



**Exploring the
Agrobacterium genome
to facilitate *in planta*
transformation**

*Greg Goralogia
and Steve Strauss*

*OSU College of
Forestry*



Oregon State
University

Agenda

1. Perspectives & experimental system
2. Hopes and approaches for tissue culture-free “*in planta*” transformation
3. Surveying wild *Agrobacterium* strains for novel morphogenic capability

Regeneration & transformation continue to be major limiting factors for gene editing & engineering in plants, and especially trees

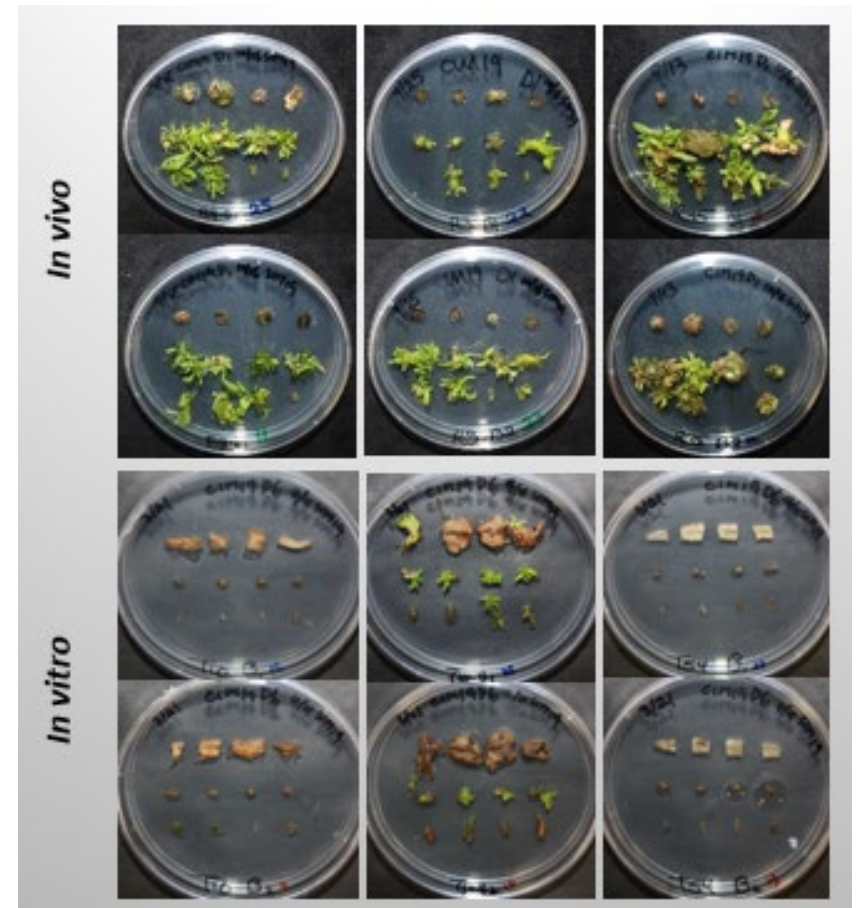
- Species and genotypic differences often dramatic
- Slow, costly, complex customization efforts usually needed
- On top of often large social/regulatory constraints, often a “deal breaker”



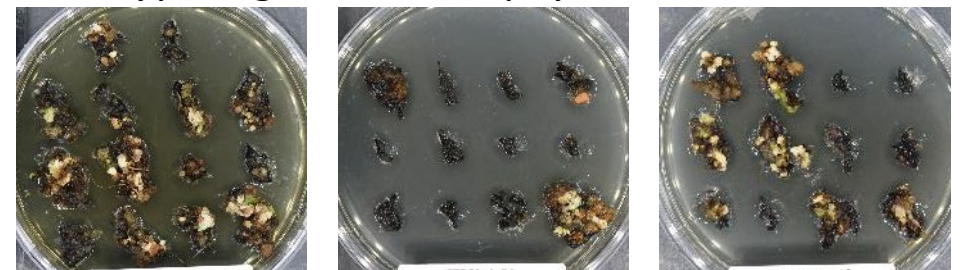
Our experimental system features

- Woody (forest) trees
- Elite clones, not seed-derived
- High physiological diversity
 - Growth environment, age, explant type and source
- Great tissue sample heterogeneity
- Common necrotic responses
- Very high genetic diversity of forest trees

