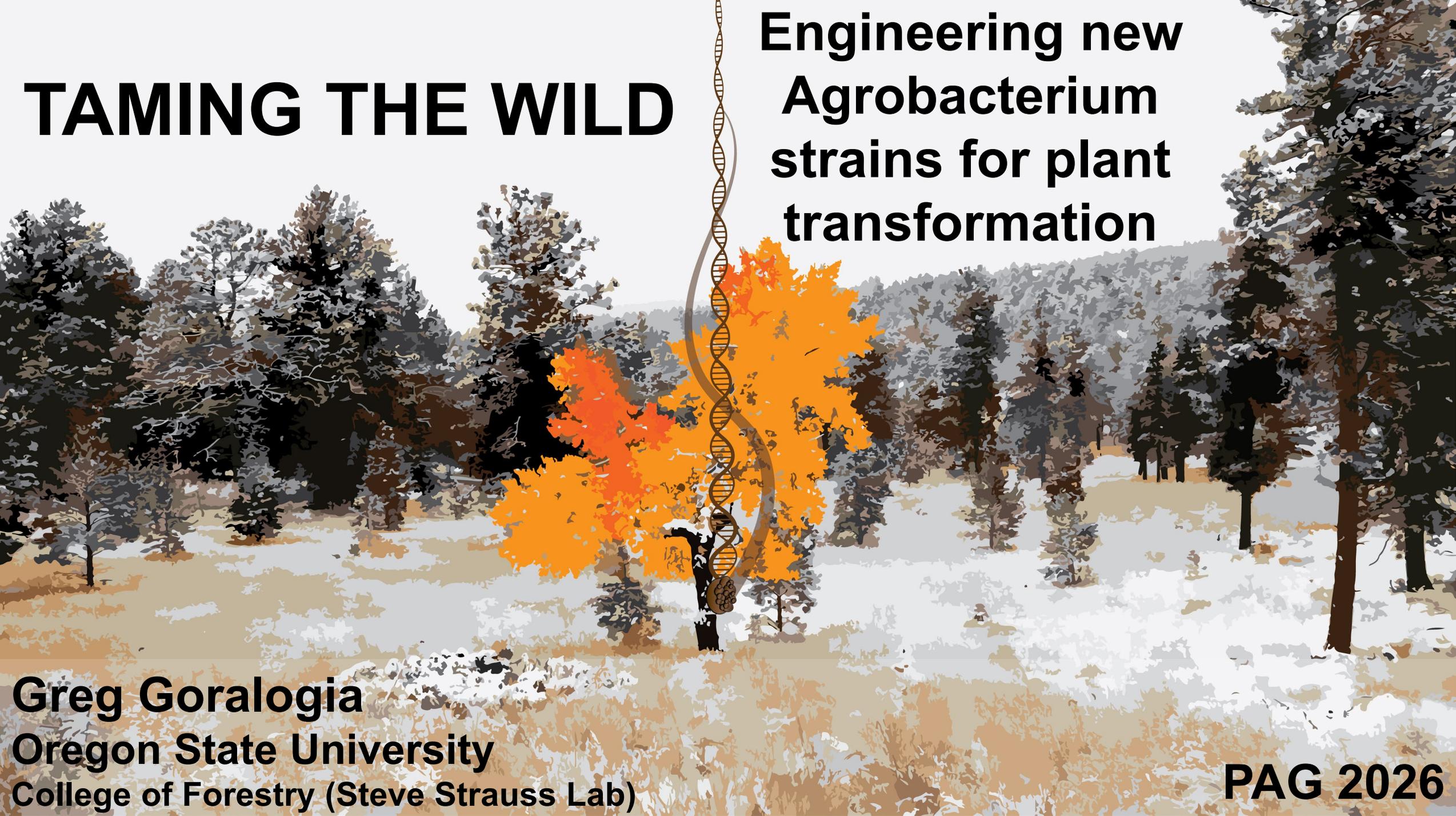


TAMING THE WILD



**Engineering new
Agrobacterium
strains for plant
transformation**

Greg Goralogia
Oregon State University
College of Forestry (Steve Strauss Lab)

PAG 2026

Inefficient transformation remains a bottleneck for biotechnology in many species, including forest trees and specialty crops

Hybrid Poplar

Populus tremula x alba 717-1B4

Populus tremula x tremuloides 353-53



Hop

Humulus lupulus

Fuggle, Cascade, Saaz



Eucalypts

Eucalyptus grandis x urophylla

E. globulus, *E. nitens*, *E. dunnii*



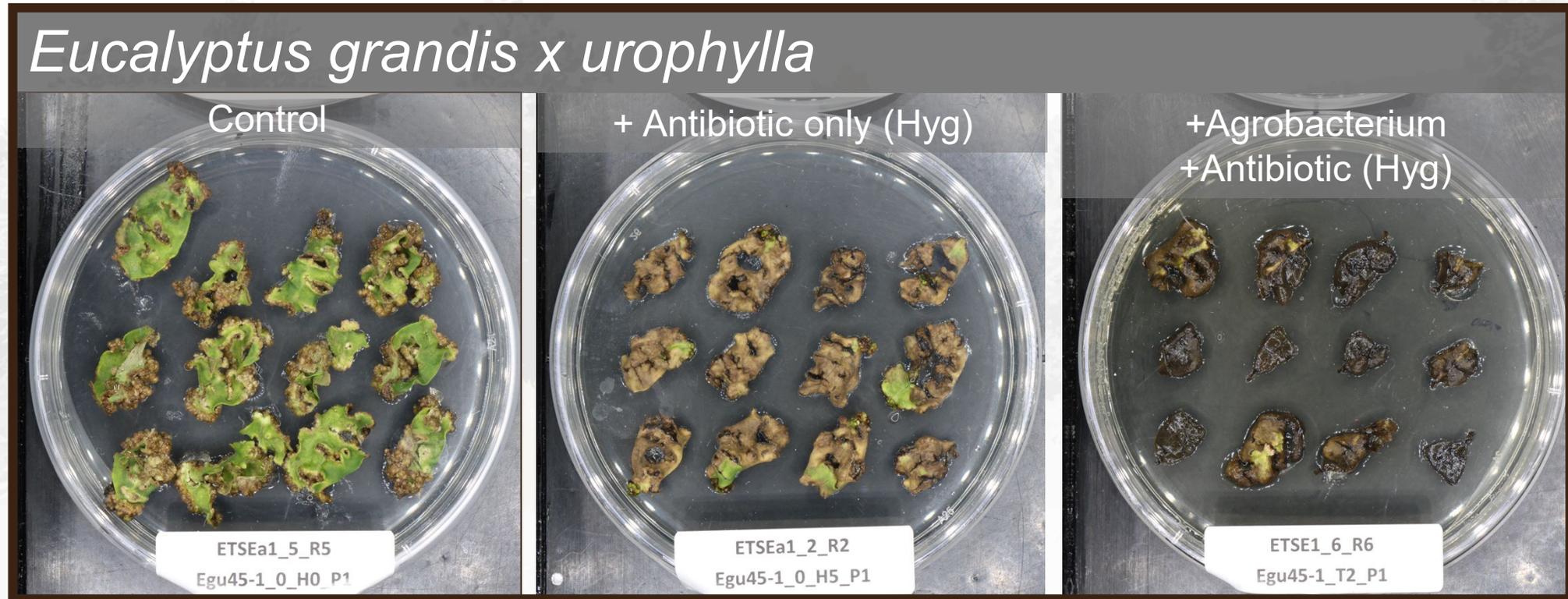
Black Cottonwood

Populus trichocarpa

(~1500 genotype GWAS population)

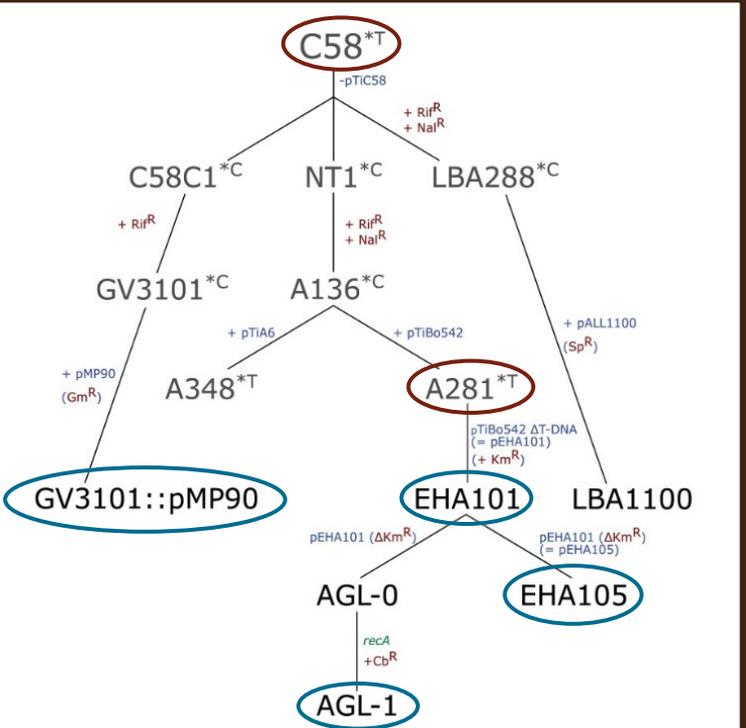
SKWB24-2, SLMB28-1, Nisqually-1

Poor DNA delivery, strong defense responses, and difficult regeneration are common themes in our species

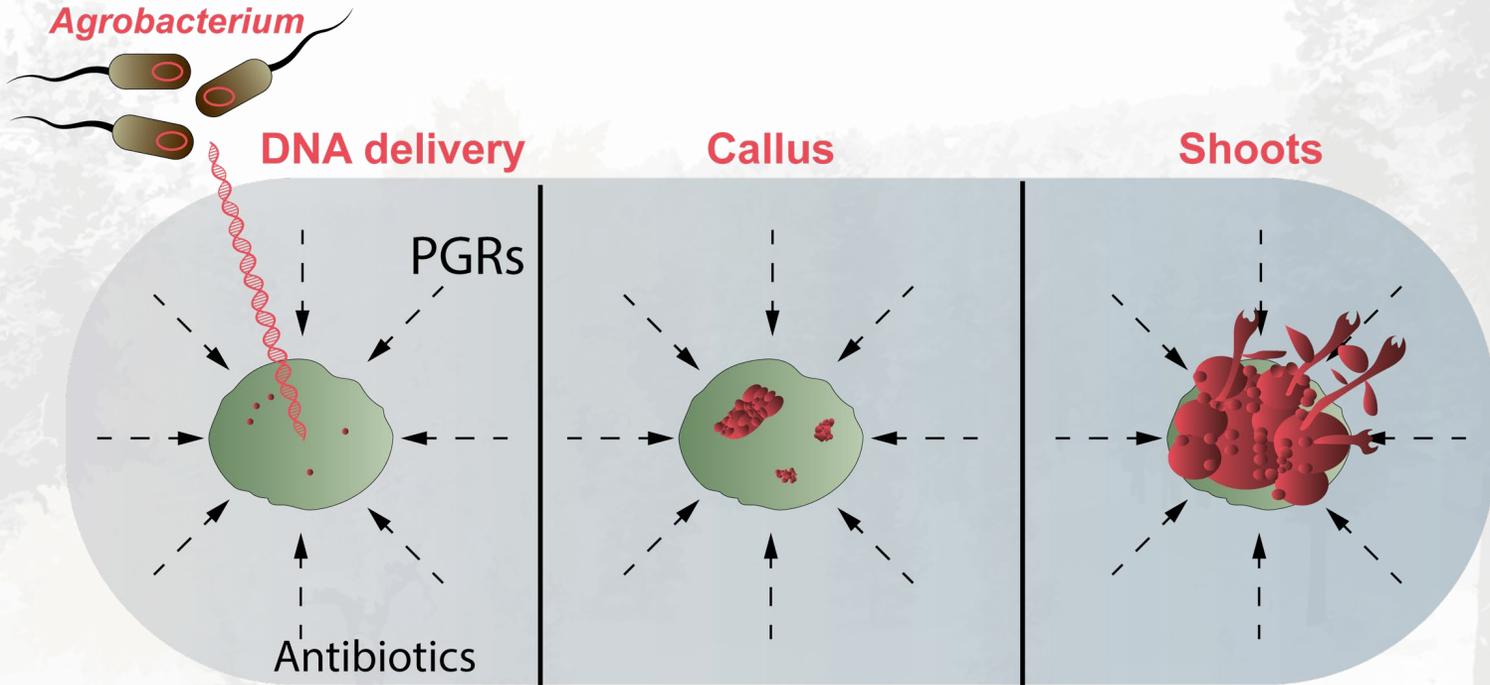
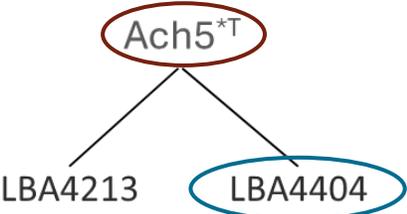


