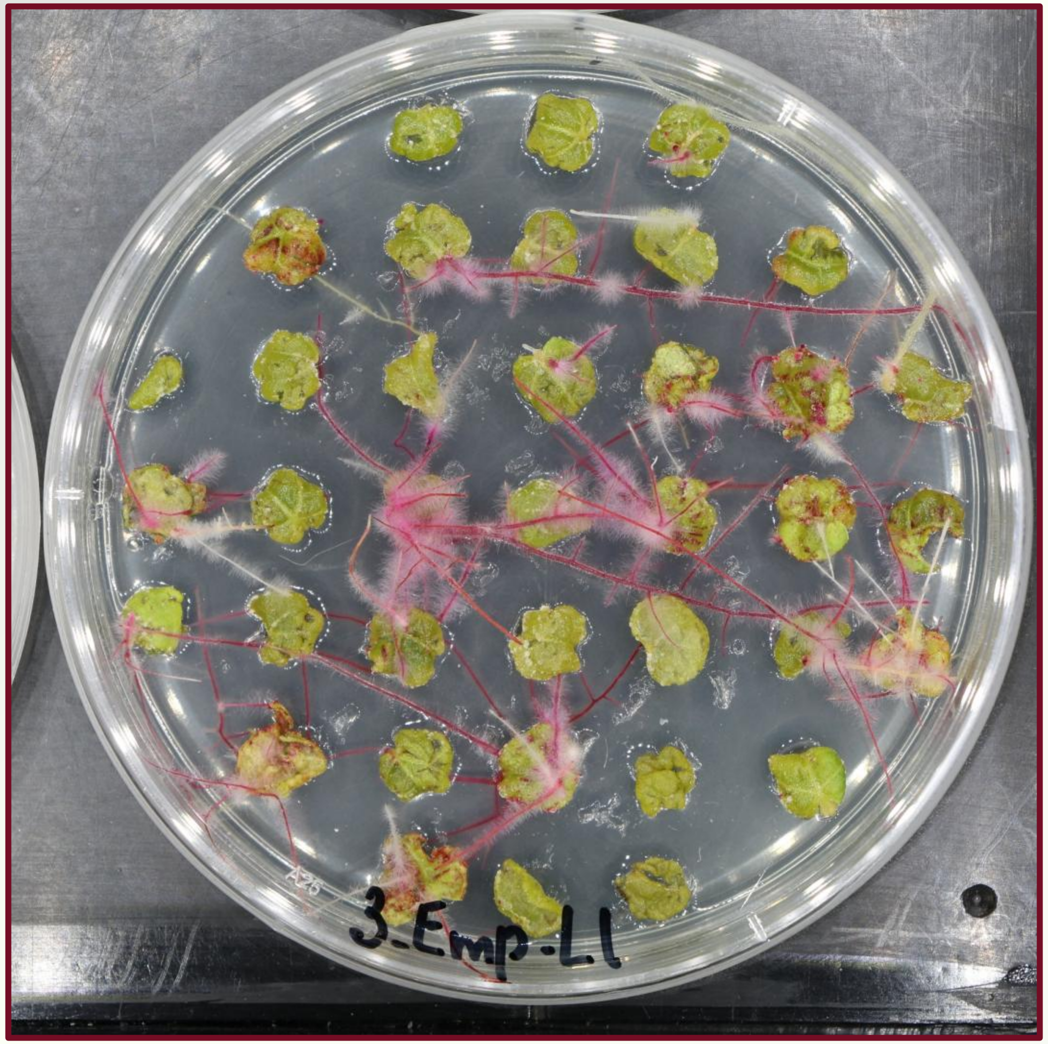
The “kitchen sink” RESET construct

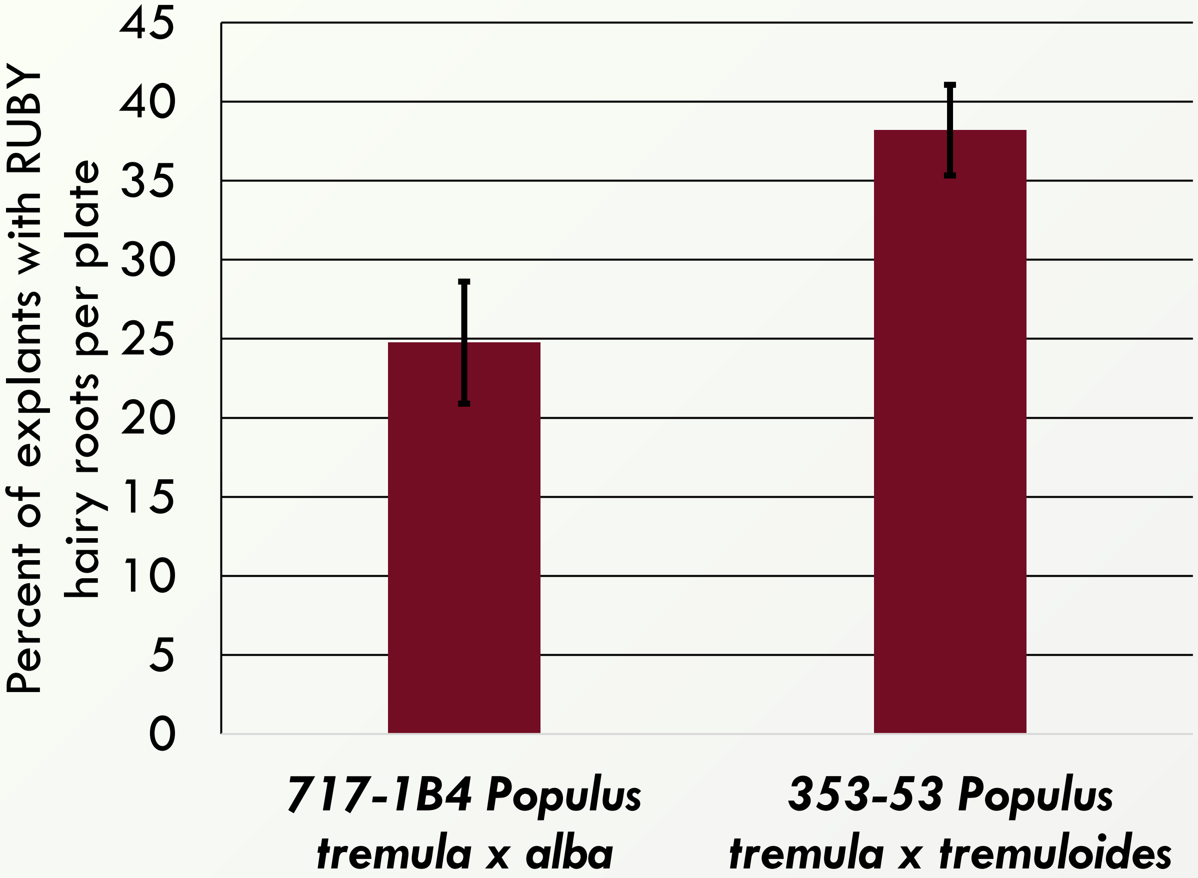


- 39kbp in size in this configuration
- 14 transcriptional units
- 16 independent peptides

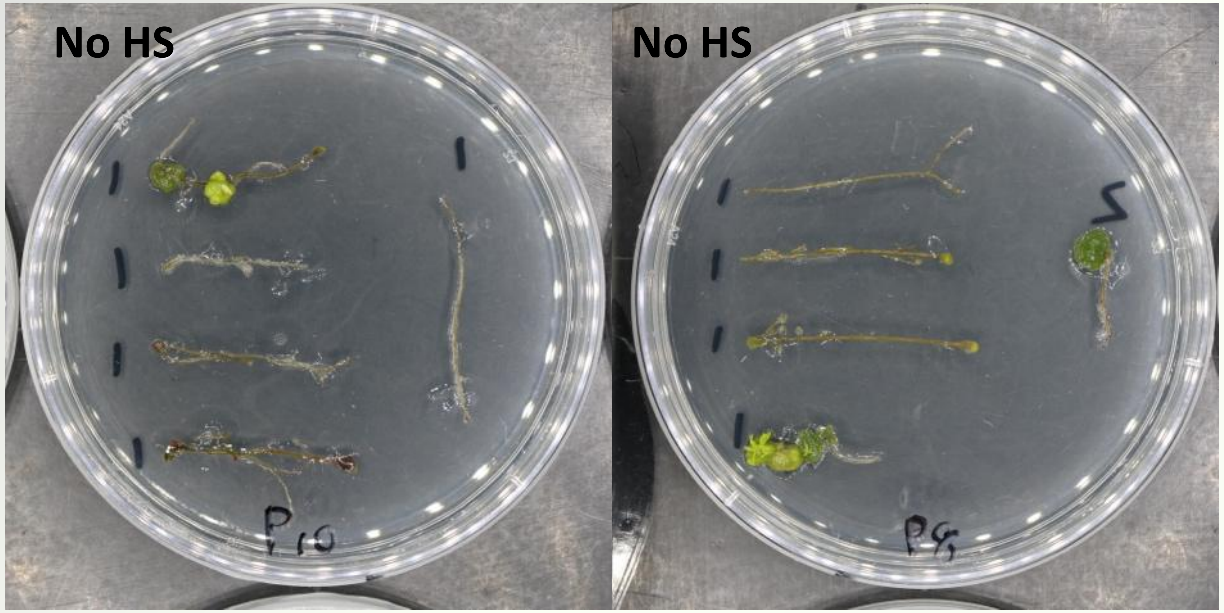
- Included 3 marker genes to identify transgene insertion (GFP, DsRed, and RUBY), excision, and truncations
- Includes gene editing through CRISPR-Cas9
  - tRNA-arrays targeting *RGA1* gene for semi-dwarfism
- Hygromycin selection gene present but no selection was used in these experiments

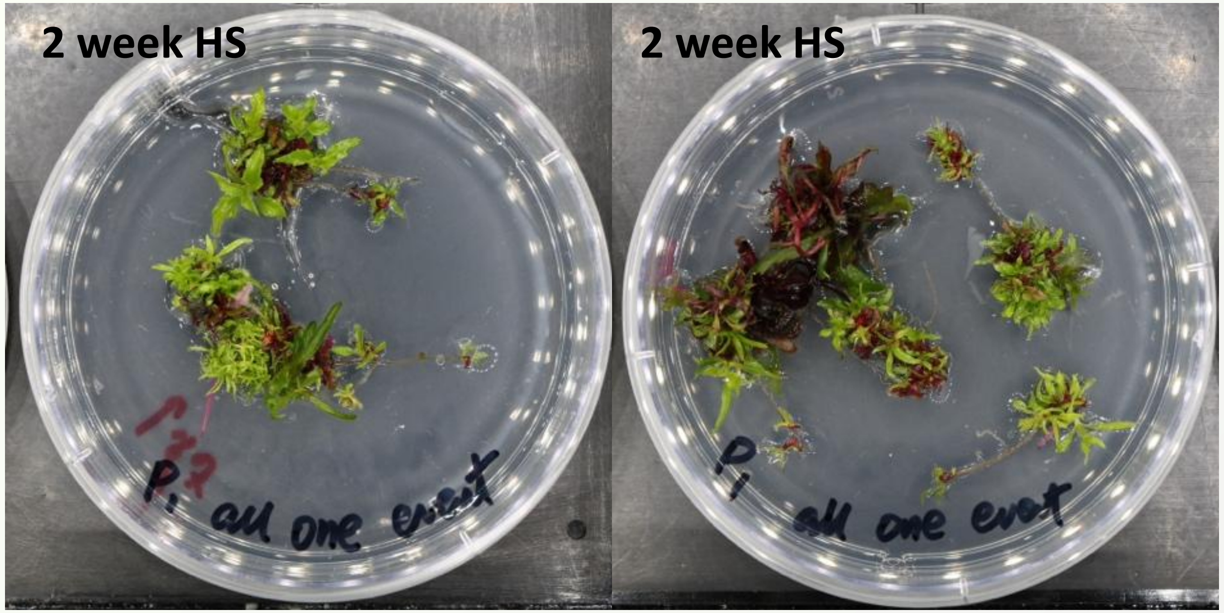
Testing the system: We efficiently generated transgenic hairy roots in two poplar genotypes for regeneration analysis





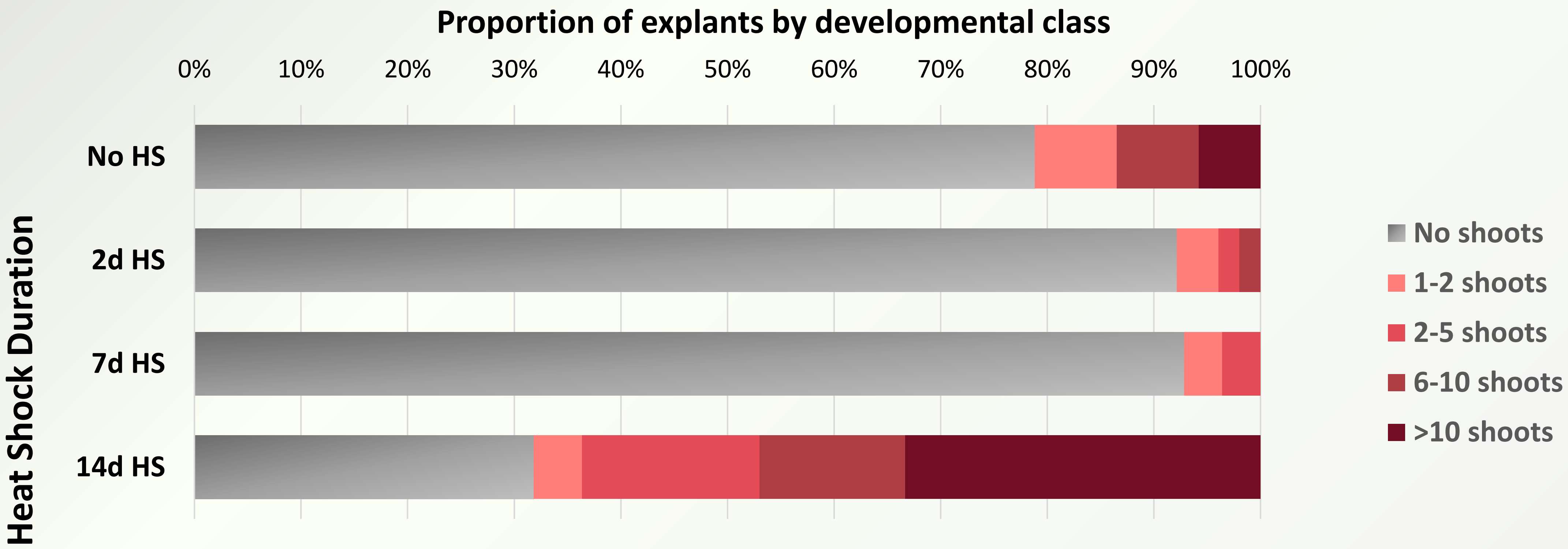
Two weeks of pulsed heat shock resulted in efficient shoot regeneration and excision from hairy roots



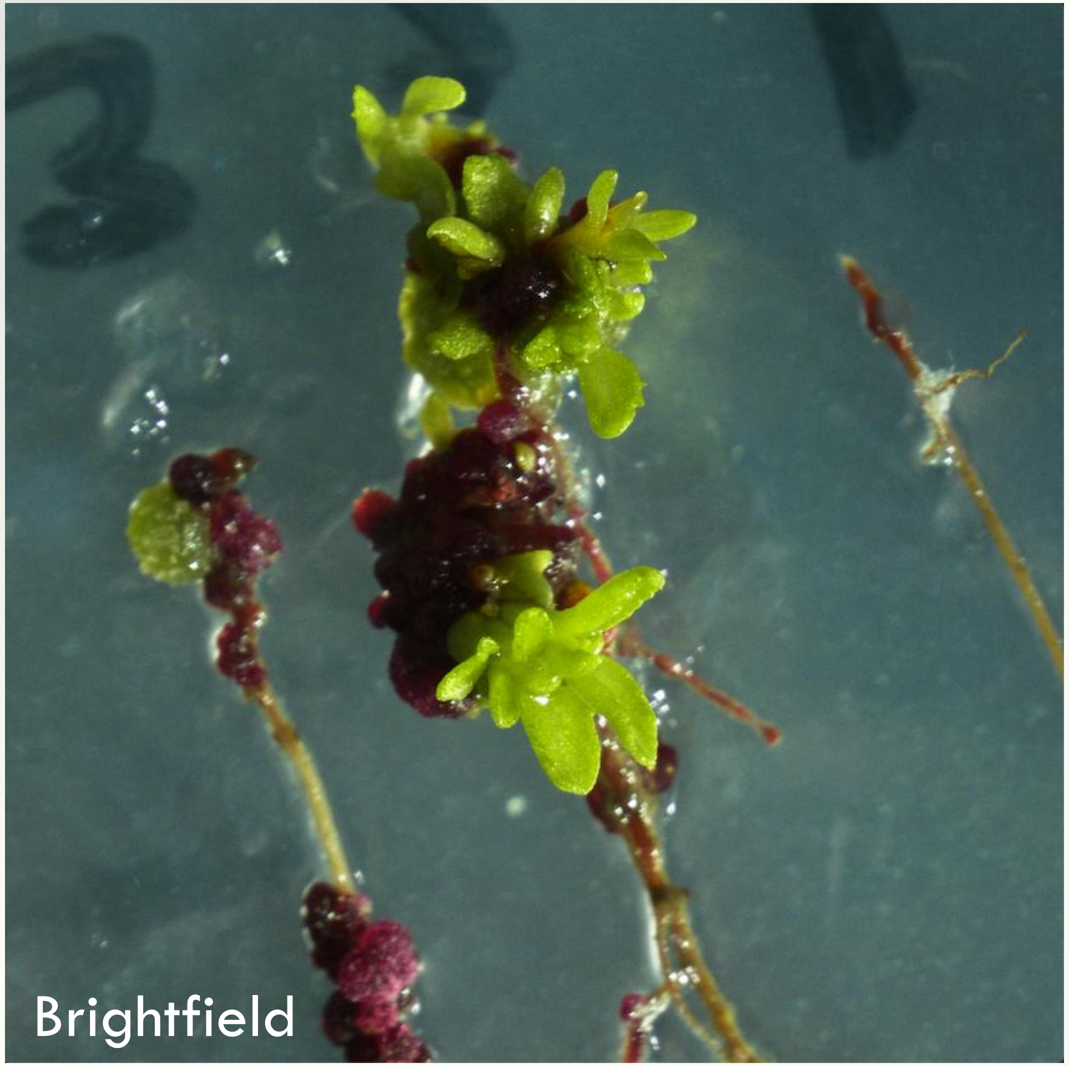


- Four hours heat shock at 39 degrees Celsius
- RUBY vs. non-ruby shoots can be easily identified for propagation, then other reporters examined by fluorescent microscopy after isolation

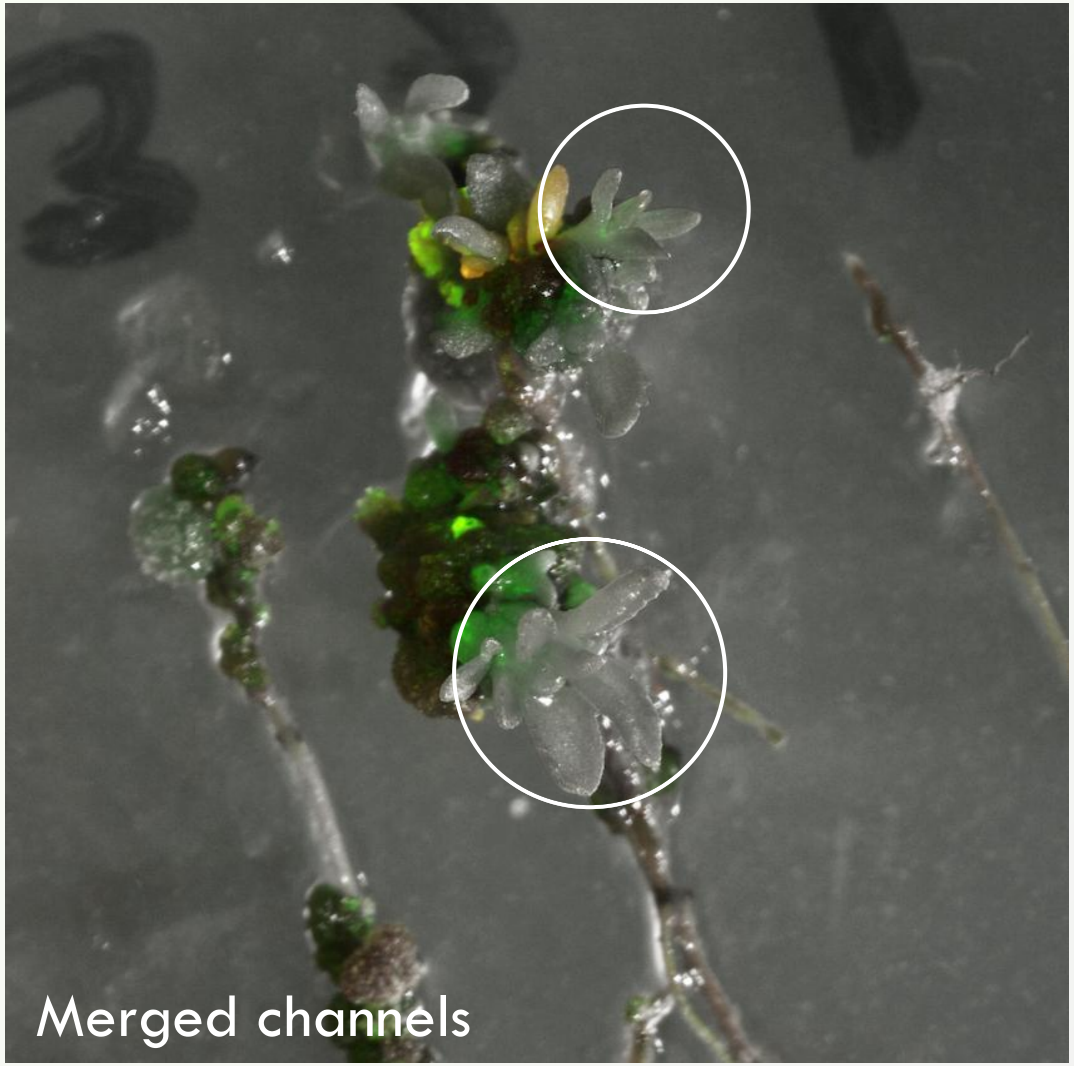
Longer heat-shock (HS) duration improved shoot regeneration rates per explant (segments of hairy roots)



Using multiple reporters (GFP, DsRed and RUBY), we can find shoots with excised transgenes



Brightfield



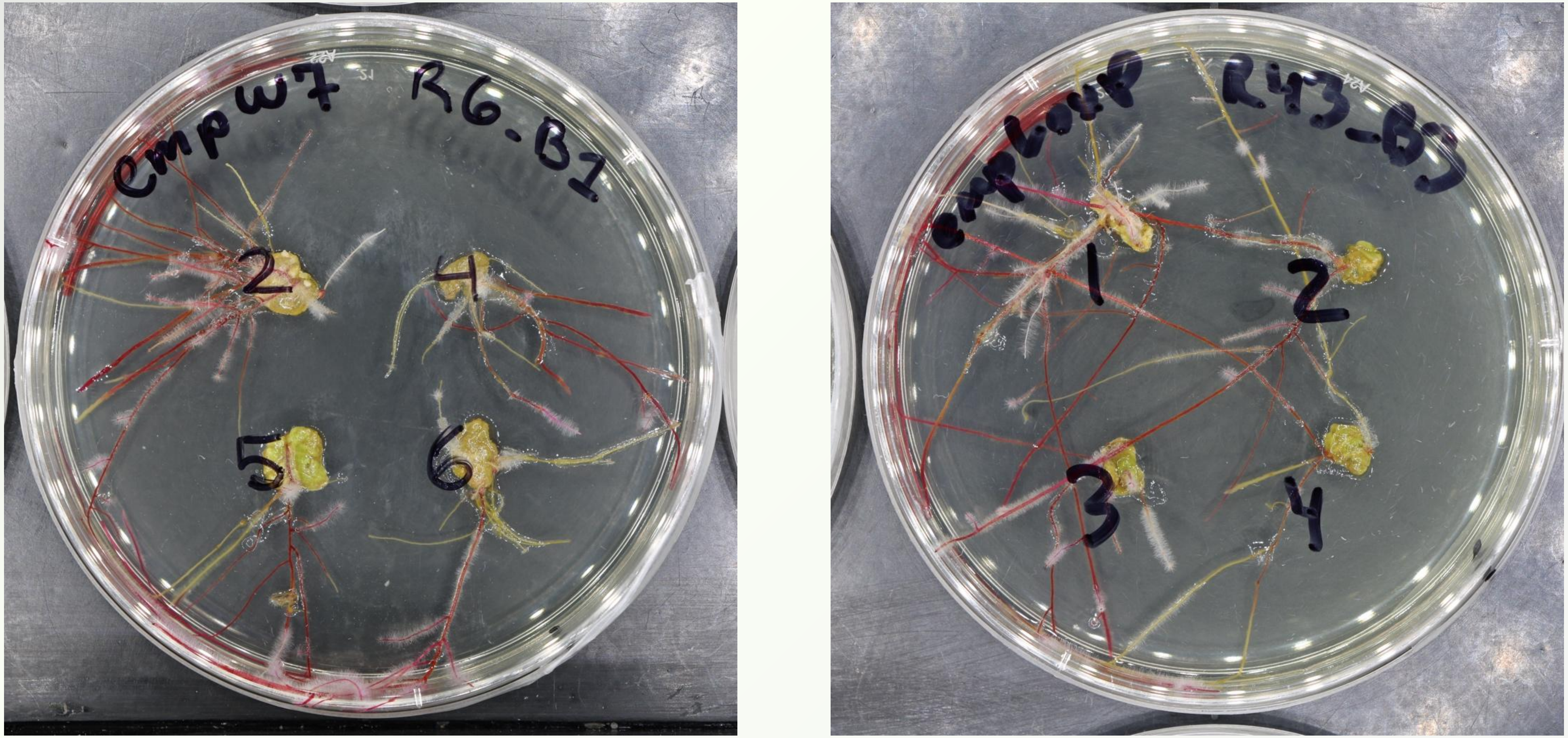
Merged channels

After transfer of regenerating root explants, elongated shoots without marker genes can be identified