- Elite clones, not seed-derived
- High heterozygosity: each genotype a new adventure in culture
- High physiological diversity and common defense responses

AMT remains the most common method – but little has changed in the 30-40 years since these first lab strains were made



Adapted from De Saeger et al. (2021)



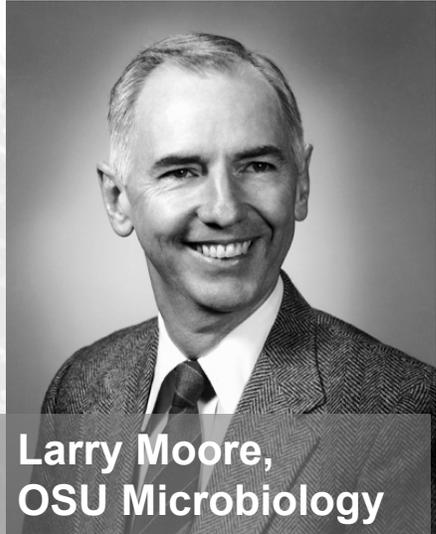
Are there better strains out there?

How do we survey most efficiently?

How do we turn new strains into laboratory tools?

Local history of *Agrobacterium* research enabled this project

Agro strains and molecular biology



Larry Moore,
OSU Microbiology

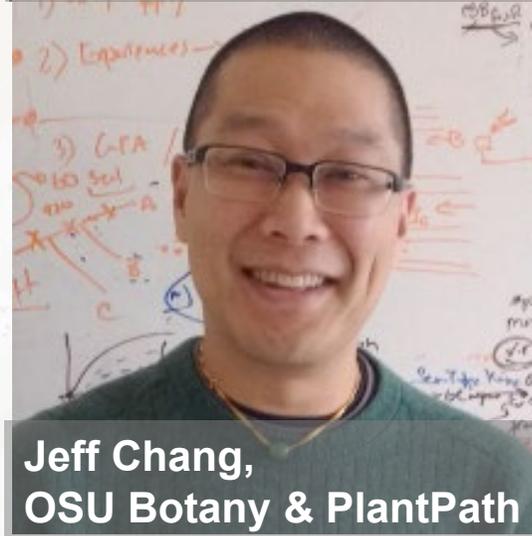


Walt Ream,
OSU Microbiology

Strain genomics

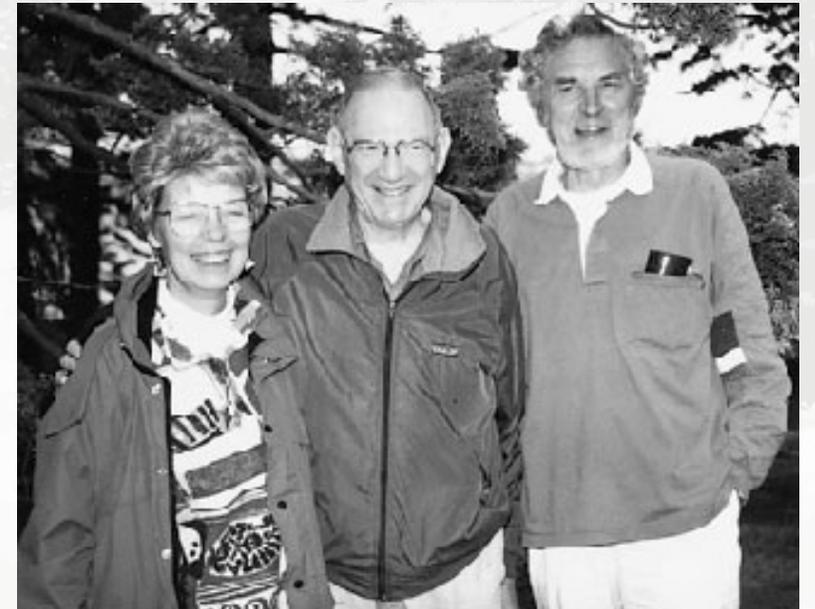


Alex Weisberg,
OSU Botany & PlantPath



Jeff Chang,
OSU Botany & PlantPath

Early disarmed and intermediate strains (UW)



Mary-Dell
Chilton

Milton
Gordon

Eugene
Nester



Melodie Putnam, OSU Plant Clinic

Local history of *Agrobacterium* research enabled this project

Efficacy of different *Agrobacterium tumefaciens* strains in transformation of pinaceous gymnosperms

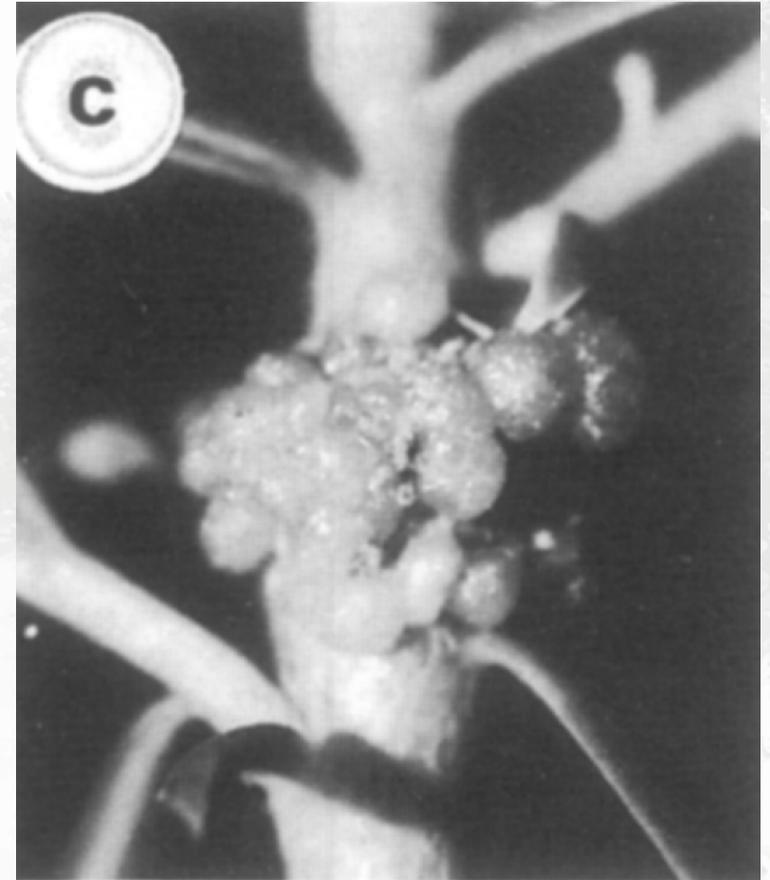
JOHN W. MORRIS§, LINDA A. CASTLE and ROY O. MORRIS†*

Department of Biochemistry, 322 Chemistry Building, University of Missouri-Columbia, Columbia MO 65211, U.S.A.;

† Departments of Forest Science and Agricultural Chemistry, Oregon State University, Corvallis, Oregon 97331, U.S.A.

(Accepted for publication October 1988)

	Host				Opine	Plant origin	Reference
	<i>Pseudotsuga</i>	<i>Pinus</i>	<i>Tsuga</i>	<i>Abies</i>			
<i>Agrobacterium tumefaciens</i>							
15955	20	0	20	21	oct	<i>Lycopersicon</i>	25
3667	100	25	65	70	nop	<i>Rosa</i>	33
A6	10	0	25	32	oct	<i>Rubus</i>	25
Ach5	40	0	25	53	oct	<i>Prunus</i>	17
Ach5C3	0	0	0	0	none		14
B1/74	85	30	75	85	nop	<i>Prunus</i>	1
B234	75	40	20	70	nop	unknown	1
B3/73	100	30	70	90	nop	<i>Acer</i>	1
B4/73	40	35	55	75	nop	<i>Acer</i>	1
C2/74	80	60	50	70	nop	<i>Prunus</i>	1
C58	25	9	7	29	nop	<i>Prunus</i>	25



Induced gall (strain B3/73) on Douglas fir seedling

A fully sequenced public collection of diverse *Agrobacterium* is the main resource for our study

RESEARCH

RESEARCH ARTICLE SUMMARY

PLASMID EVOLUTION

Unexpected conservation and global transmission of agrobacterial virulence plasmids

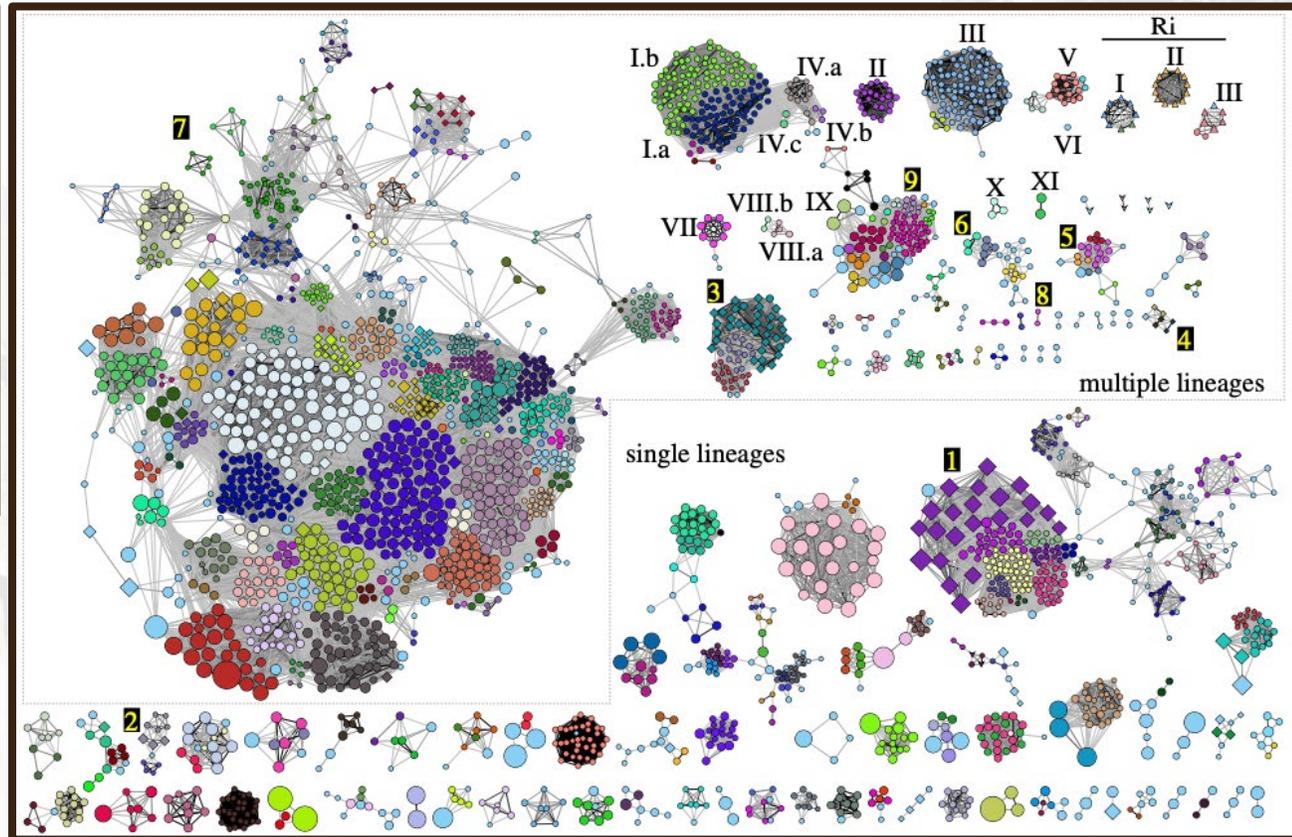
Alexandra J. Weisberg, Edward W. Davis II, Javier Tabima, Michael S. Belcher, Marilyn Miller, Chih-Horng Kuo, Joyce E. Loper, Niklaus J. Grünwald, Melodie L. Putnam, Jeff H. Chang*