Mixtures of RUBY and green RESET shoots in late-stage propagation

Populations of putative excised RESET shoots for further molecular analysis

Tweaking and extending the system: We made new transformations to better quantify frequency and integrity of excision



Tracked individual hairy root insertion events through the transformation and excision process

A concurrent strand in the lab: Trying to improve Cre excision in face of DNA methylation

Full Paper

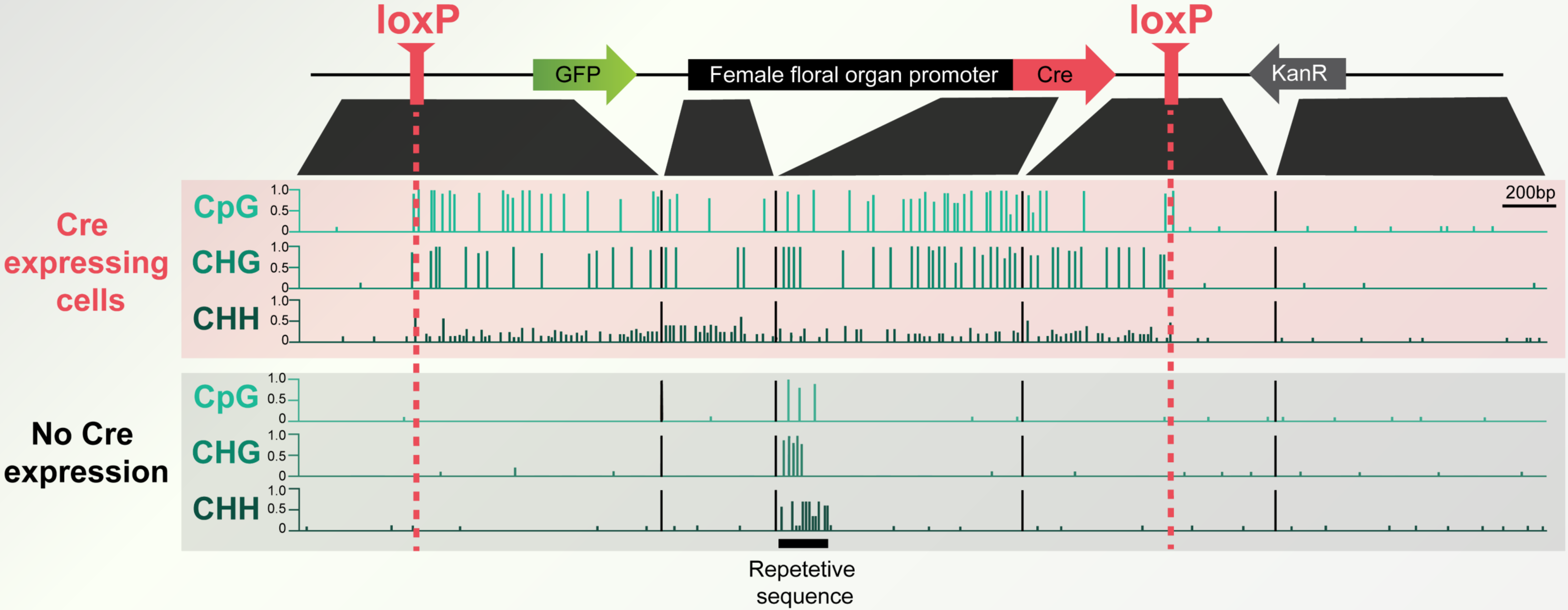
New Phytologist

DNA methylation occurring in Cre-expressing cells inhibits loxP recombination and silences loxP-sandwiched genes

Ruochen Liu, Qin Long, Xiuping Zou, You Wang and Yan Pei

Chongqing Key Laboratory of Application and Safety Control of Genetically Modified Crops; Biotechnology Research Center, Southwest University, No. 2 Tiansheng Road Beibei, Chongqing 400715, China

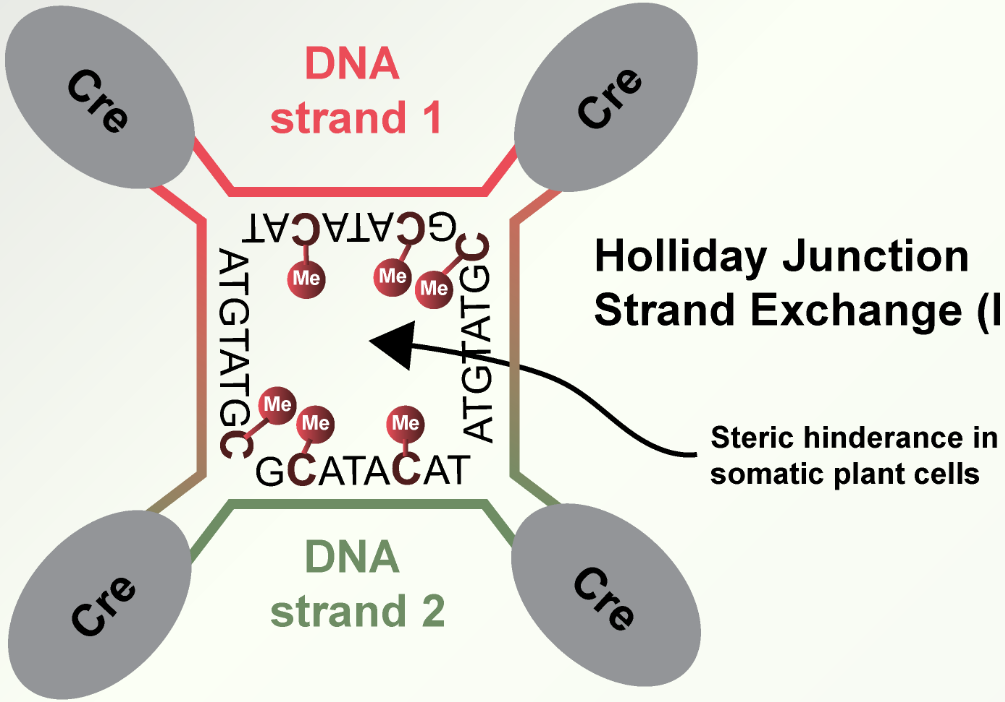
Cre can methylate transgene regions flanked by its recognition site loxP



Modified from Liu et al. 2021 *New Phytologist*

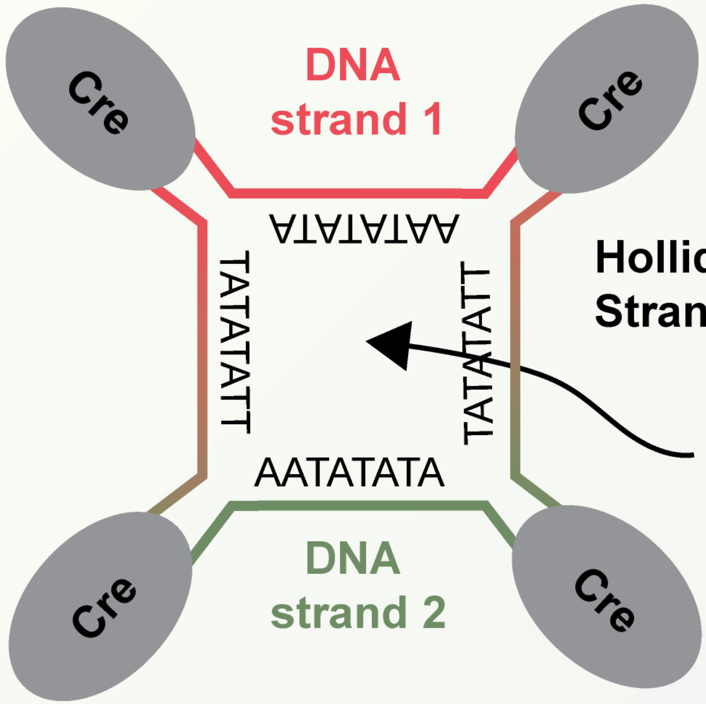
We made several variations of RESET constructs, including changes to flanking lox sites designed to be resistant to DNA methylation

Removal of cytosines, sites of DNA methylation



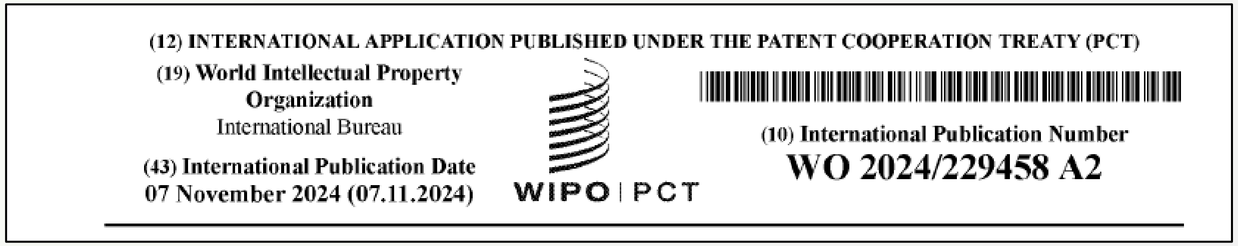
Holliday Junction Strand Exchange (loxP)

Steric hinderance in somatic plant cells



Holliday Junction Strand Exchange (LoxW)

Increased recombination efficiency in plant somatic cells



(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

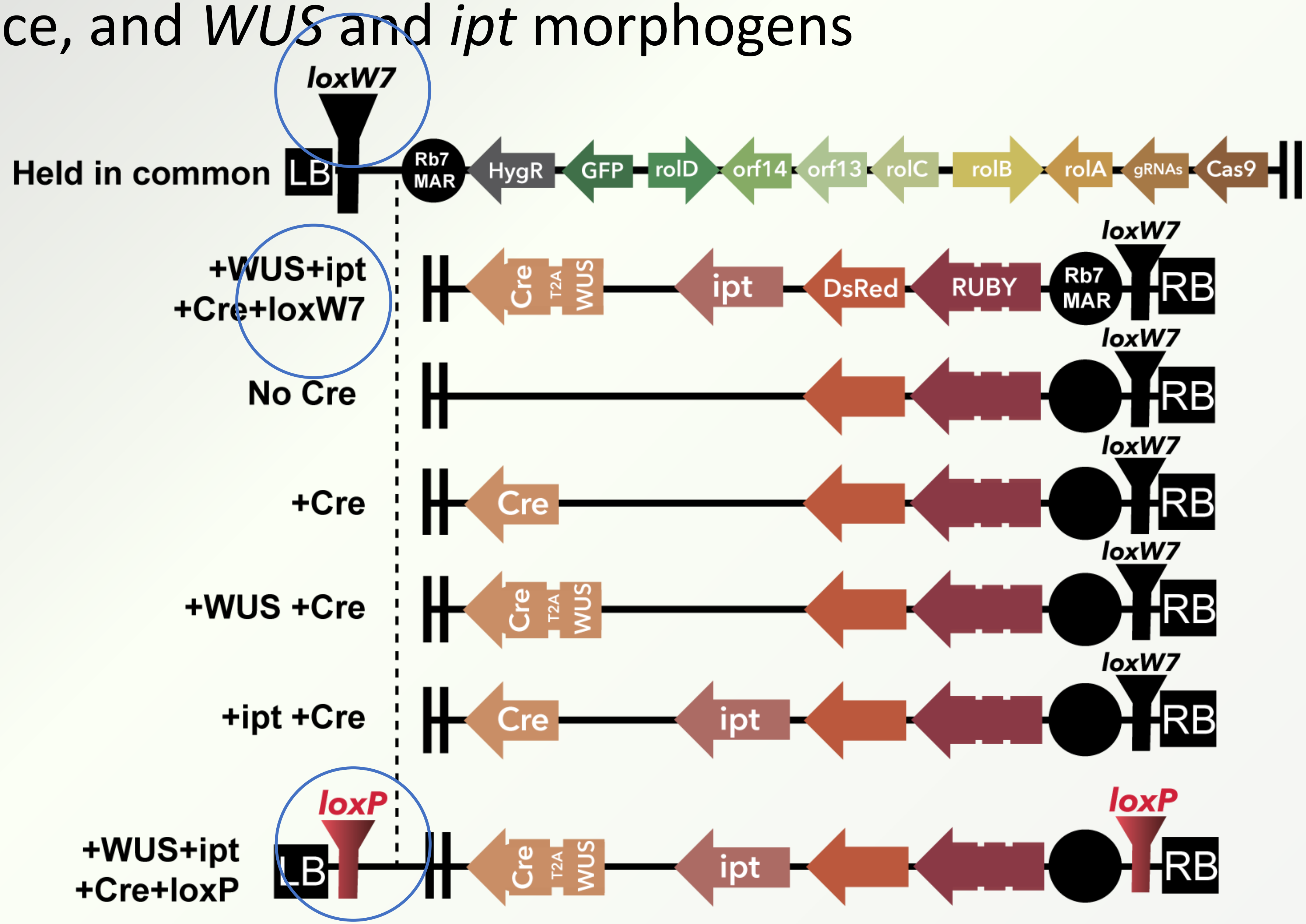
(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
07 November 2024 (07.11.2024)