Diversification of plasmids in a genus of pathogenic and nitrogen-fixing bacteria

Alexandra J. Weisberg¹, Marilyn Miller¹, Walt Ream², Niklaus J. Grünwald³ and Jeff H. Chang¹

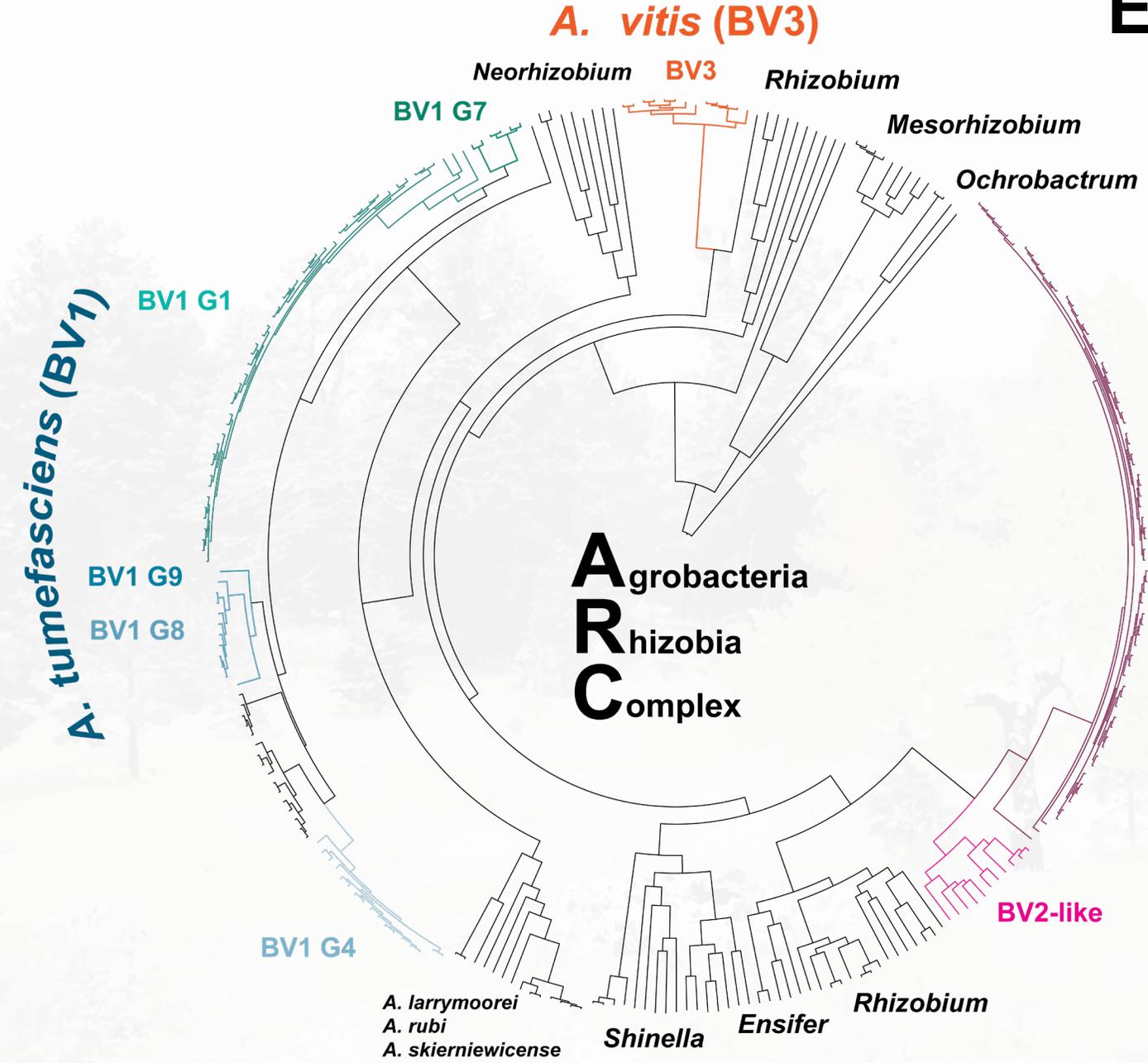
¹Department of Botany and Plant Pathology, and ²Department of Microbiology, Oregon State University, Corvallis, OR 97331, USA

³Horticultural Crops Research Laboratory, United States Department of Agriculture and Agricultural Research Service, Corvallis, OR 97330, USA



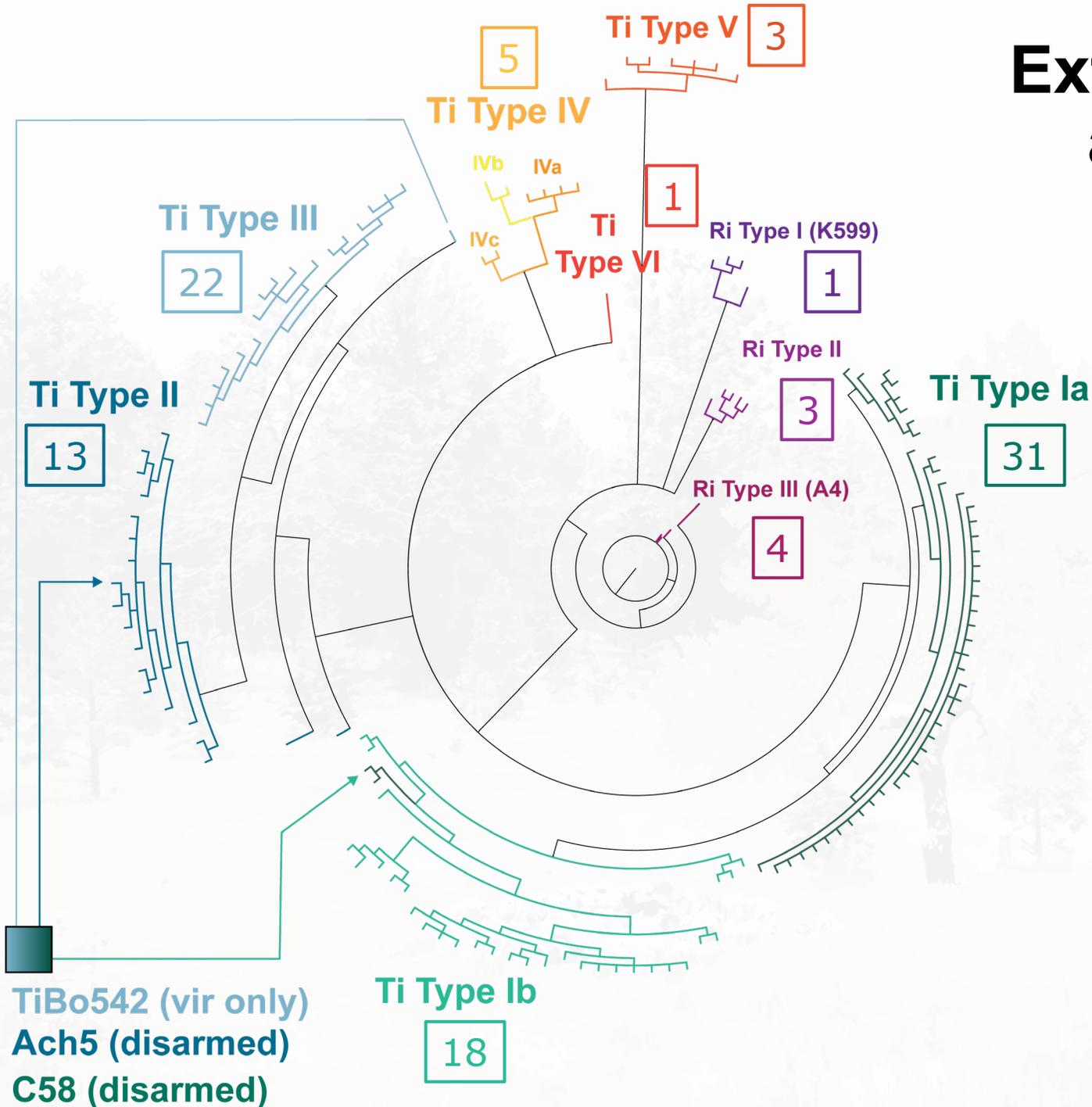
Complex network of accessory plasmids in *Agrobacteria* and *Rhizobia* species (From Weisberg et al. 2021 *Phil. Trans. R. Soc. B*)

Extensive collection diversity at the chromosomal level



- At least ten species-level taxonomic groups based on sequence
- Parasitic (+Ti/Ri) strains are paraphyletic
- Biovar 2 (*A. rhizogenes*) have had a recent evolutionary bottleneck (~2mya)
- Related ARC species can be used for transformation if Ti/Ri is introduced

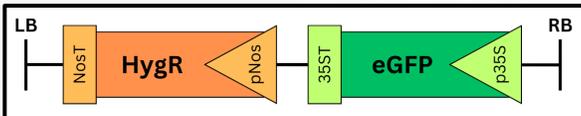
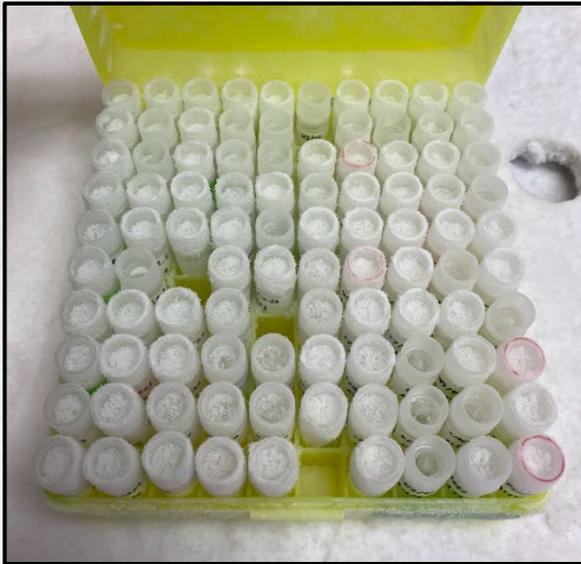
Extensive collection diversity at the Ti/Ri plasmid level



- Plasmids include DNA transfer machinery and T-DNA region (crown gall plant hormone genes)
- Most types can be biovar 1 (*tumefasciens*) or biovar 2 (*rhizogenes*)
- Strains isolated from diverse dicots, with type II and type III Ti more likely to be herbaceous than woody
- Ri plasmid diversity underrepresented in public collections

We used a high throughput phenomics platform to quantify transformation and regeneration using wild strains

Insert binary vector



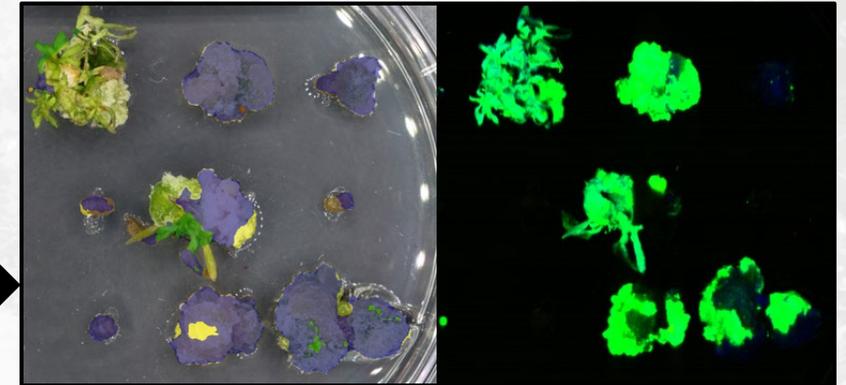
Kanamycin selection for binary plasmid in Agro