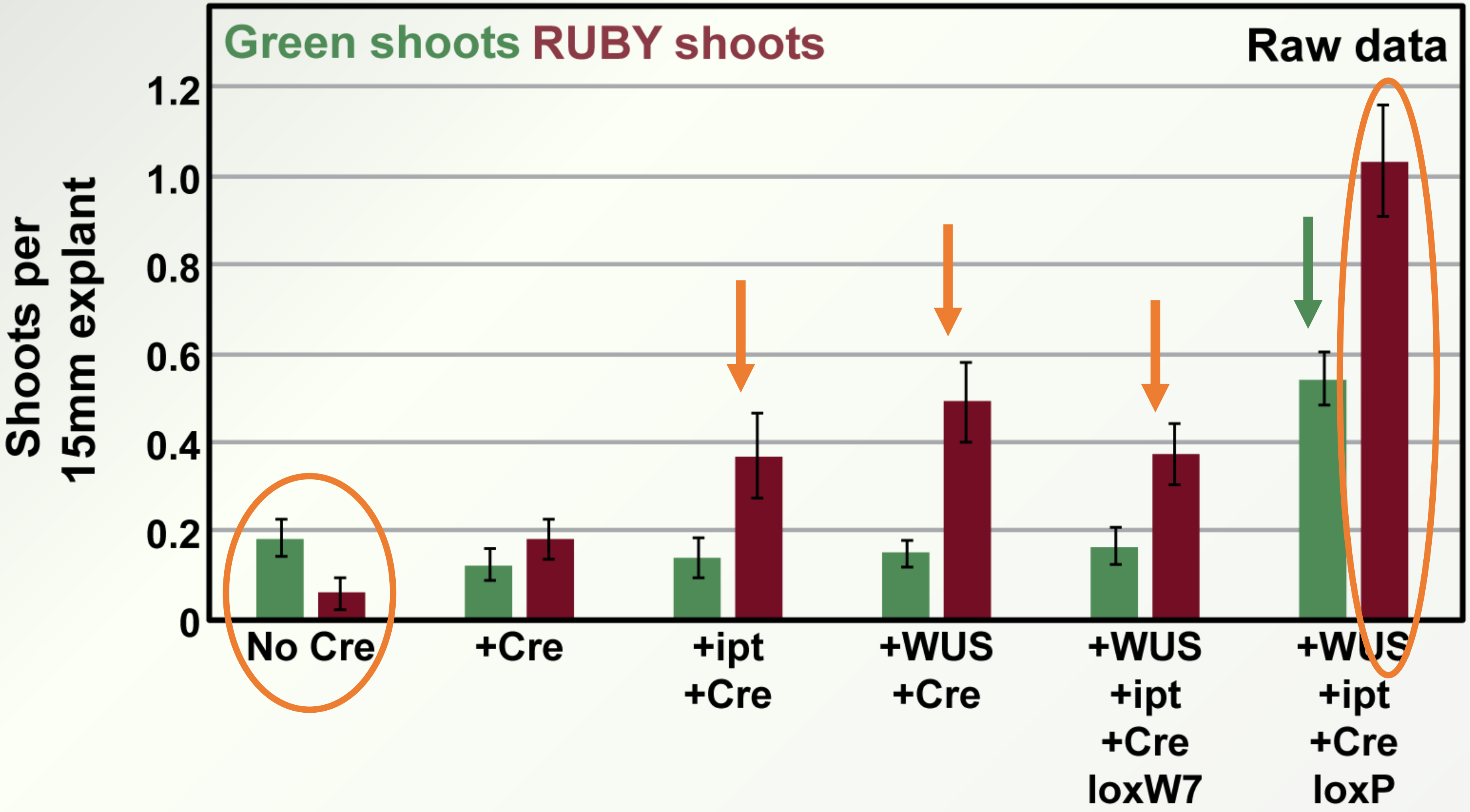
WIPO | PCT

(10) International Publication Number
WO 2024/229458 A2

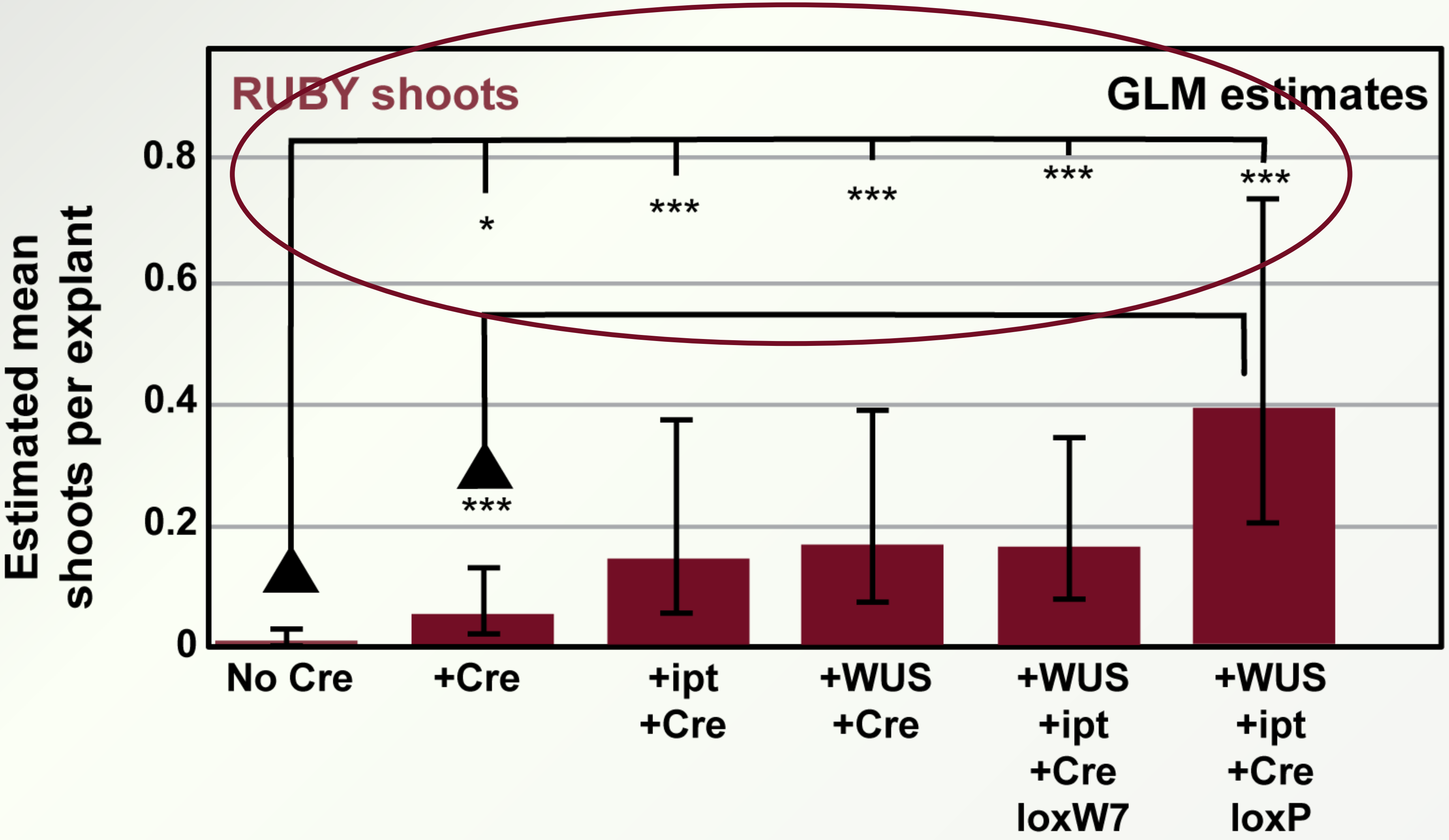
We tested the effect on shoot regeneration of a new lox site, Cre presence, and *WUS* and *ipt* morphogens



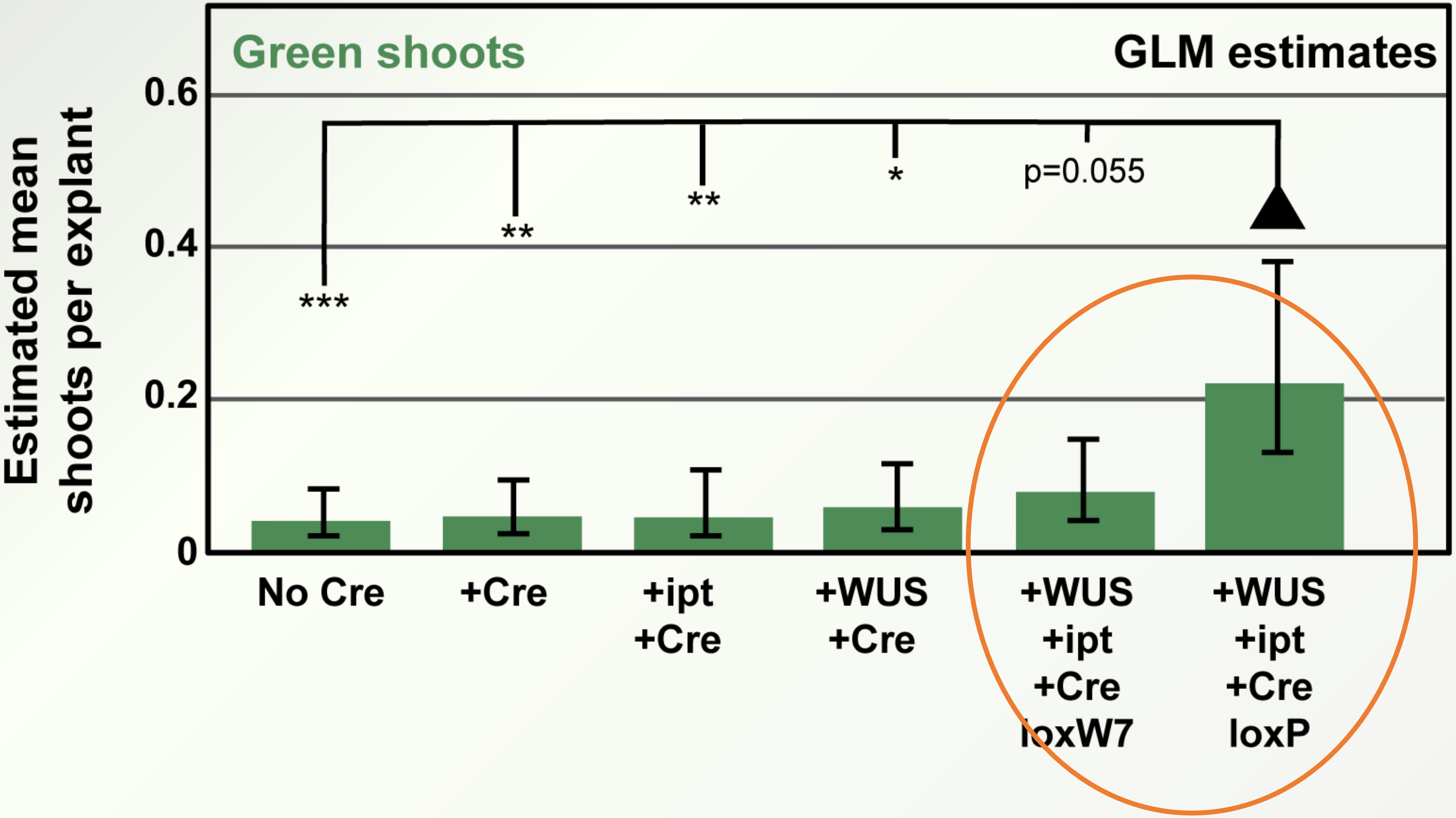
loxP-flanked RESET constructs gave the highest shoot regeneration after heat shock induction of transgenic roots