Transform plants



- Hybrid poplar (*easiest*)
- Black cottonwood (*moderate/hard*)
- Eucalyptus (*hard*)

Phenomics Analysis



- Transgenic tissue
- Regeneration
- Browning

Screening was performed using a two-stage strategy



Hybrid Poplar
Populus tremula x alba 717-1B4

Stage I

100 strains

Low replication
(3 plates)

No plant hormones

Minimal selection
(Hygromycin)

3w 7w 10w



- Transgenic tissue
- Regeneration
- Browning

Stage II

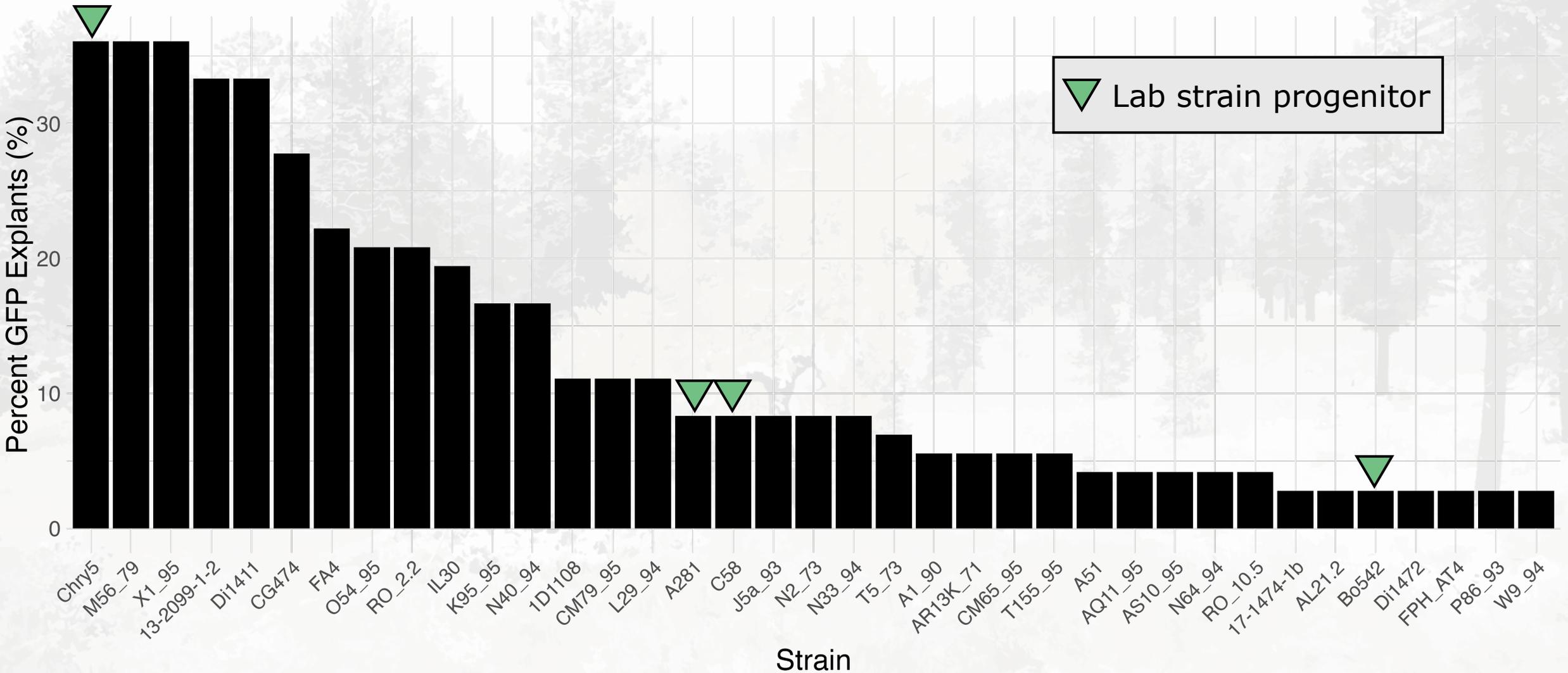
Repeat in other species
or treatment conditions

30 strains
high replication
(10 plates)

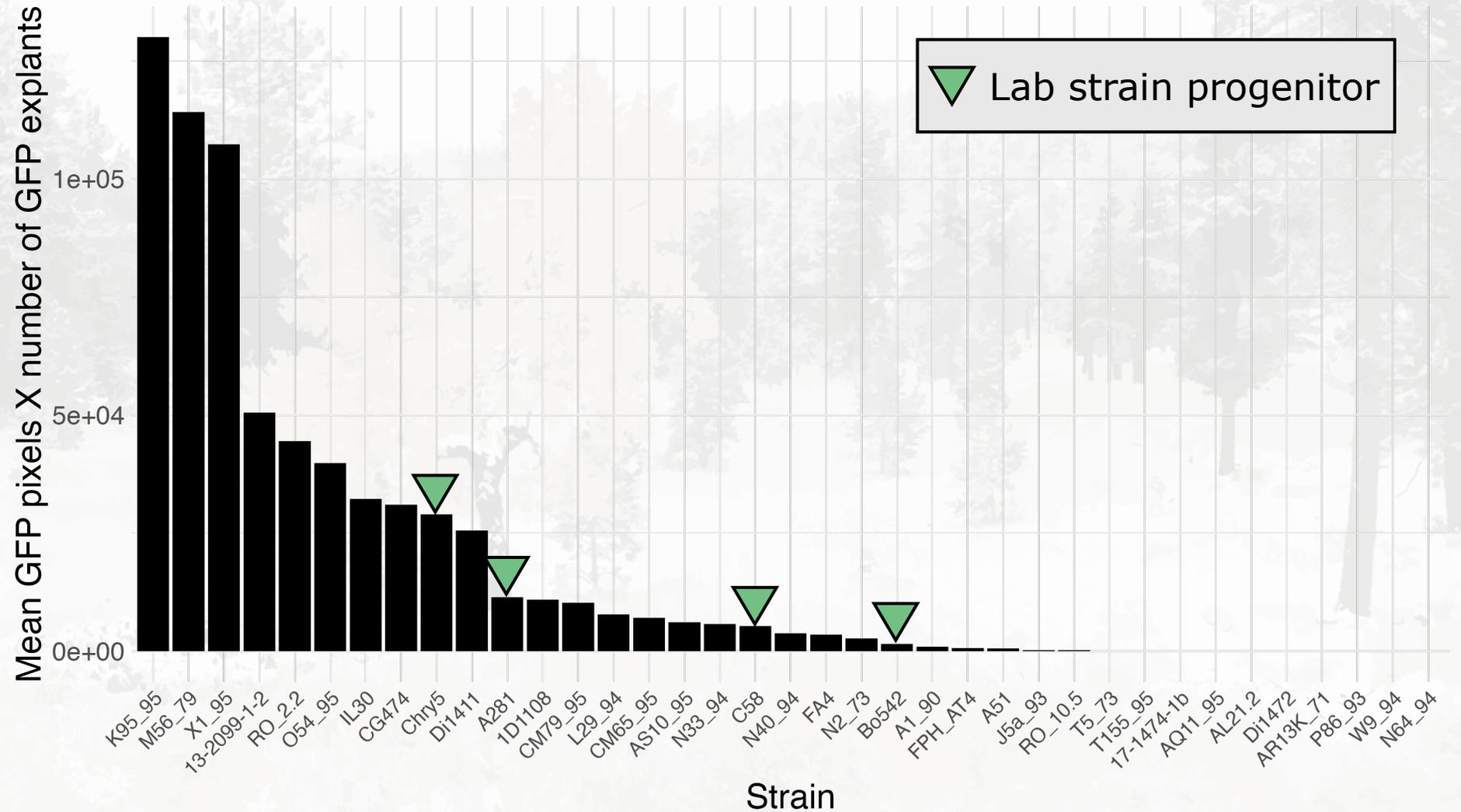
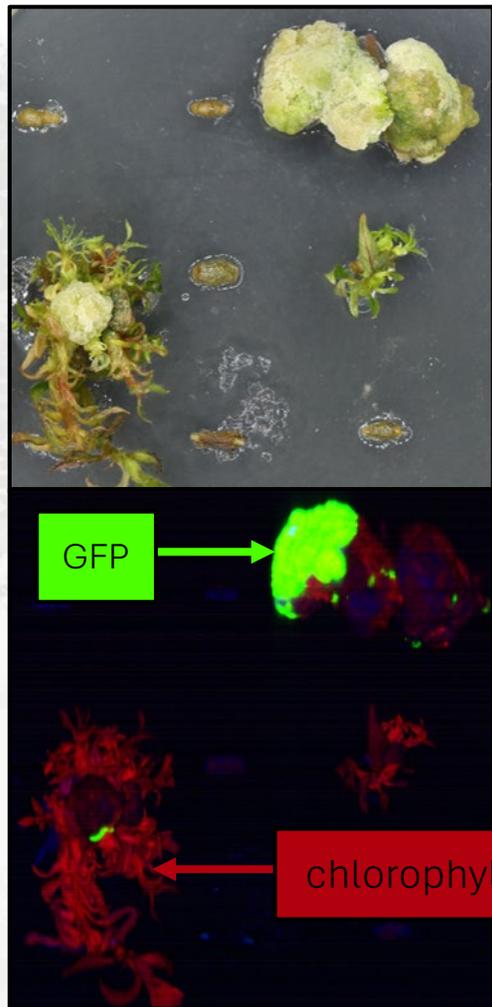
Select:
20 good strains
10 bad* strains

(*bad strains retained for mechanistic insight)

Many wild strains in our initial screens were competent transformers compared to lab strain progenitors

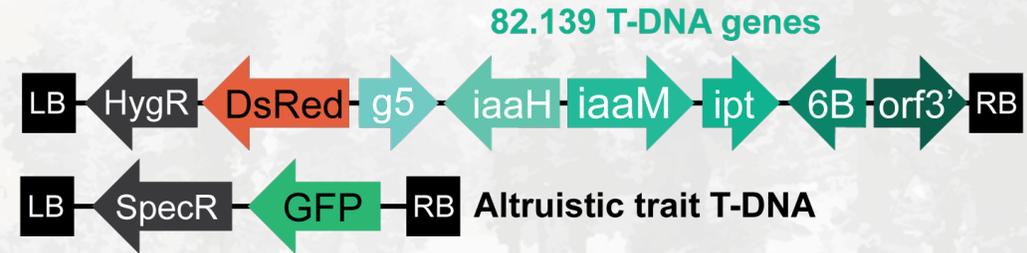
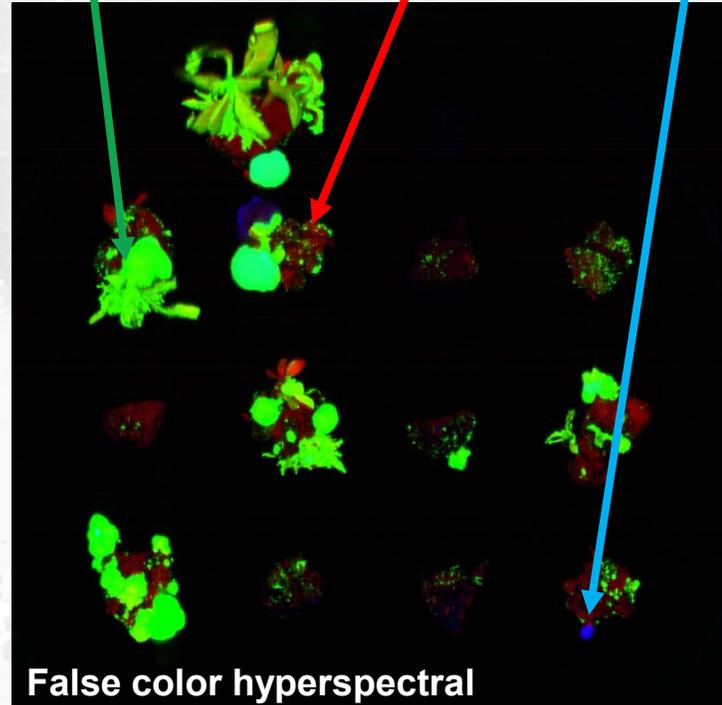
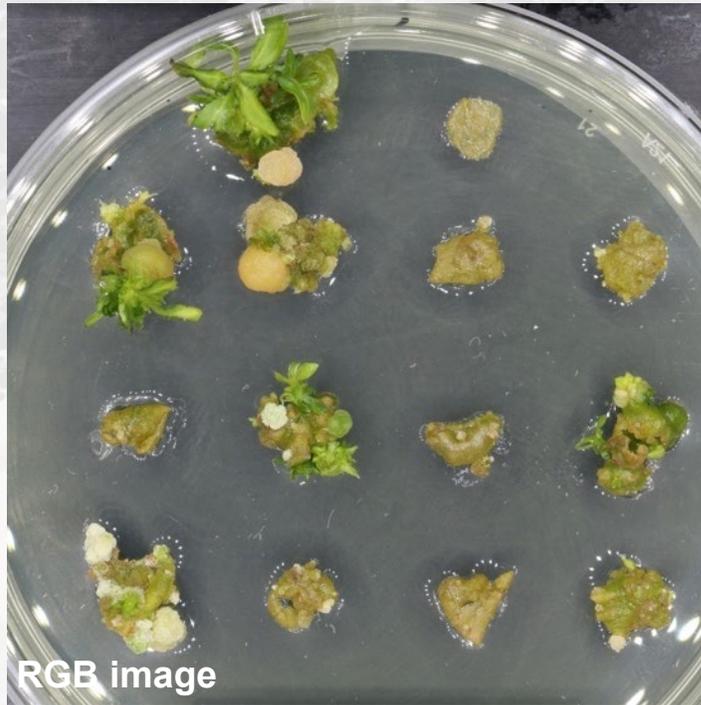