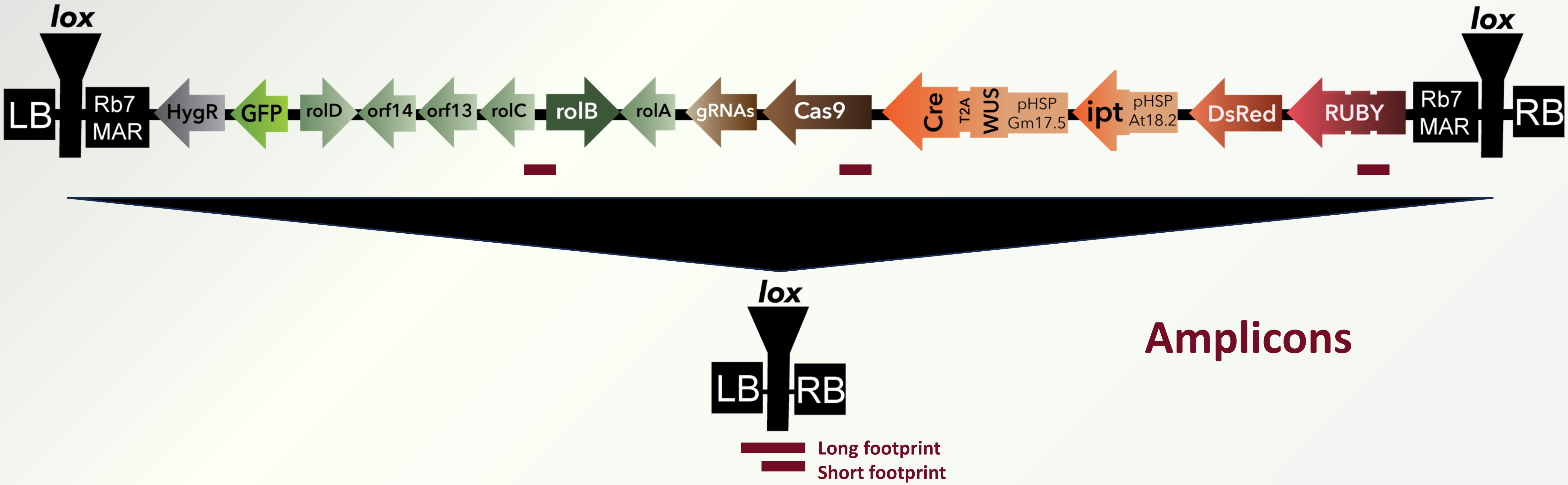
Cre expressing RESET constructs had a significant benefit for transgenic shoot regeneration



loxP-flanked RESET constructs had superior numbers of excised shoots versus loxW7 variants



To figure out if the shoots without RUBY, GFP, and DsRed were completely excised, we used a panel of PCR amplicons

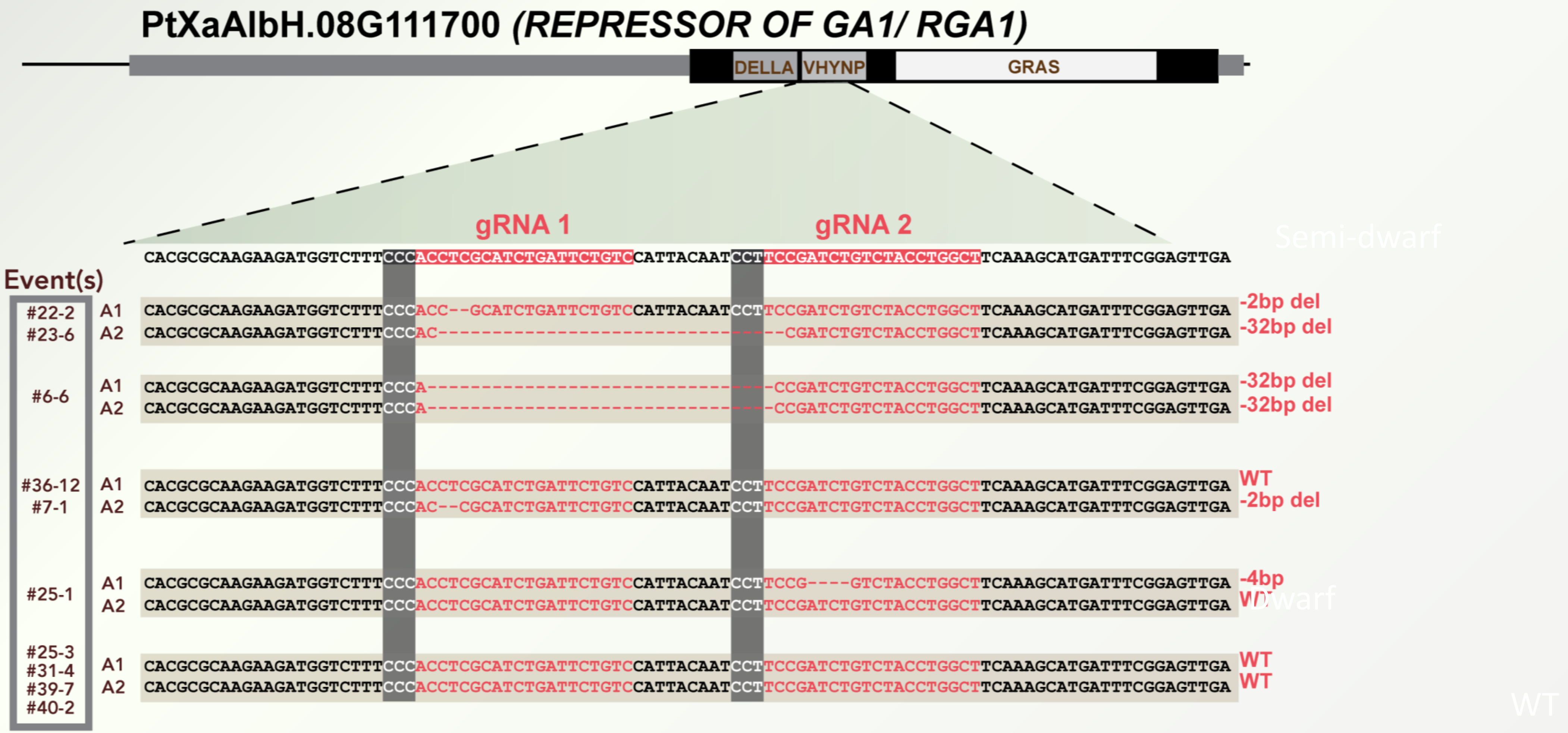


The presence of any transgene band eliminated a shoot as being categorized fully excised (partial chimera)

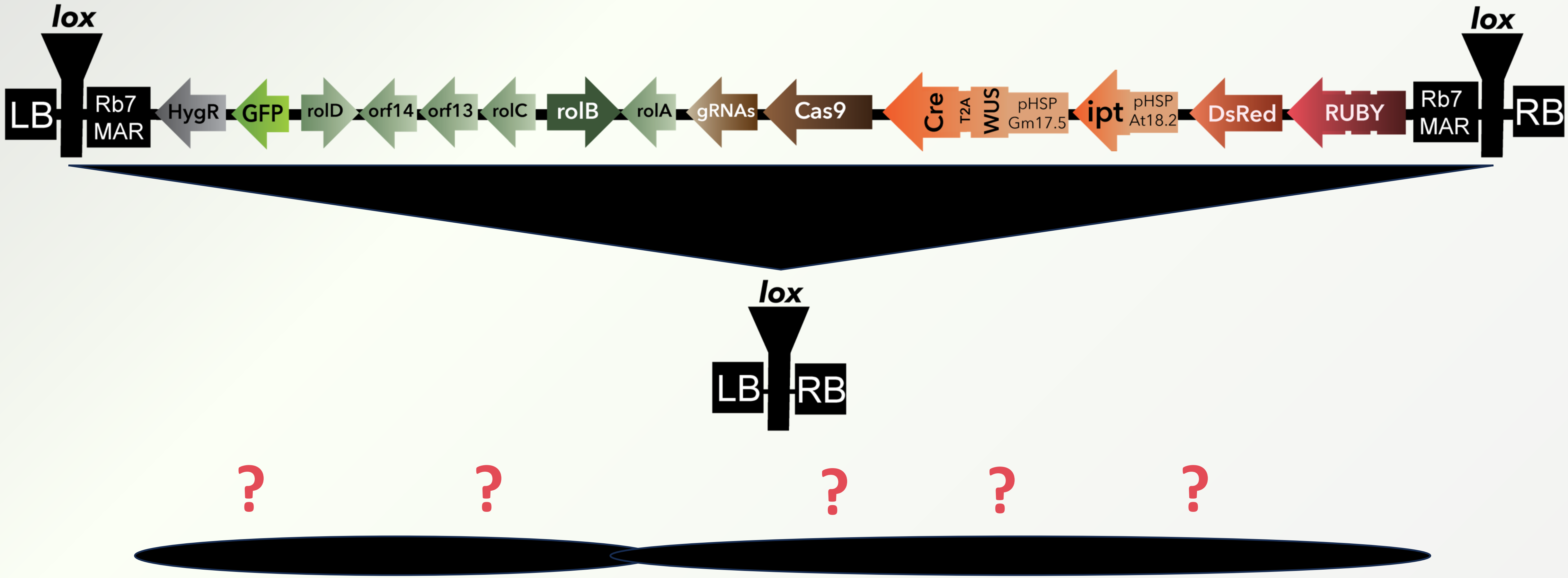
Two footprint amplicons were included in case of truncation of the T-DNA left border

While many escape shoots were found, high rates of complete excision were found in product shoots

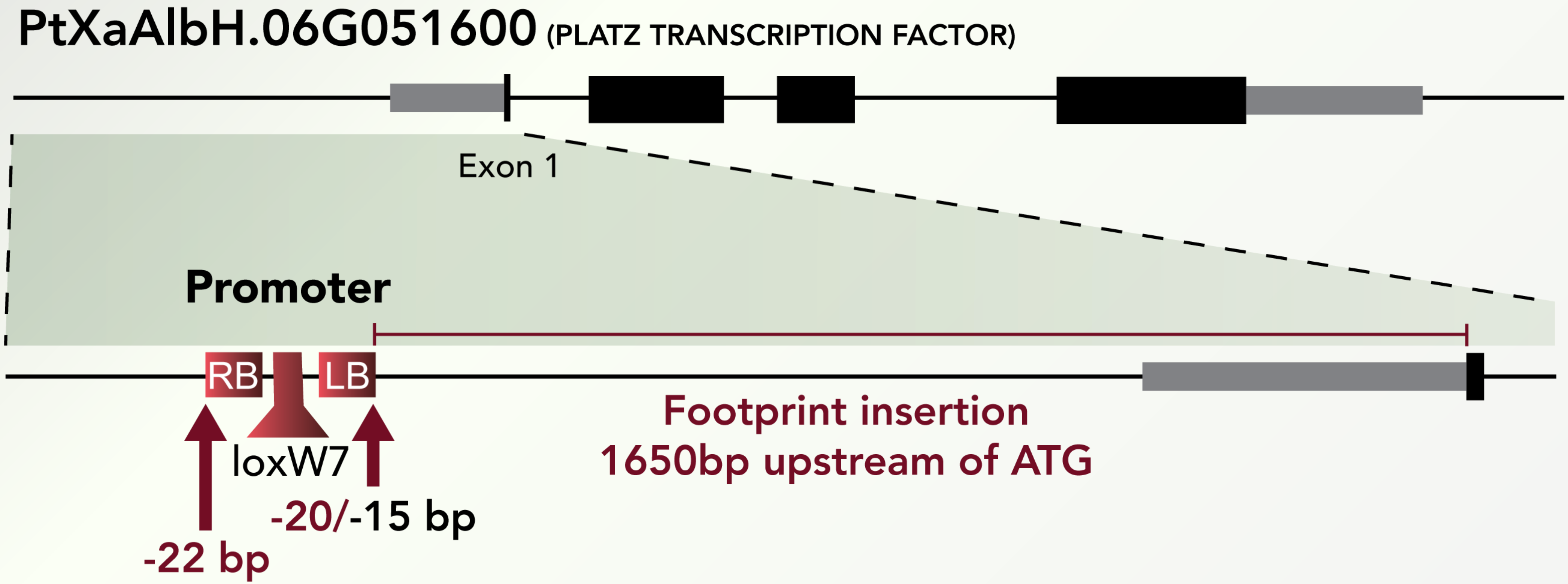
60% of excised events showed editing in at least one allele of the target locus, which is typical for poplar



Where did our transgenes insert? How did the excision process resolve the footprints into final configurations?



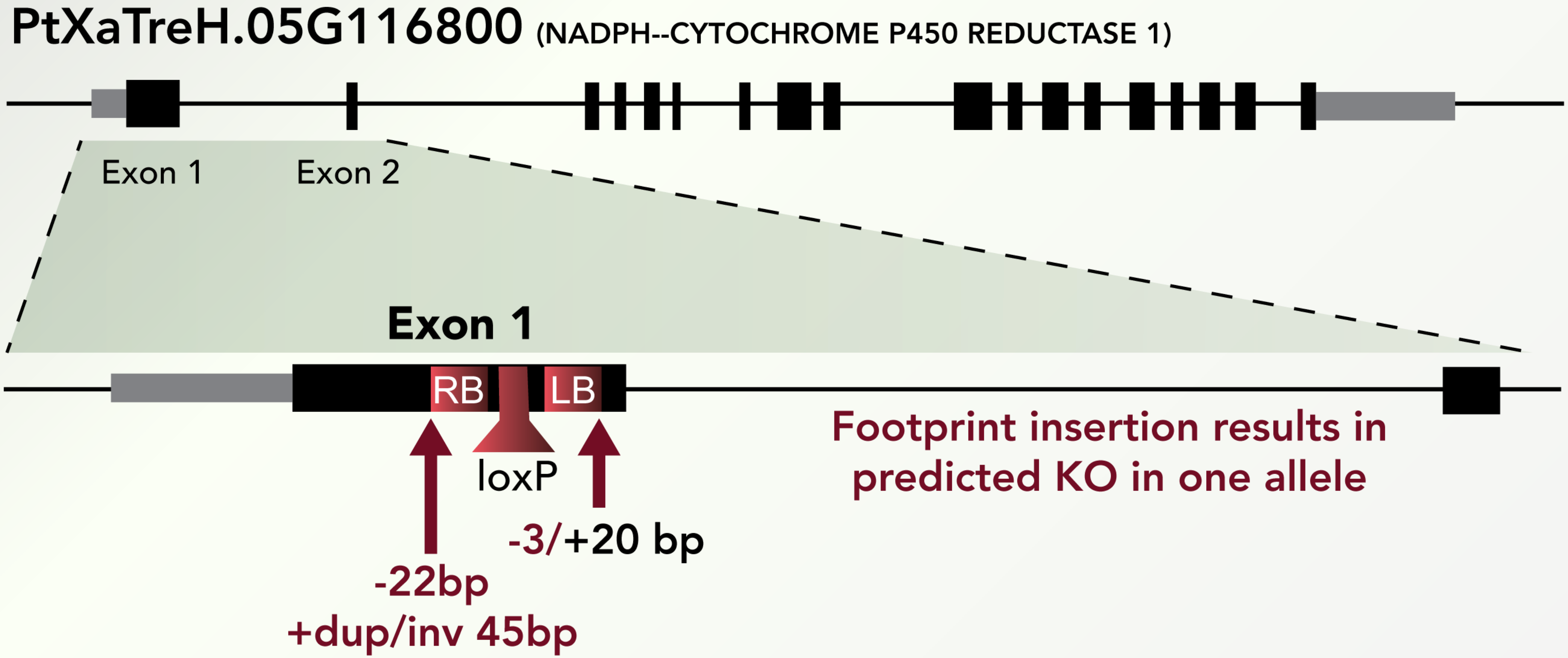
We used TAIL-PCR and WGS to find where transgenes landed and resolved into smaller footprints



PtXaAlbH.06G051600 (PLATZ TRANSCRIPTION FACTOR)

Footprint insertion
1650bp upstream of ATG

We did find some events where the footprint inserted into an exon of one allele

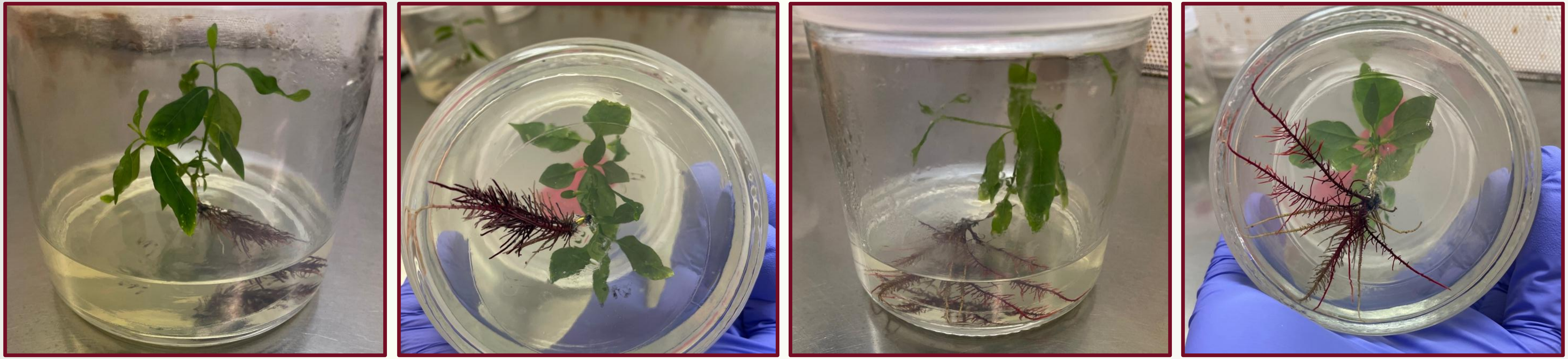


Footprint insertion results in predicted KO in one allele

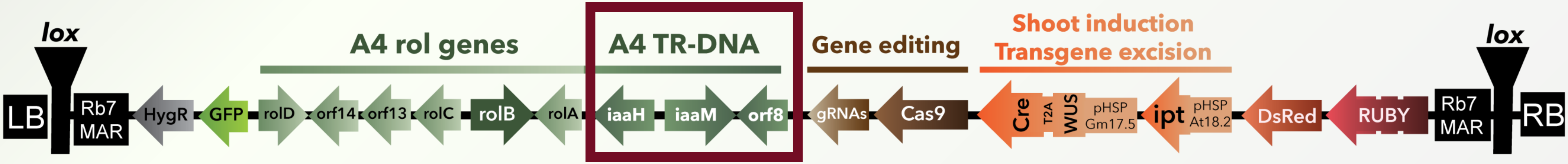
RESET elements

- Background
- The basic RESET system
- **Activities to improve it**

Does this work in other, more recalcitrant species?

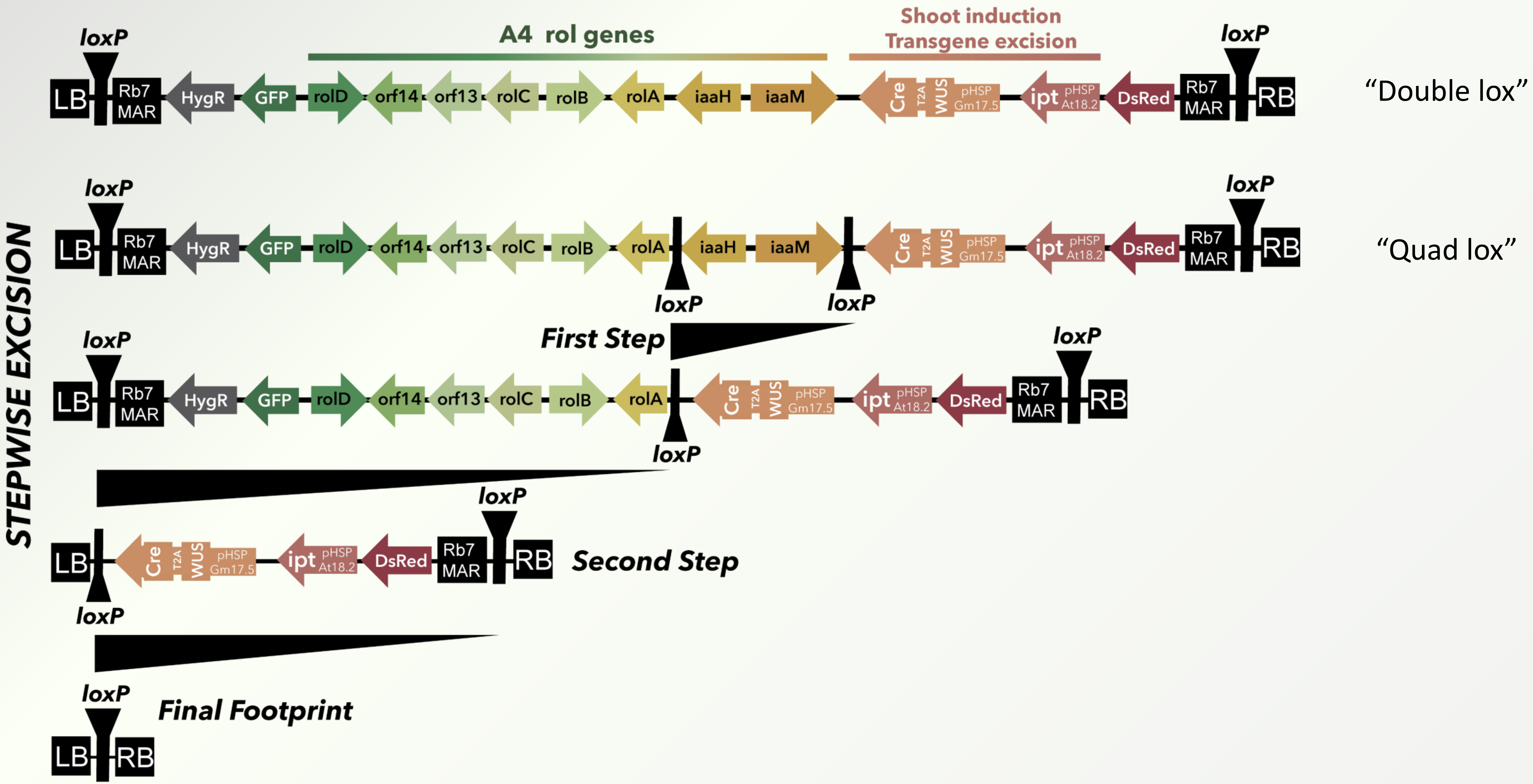


Eucalyptus grandis x urophylla RESET composite plants



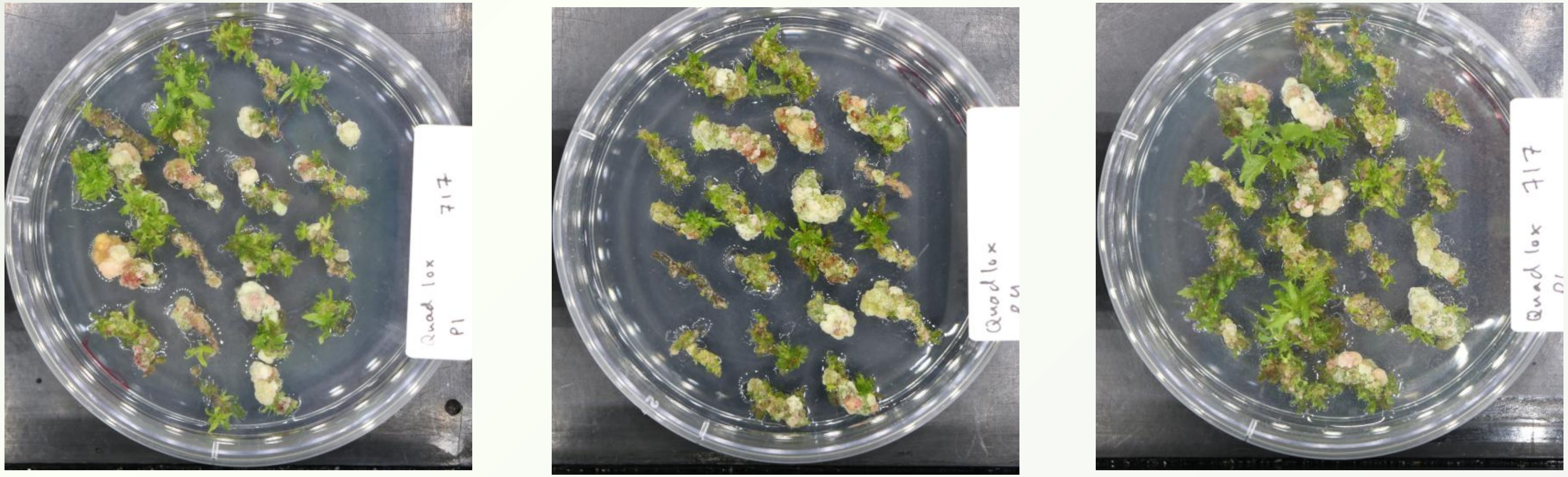
So far, adding the iaaH/M genes is essential for hairy-roots, but also seems to interfere with shoot development

Attempting to accelerate excision by addition of internal loxP sites

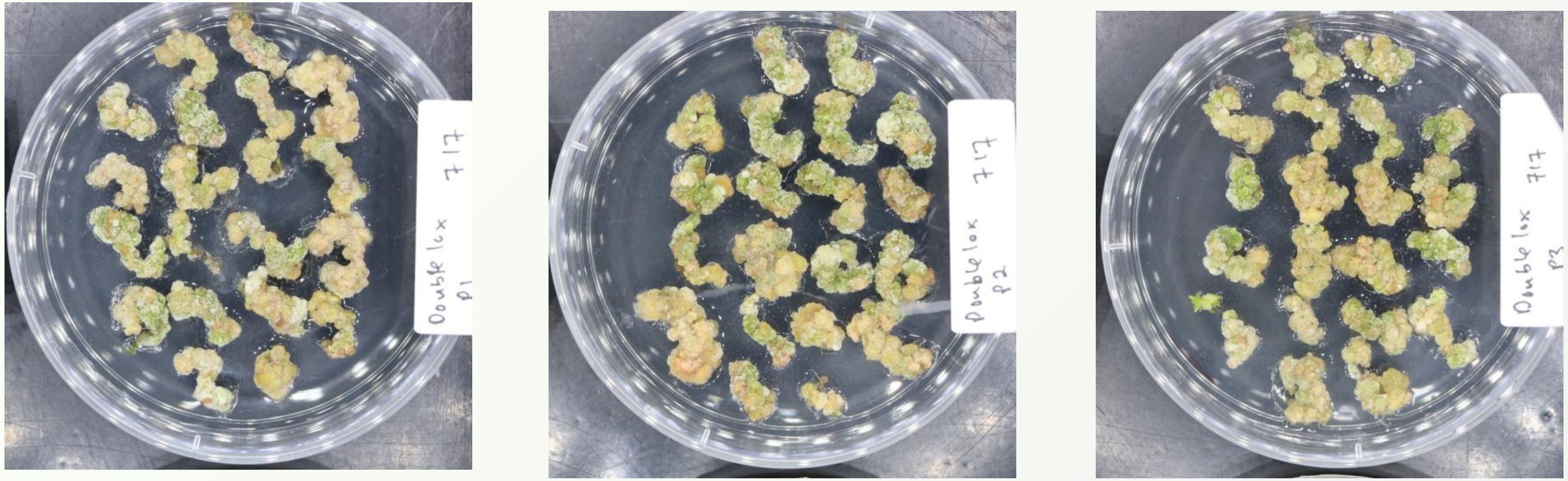


QuadLox showed improve shoot regeneration over double lox configurations

“QuadLox”