We are cautious about using transgenic callus area phenotypes, as gall size is highly variable among strains



We are also interested in passive “shooty” regeneration behavior as a tool using a co-transformation approach

GFP (Trait T-DNA) Chlorophyll DsRed (Agro T-DNA)



Plant Biotechnology Journal



Plant Biotechnology Journal (2025) 23, pp. 3841–3850

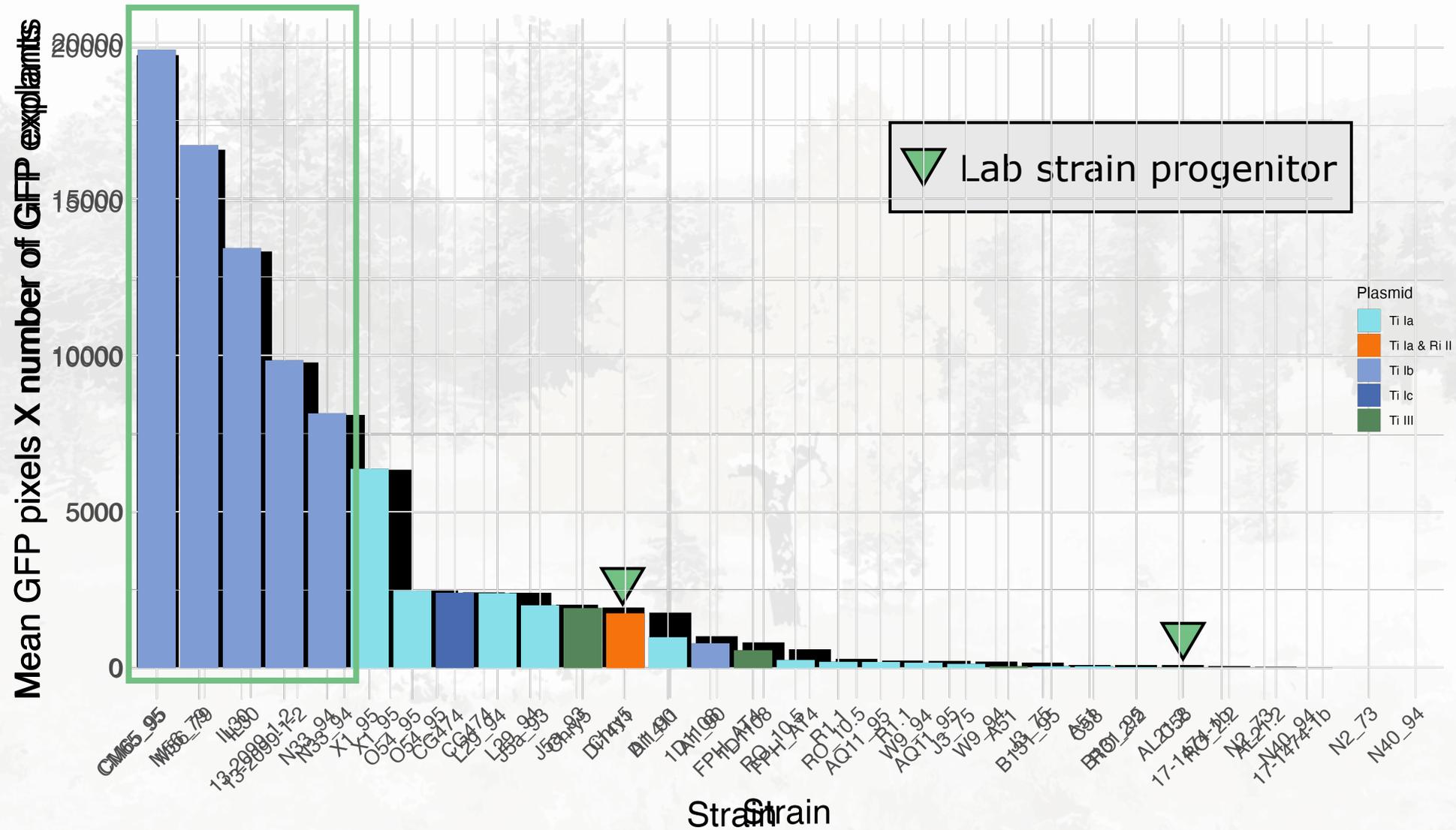
doi: 10.1111/pbi.70159

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* 

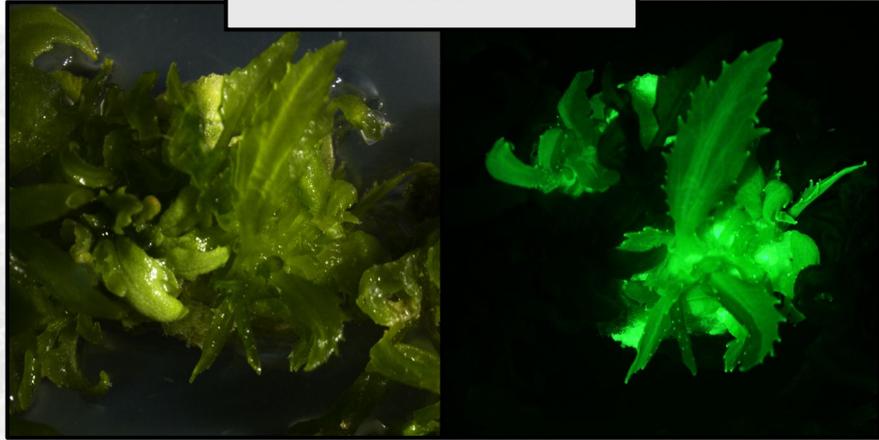
Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon, USA

Some wild strains spur transgenic shoot regeneration in the absence of exogenous hormones

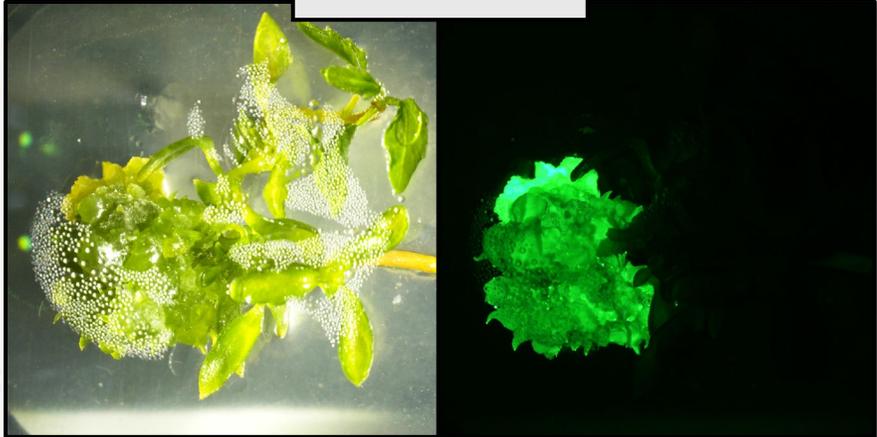


Ti plasmid type 1b was the most efficient at transgenic shoot formation

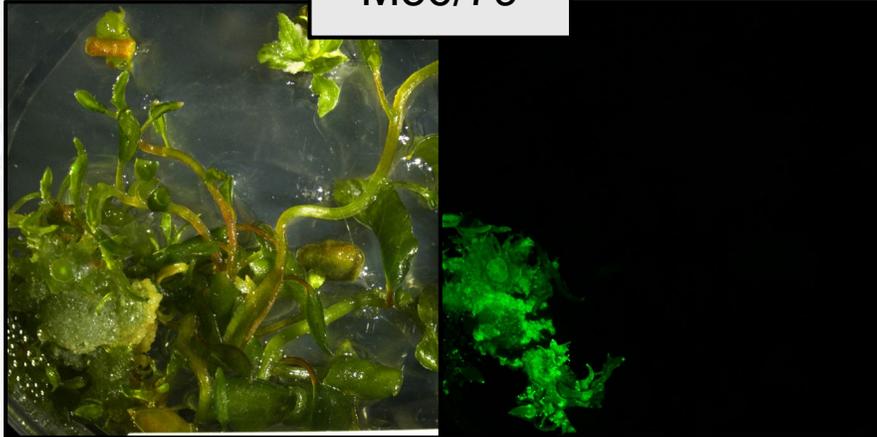
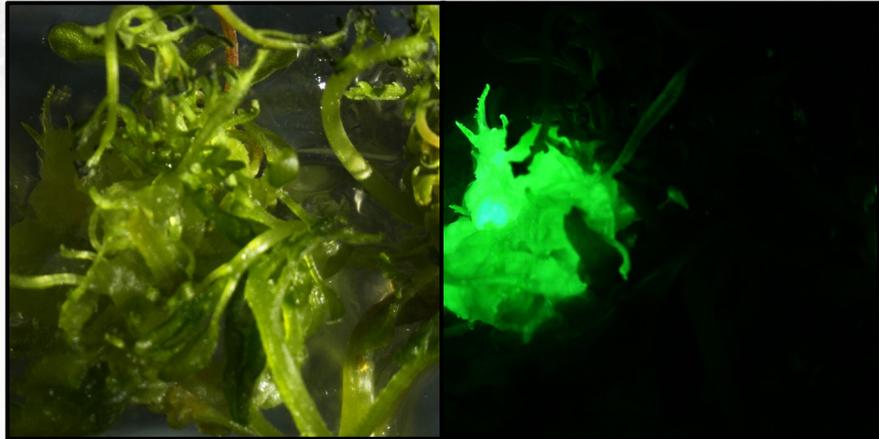
13-2099-1-2