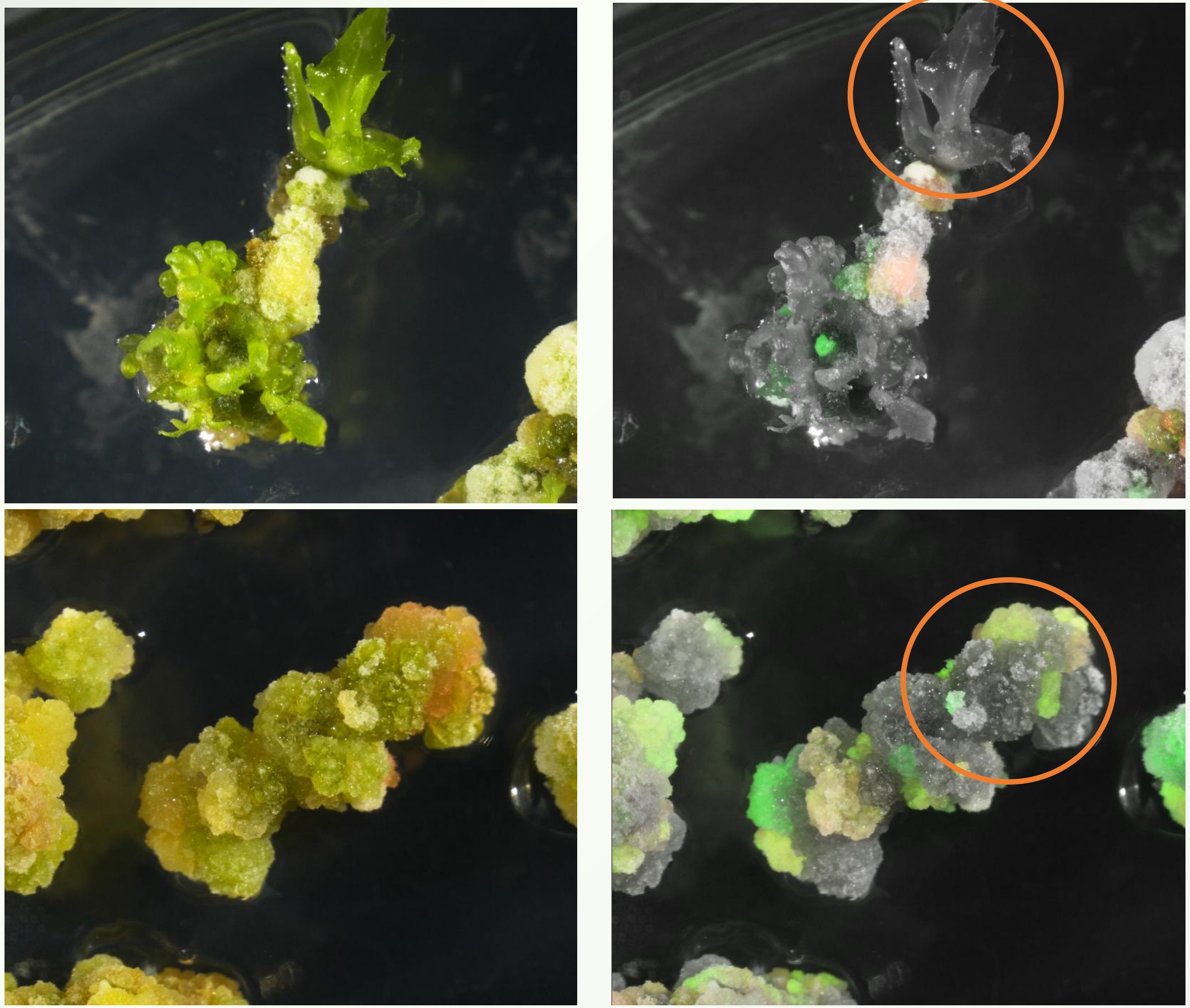
“Double lox”



QuadLox also showed impressive excision rates

Brightfield

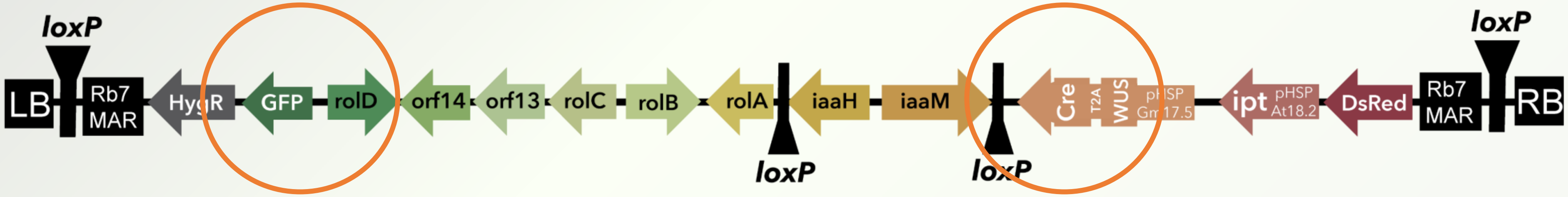
GFP and DsRed

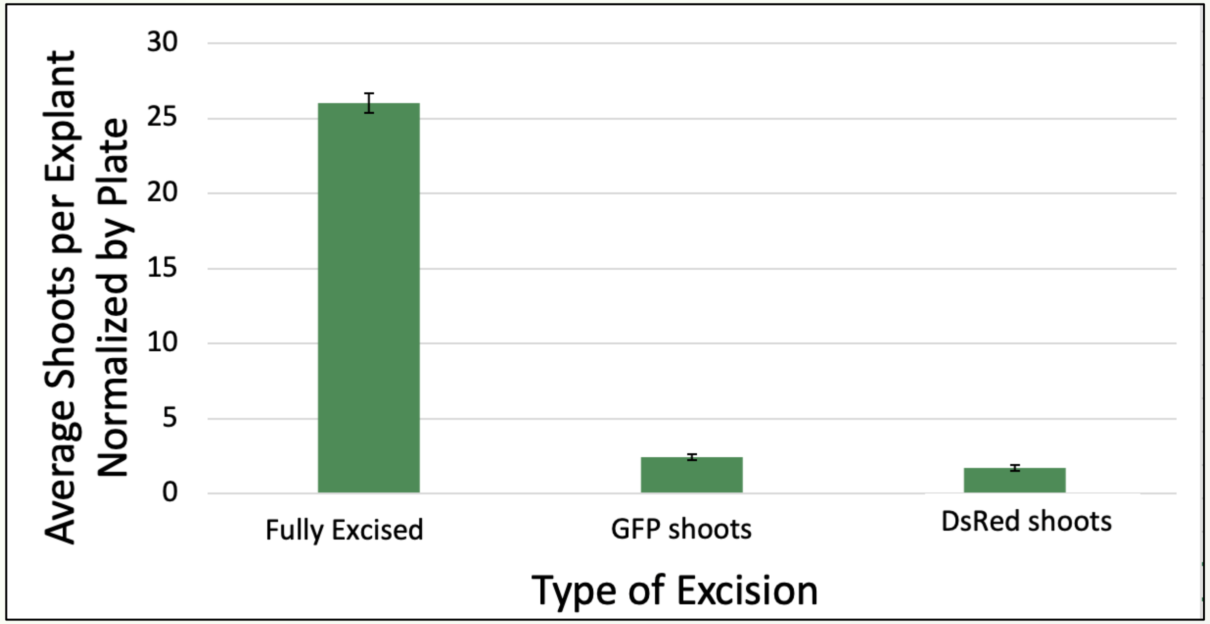


“QuadLox”

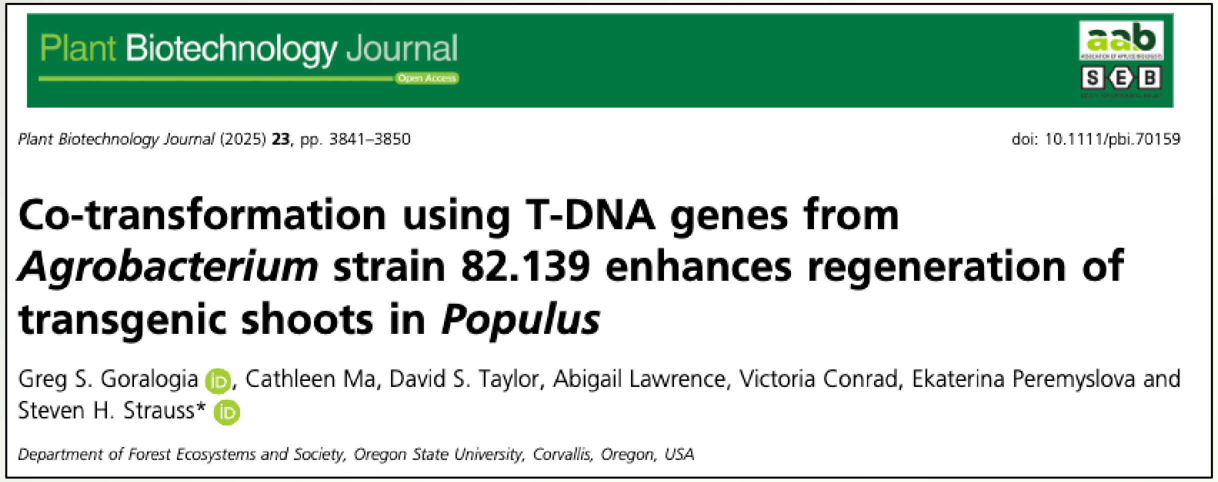
“Double lox”

Final excision has the potential to remove Cre too early - but a low rate of partially excised tissues observed





We are also working on alternative morphogens such as gene 6b isolated from a “shooty” strain of Agrobacterium



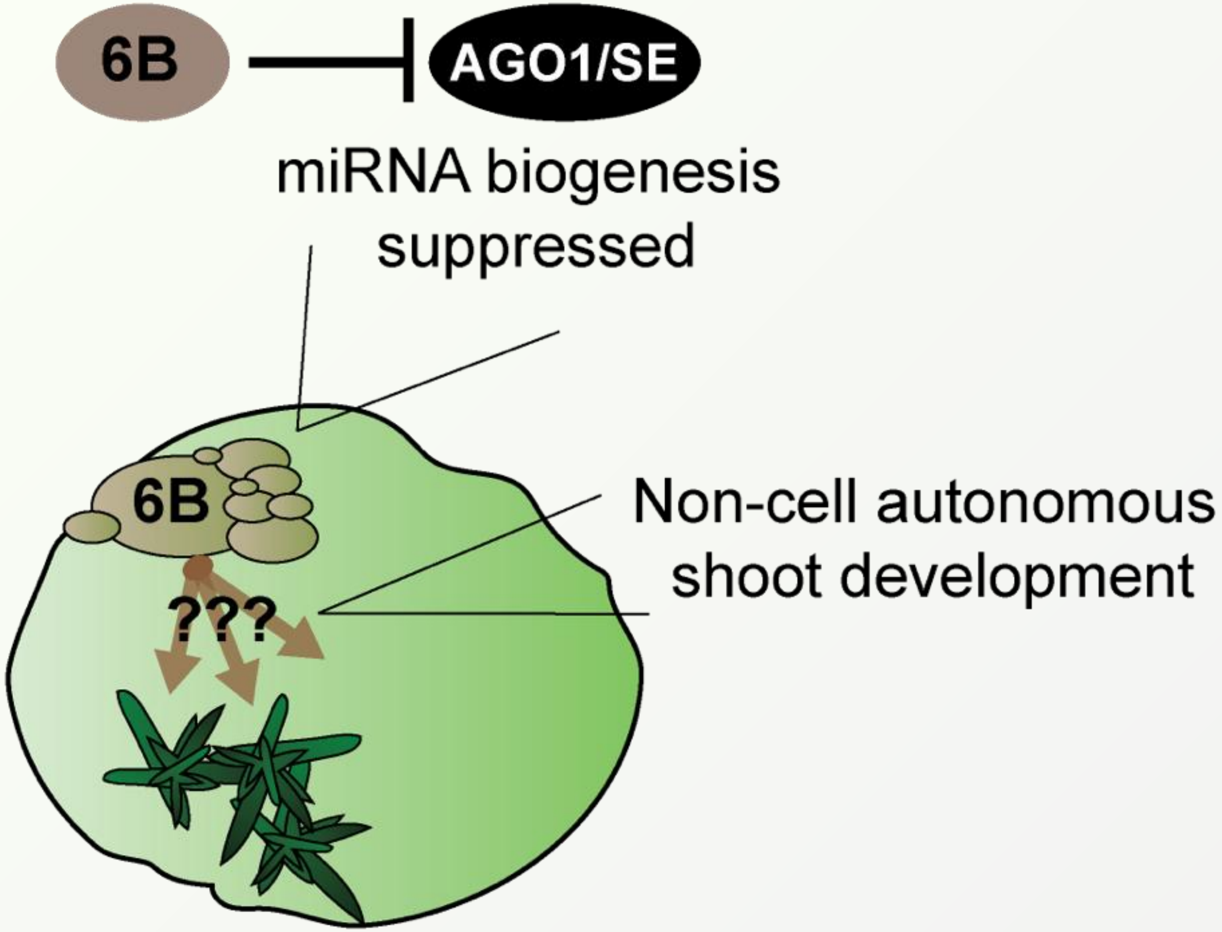
Plant Biotechnology Journal

Plant Biotechnology Journal (2025) **23**, pp. 3841–3850 doi: 10.1111/pbi.70159

Co-transformation using T-DNA genes from *Agrobacterium* strain 82.139 enhances regeneration of transgenic shoots in *Populus*