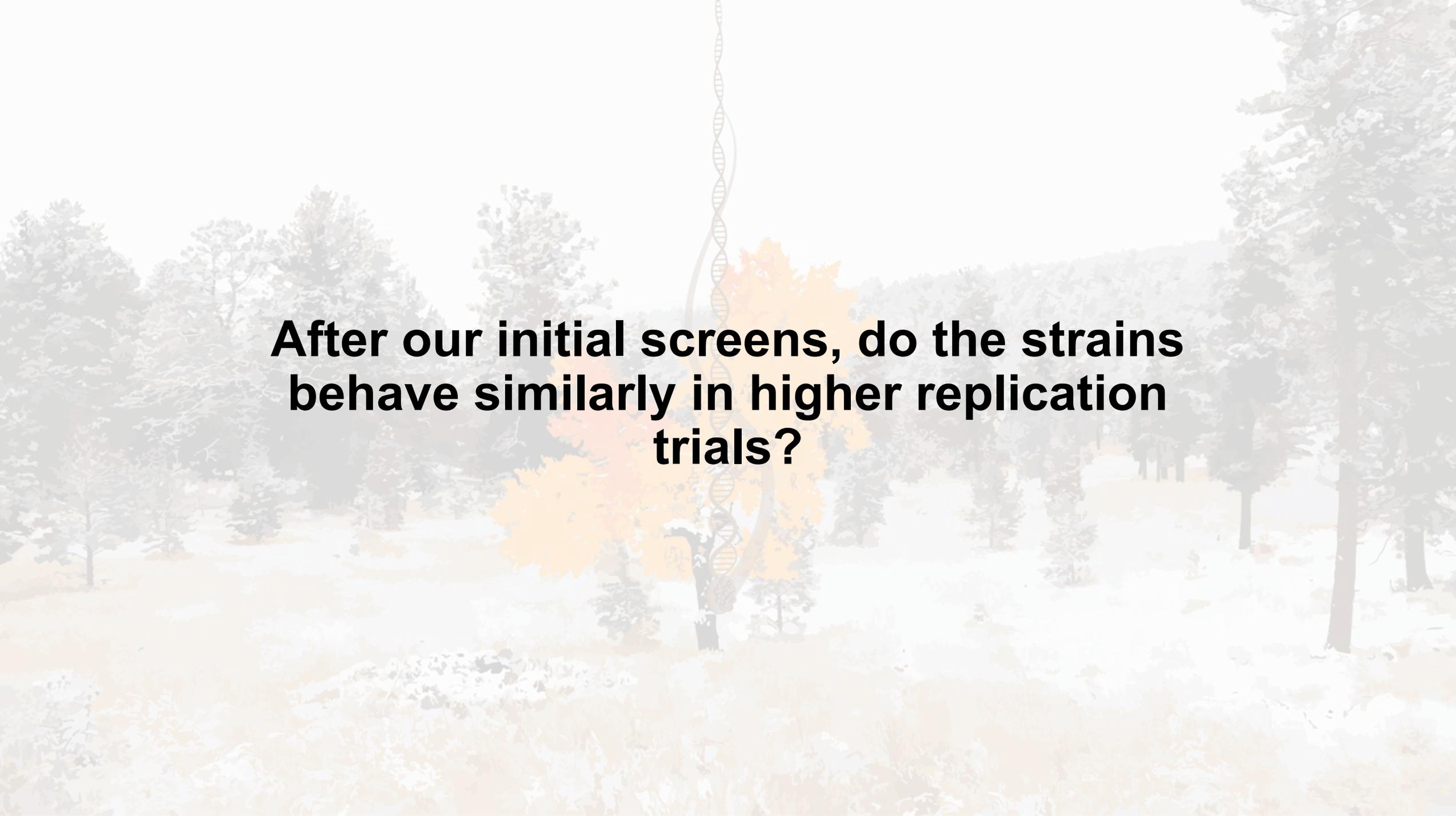


CM65/95



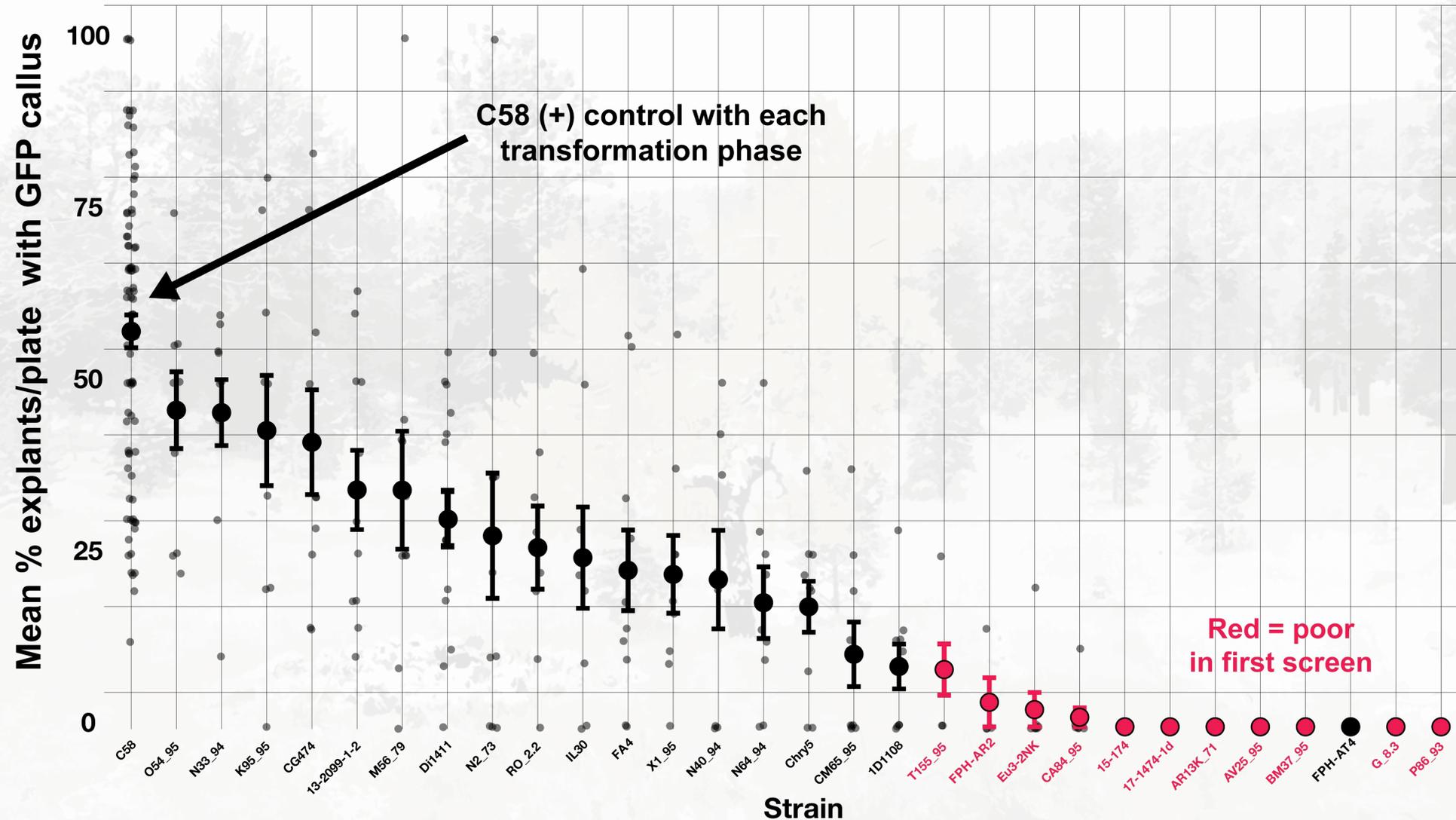
M56/79



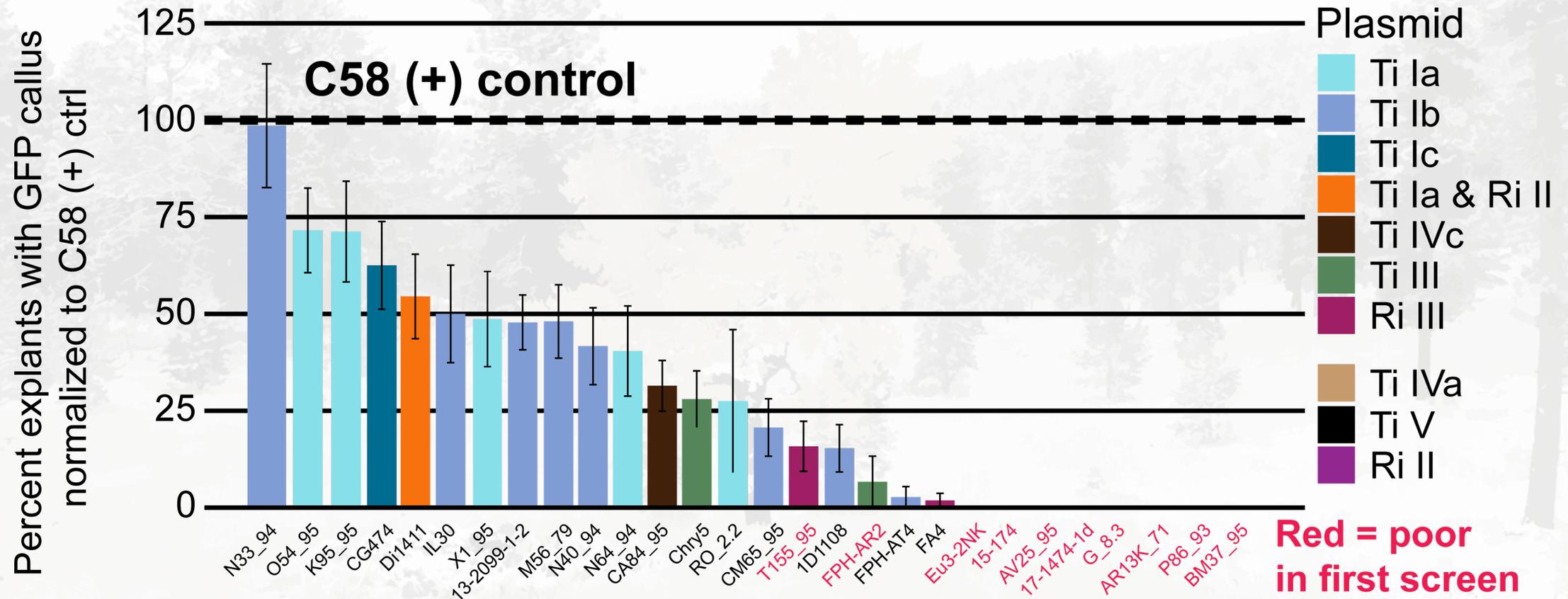
The background features a soft-focus landscape of a forest with various trees. A vertical DNA double helix is positioned in the center, extending from the top to the bottom. A tree with bright orange and yellow autumn foliage is also centered, partially overlapping the DNA helix. The overall scene is dimly lit, with a pale, hazy sky.

**After our initial screens, do the strains
behave similarly in higher replication
trials?**

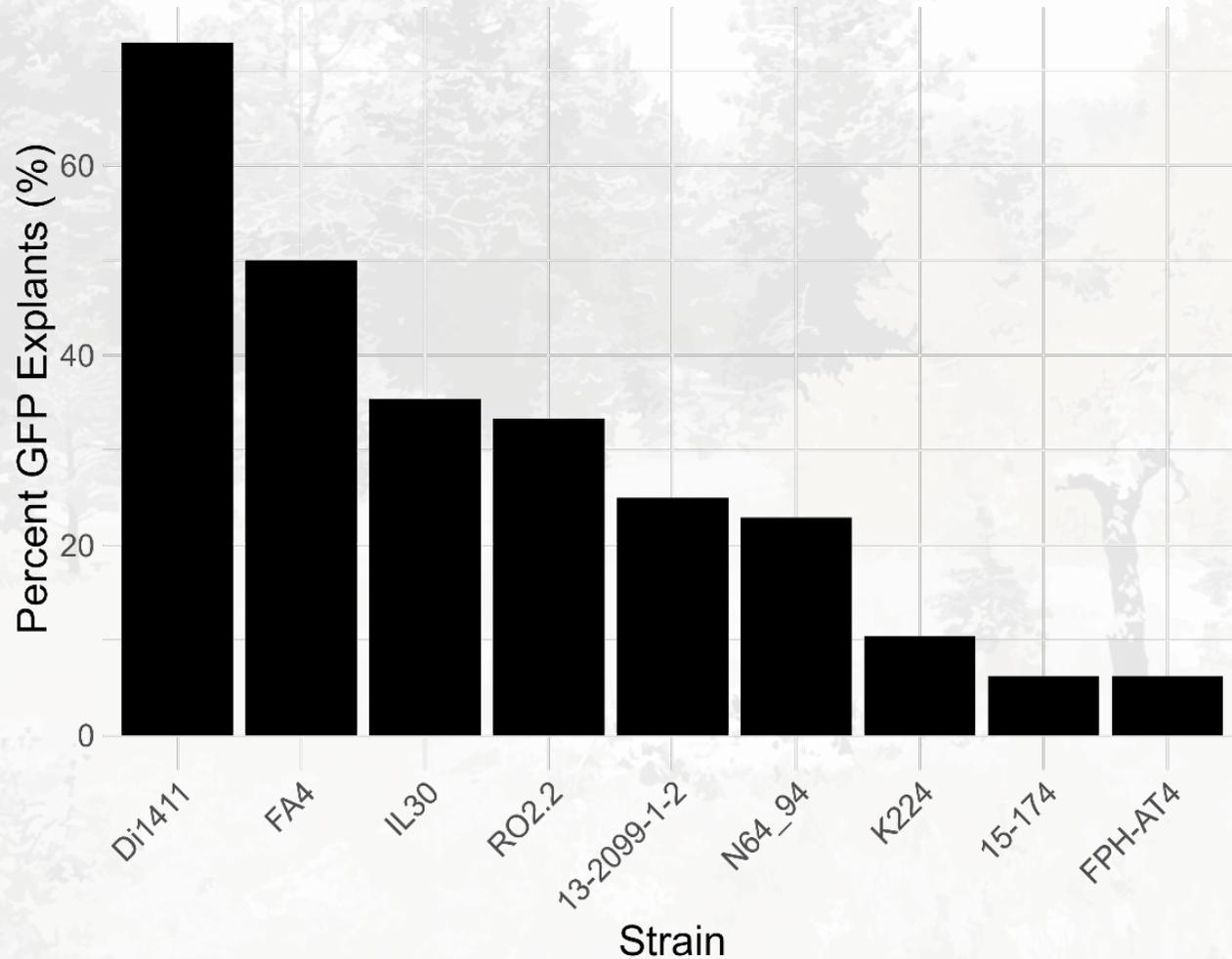
Higher replication trials show consistent behavior in hybrid poplar, though C58 outperformed other strains