Greg S. Goralogia, Cathleen Ma, David S. Taylor, Abigail Lawrence, Victoria Conrad, Ekaterina Peremyslova and Steven H. Strauss*

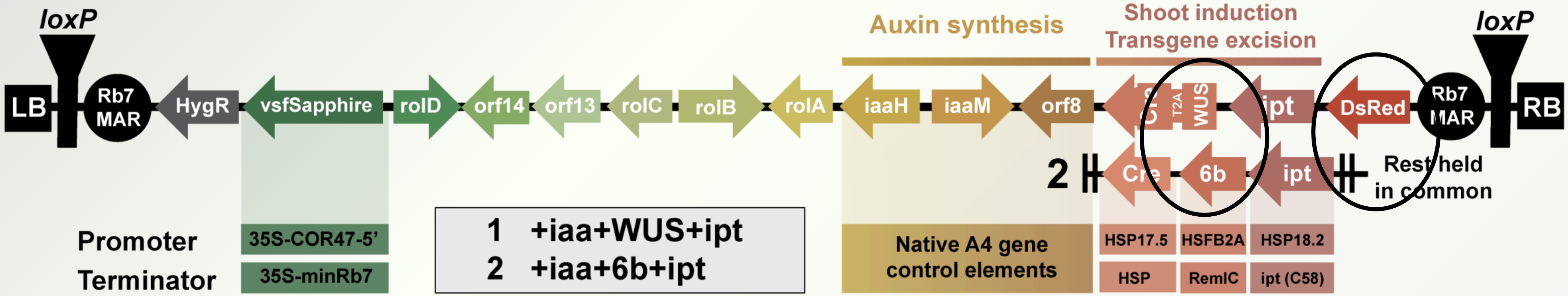
Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon, USA



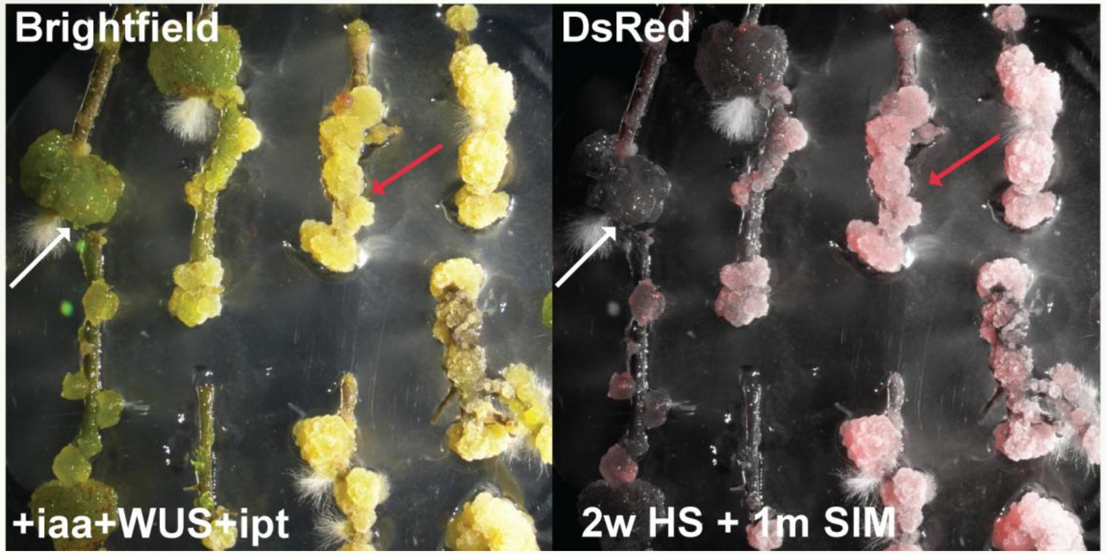
miRNA biogenesis suppressed

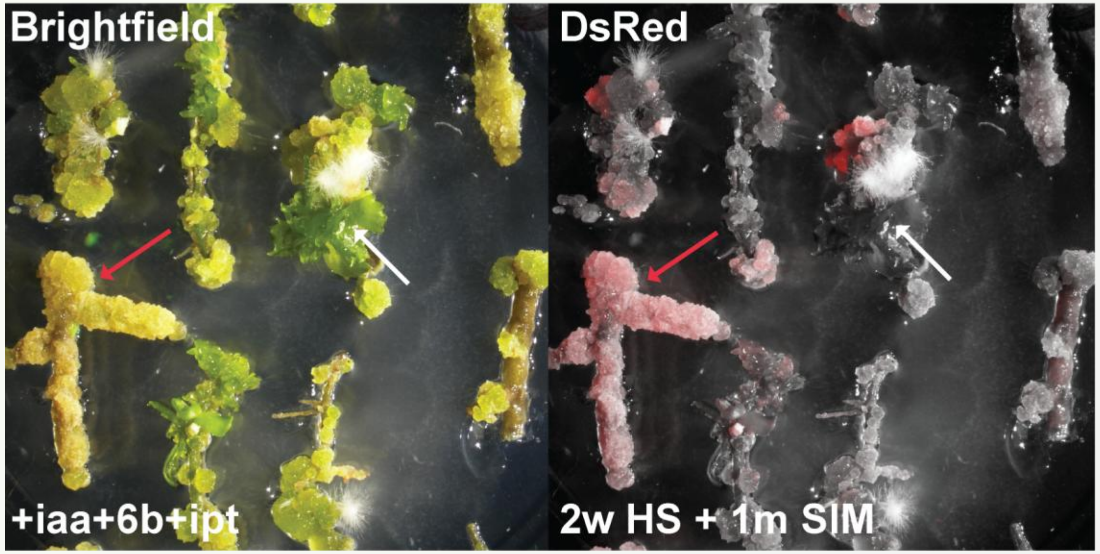
Non-cell autonomous shoot development

Gene 6b showed improved excision and shoot regeneration vs. WUS

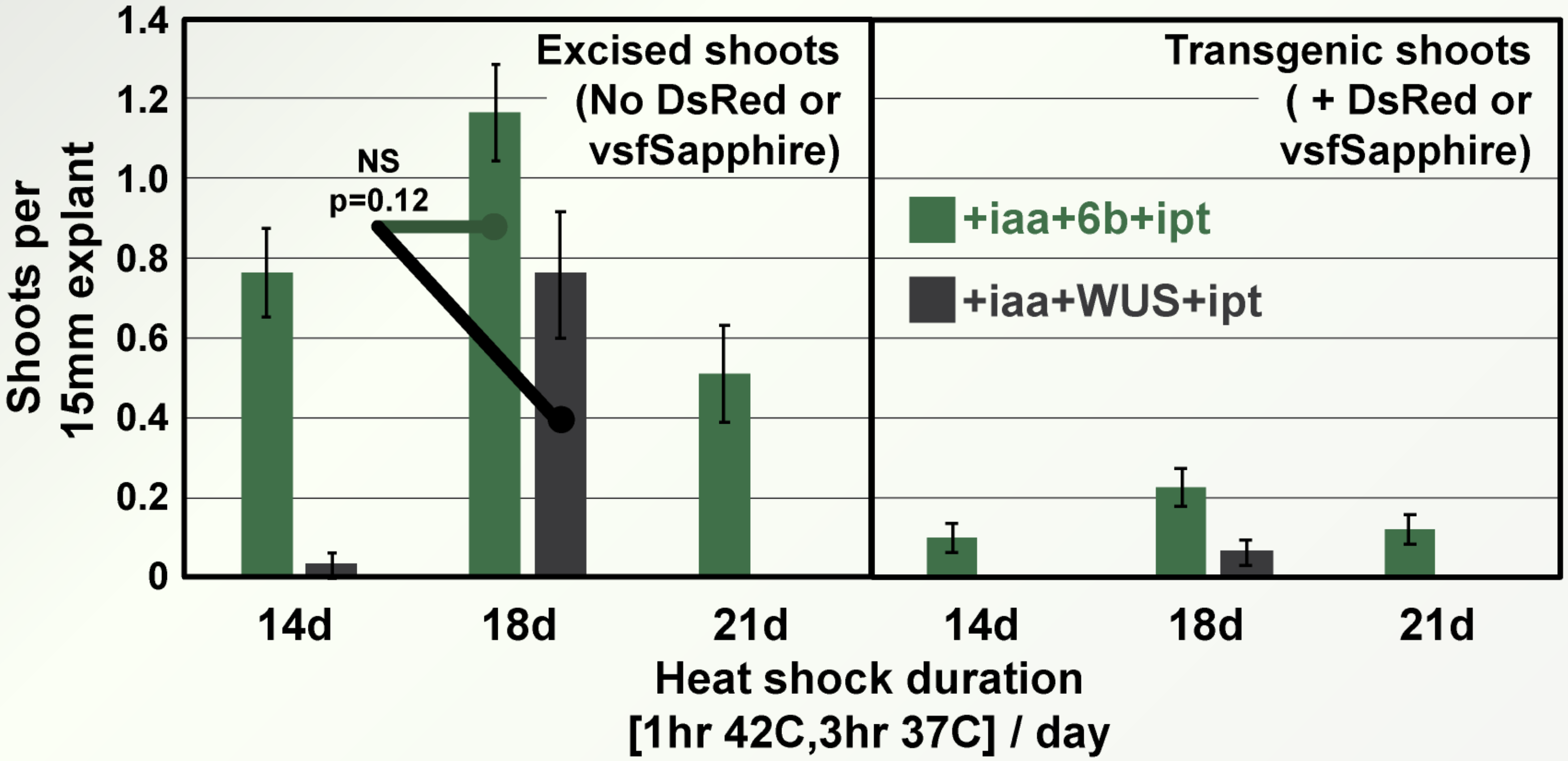


1 +iaa+WUS+ipt
2 +iaa+6b+ipt





Gene 6b also showed improved excision and shoot regeneration vs. WUS



In summary: RESET system is functional for editing and transformation in poplar

- High rates of hairy root transformation
- High rates of editing in excised shoots
- Significant numbers of escape shoots, but imposed weak selection
- Will the system function broadly in clonal woody plant species?
  - Eucalypts problematic so far – but known to be slow and variable -- testing ongoing
  - Also under study by collaborators in several other species

Biologically clean but legally still a mess….

Rationalizing plant biotech regulations: The case of accessory DNA

Steven H. Strauss*[1], Wayne Parrott*, Chris Willig, Greg Goralogia, Katie Toomey, Ray Shillito and Alan Wenck

Request for Information on Modified Organisms Subject to the Plant Protection Act

A Proposed Rule by the Agriculture Department on 05/15/2026

This document has a comment period that ends in 11 days. (06/15/2026)

4 comments received. View posted comments

https://www.federalregister.gov/documents/2026/05/15/2026-09833/request-for-information-on-modified-organisms-subject-to-the-plant-protection-act

My deep thanks to the people who did the real work !

Victoria Conrad
Undergraduate

Sydney Gould
Undergraduate

Cathleen Ma
Tissue culture and transformation

Kate Peremyslova
Tissue culture and transformation

Greg Goralogia
Postdoc FES

Scientific assistance

Bill Gordon-Kamm (Corteva)
Todd Jones (Corteva)
Jim Thomson (ARS Albany)
Roger Thilmony (ARS Albany)
Chris Willig (OSU)
Zachary Heinhold (OSU)
Parker Wheeler and Colette Richter (OSU)

Sydney Gould & Carter Mucken

Funding sources

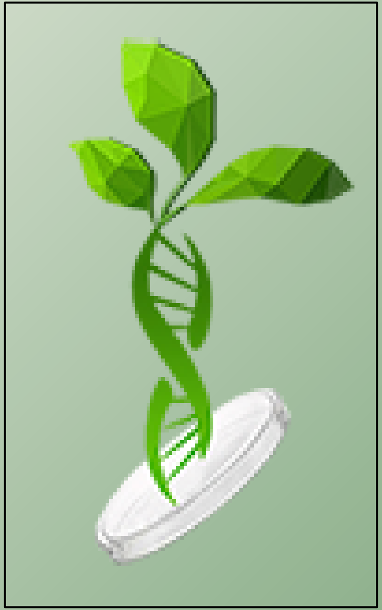
Federal grants

NIFA-Biotechnology Risk Assessment Grant (BRAG)

NSF-Plant Genome Research Program (PGRP)

GREAT TREES Consortium

Suzano, SAPPI, Arauco, Klabin, SweTree, Corteva Agriscience



Thank you