Strains from several Ti/Ri backgrounds and chromosomal groups show high rates of TG callus production

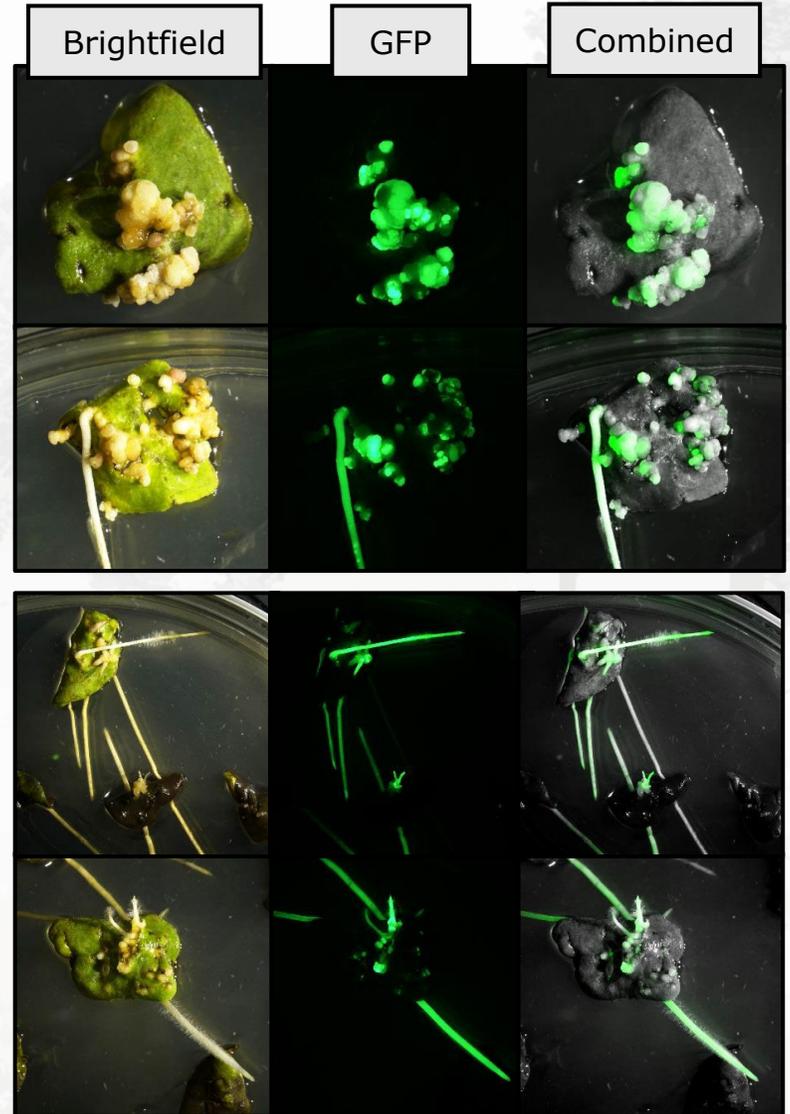


Wild strains show potential for transgenic tissue development in other recalcitrant species including *Eucalyptus*



Di1411

FA4



Collecting is never finished!

When opportunity strikes are also isolating new strains



Galls among stand of interior Douglas fir in Uinta-Wasatch Cache National Forest (*No strain isolated*)



Michele Wiseman
PhD Candidate
Gent Lab
OSU Bot&PP

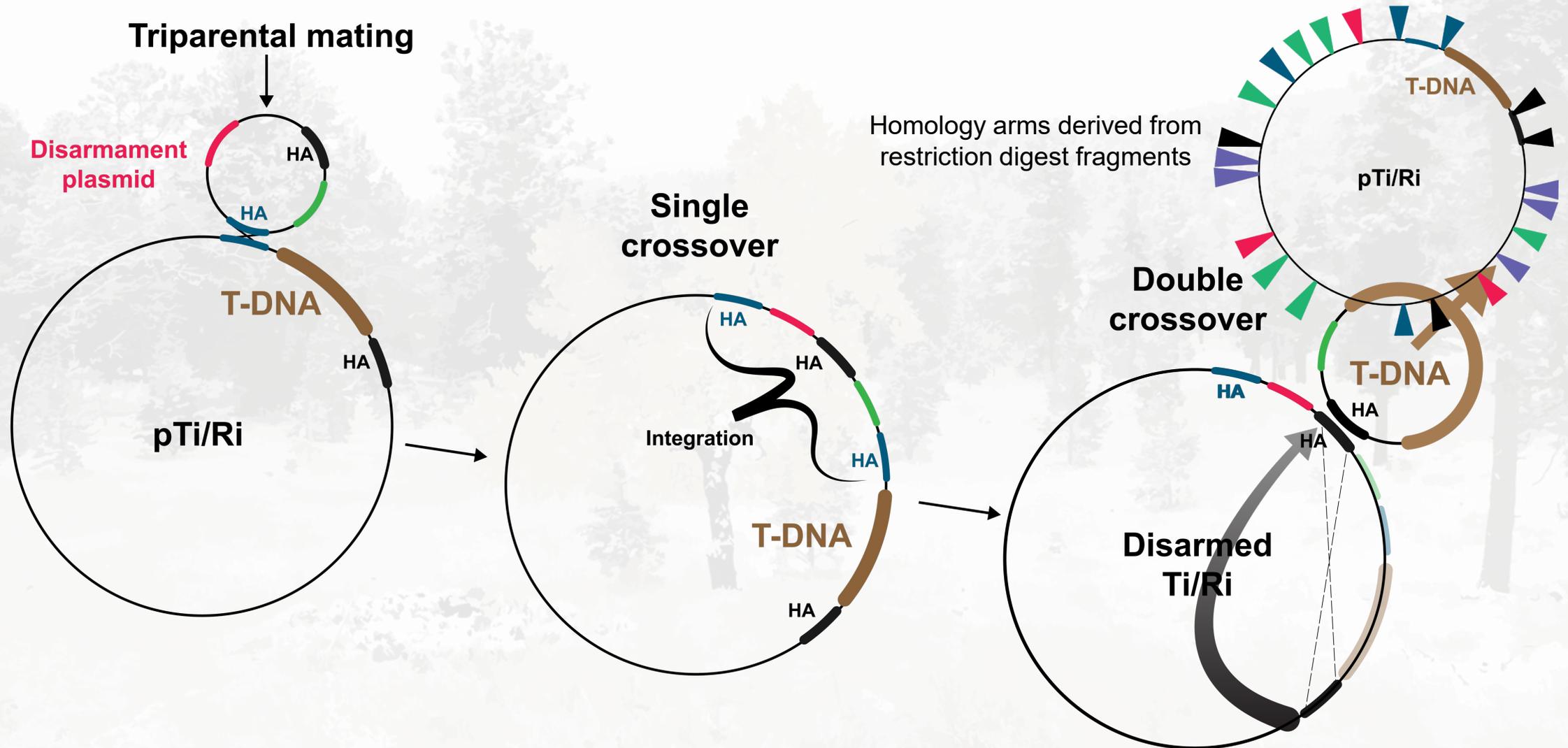


We were able to isolate a strain (BV1, Ti type Ia) from a hop gall

A landscape photograph of a forest with a DNA double helix and a tree overlay. The DNA helix is a vertical line with a double helix structure, positioned in the center of the image. A tree with yellow and orange leaves is overlaid on the DNA helix. The background is a landscape with a field of yellow and orange grasses in the foreground, a line of trees in the middle ground, and a hazy sky in the background. The overall color palette is warm and muted, with a lot of yellow, orange, and brown tones.

How best to disarm and engineer promising strains?

Conventional *Agrobacterium* disarmament

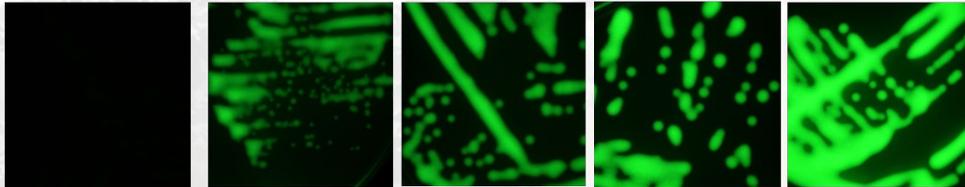


We used conventional strategies with modern cloning tools

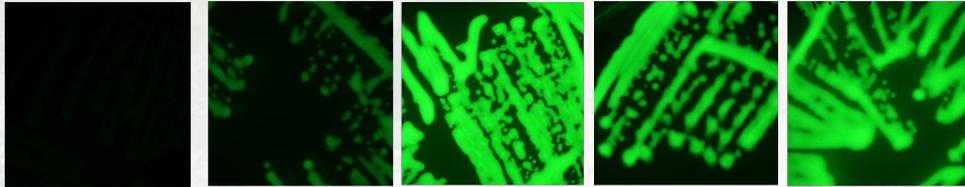
E. coli
standard
promoter

Agrobacterium
expression elements

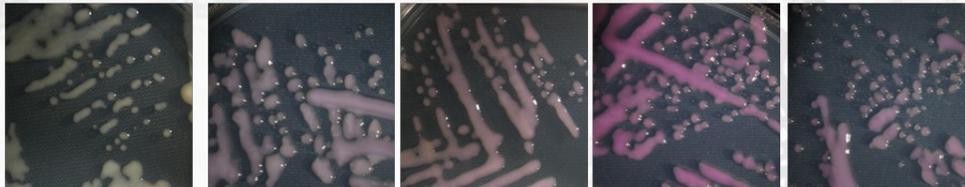
AGL1



CM65/95



AGL1



CM65/95



sfGFP

- Electroporation rather than mating
- Visualize crossover recombination outcomes
- Counterselection to remove plasmids
- Recombinases to remove residual components or markers after disarmament

eforRed



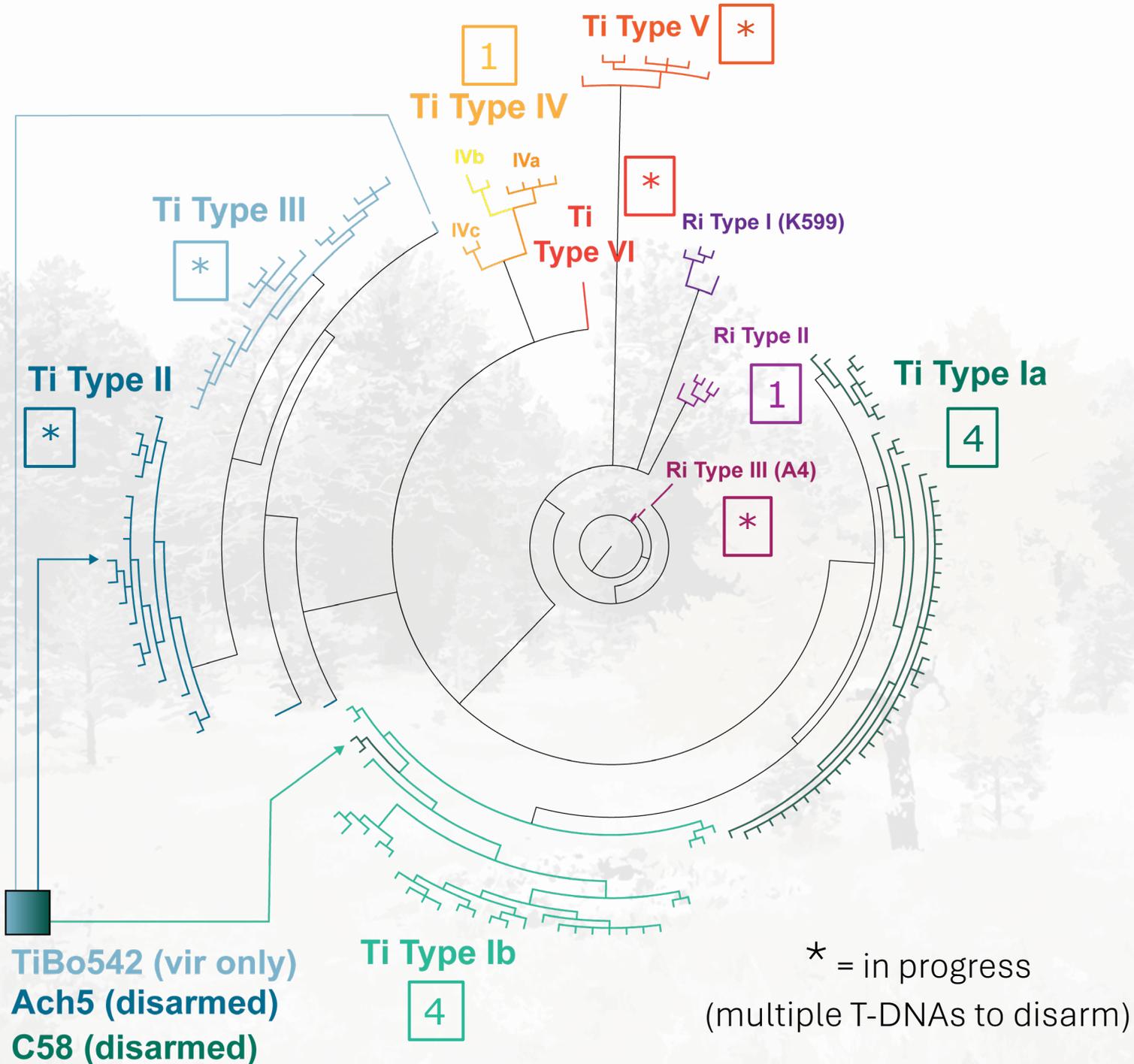
Bethani Sutliff
Undergraduate
researcher



Chris Willig
Postdoc

**We have so far
disarmed 10 strains
using this approach**

**...with more complex
edits coming soon**

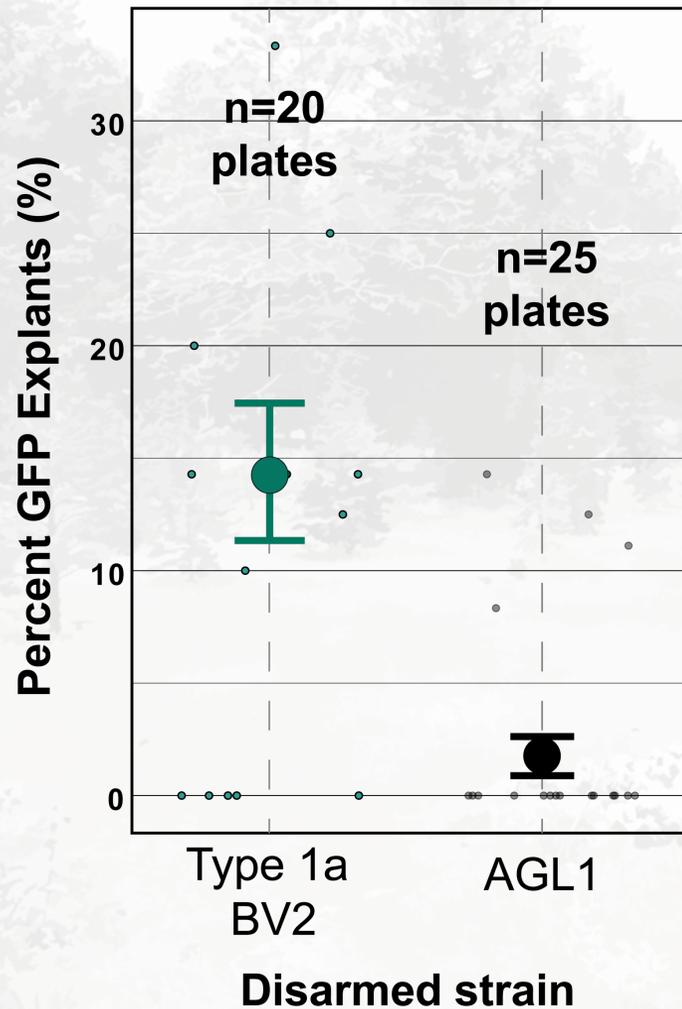


Zachary Heinhold
PhD student

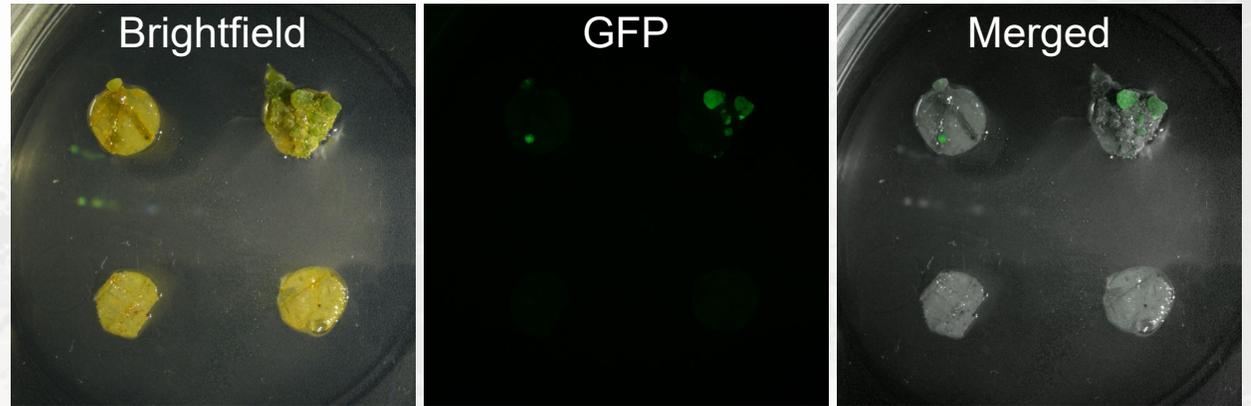


Chris Willig
Postdoc

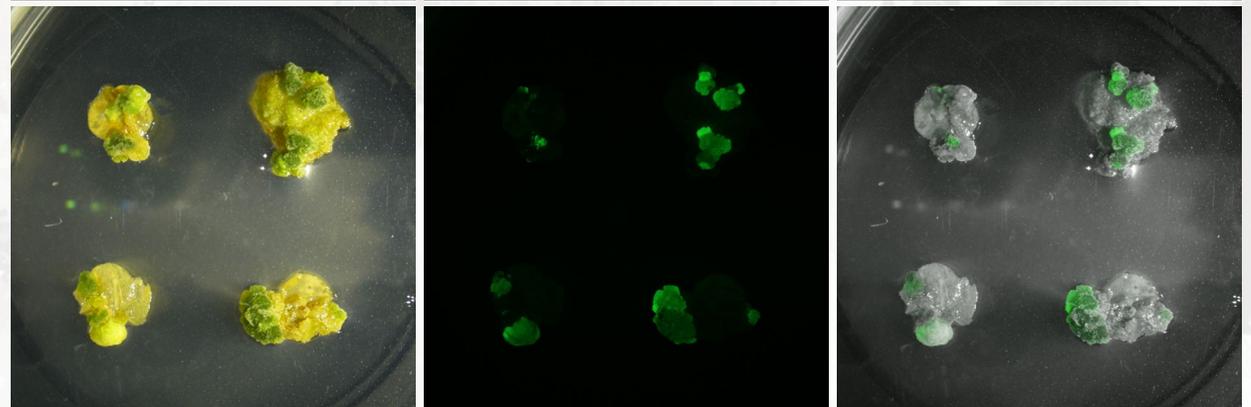
Initial testing of a disarmed Ti type 1a (BV2) against the AGL1 lab strain showed improved transformation in poplar



AGL1



T1aBV2



Summary:

Genomics and modern cloning tools make strain discovery and engineering simple compared to a few years ago

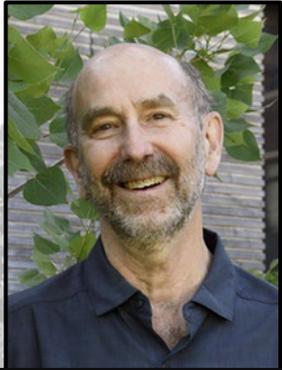
- 40% of strains had any transformation, leaving 10-20% as candidates for strain engineering
- Higher replication studies in 717 show consistent strain behavior
- Some wild strains show improved traits (browning, TG callus) in other species
- Disarmament using classical approaches but with modern amenities is efficient and simple

Next steps:

Is having more diverse lab strains useful?

- Testing in a wider variety of plant species
 - *Populus tremula x tremuloides* (353-53) with 100 strain panel
 - Systematic tests in eucalypts and hops
 - Coordinating with other groups to test in other species
- Measuring virulence gene expression when exposed to different plant species and their exudates (Jeff Anderson, OSU Botany & PP)
- Using disarmed and Ti/Ri swapped strains to understand chromosome vs. plasmid contribution to plant transformation
- Using "shooty" T-DNA genes as morphogens to improve regeneration

Acknowledgements



Steve Strauss
Professor FES



Cathleen Ma
Transformation &
Greenhouse
Experiments



Kate Peremyslova
Transformation
Experiments



Zachary Heinhold
PhD student



Chris Willig
Postdoc



Jeff Anderson
Associate Professor BPP

Forest Biotechnology Lab

Colette Richter (FRA)
Parker Wheeler (FRA)
Dylan Gregory (BPP Anderson Lab)
Bethani Sutliff (Undergraduate)
Jay Adams (Undergraduate)
Michael Nagle (LIBD)
Anthony Marroquin (Greenhouse Manager)
Dana Howe (Lab Manager)



Alexandra Weisberg (Assistant Professor BPP)

This work is supported by the U.S. National Science Foundation - Plant Genome Research Project (award no. 2424938), the GREAT Trees Cooperative & by the Wessela Graduate Fellowship at Oregon State University



Oregon State
University



2026 IN VITRO BIOLOGY MEETING
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PLANT AND ANIMAL BIOTECHNOLOGY AND GENOMICS



Dr. Indra K. Vasil, PhD

*A Witness to the History of Plant
Biotechnology in the SIVB*



PROGRAM

Dr. Delia R. Bethell, PhD

*The Society for In Vitro Biology, 80
Years of Commitment to the Teaching
and Standardization of the Science of
In Vitro Cell and Tissue Culture*



REGISTER

Join us for this once-in-a-lifetime scientific event!



A landscape with a DNA helix and a tree with autumn leaves. The background is a soft-focus scene of a field with scattered trees, some with vibrant autumn foliage in shades of orange and yellow, and others in muted greens and greys. A vertical DNA double helix structure is superimposed over the center of the image, extending from the top to the bottom. The text "Thank you for listening!" is centered in the lower half of the image.

Thank you for listening!