Populus trichocarpa



Eucalyptus grandis x urophylla

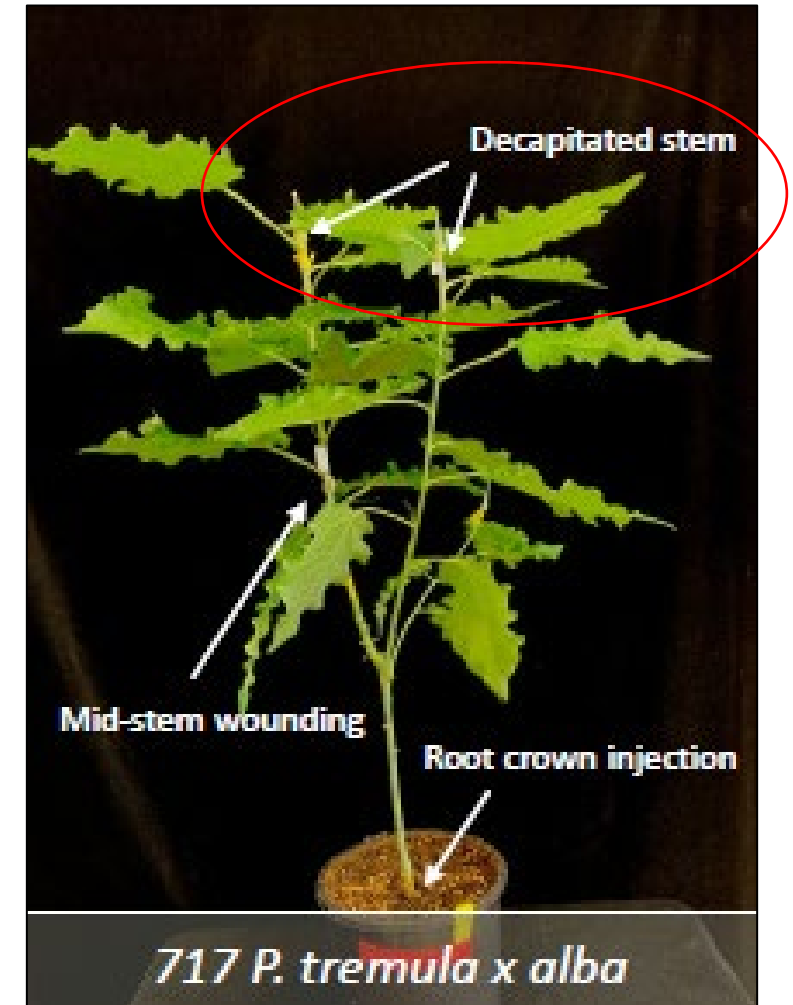


Agenda

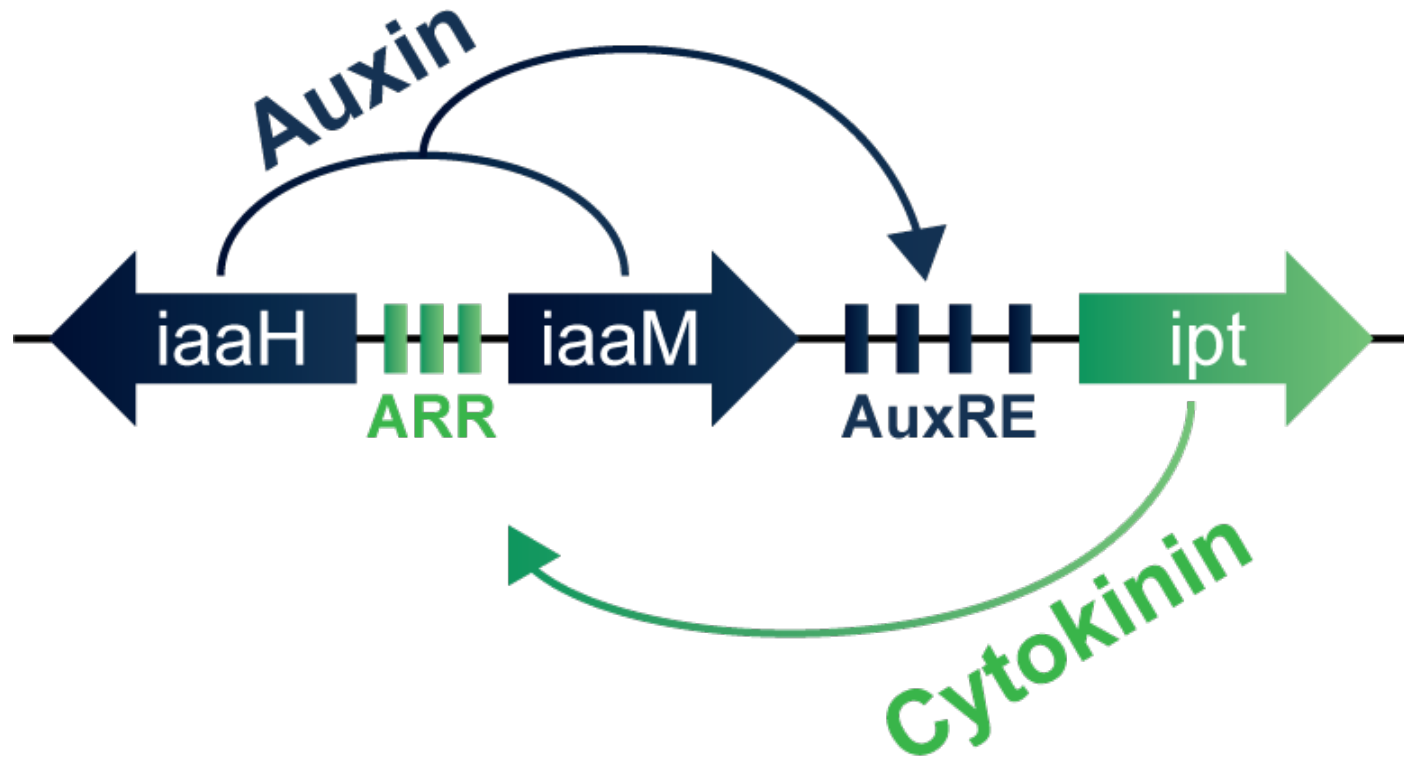
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In planta transformation of great interest

- Lower cost in media, facilities?
- Reduced customization efforts?
- Less specialized personnel could do it?
- Less genotype-dependent?
- DEV genes can help?

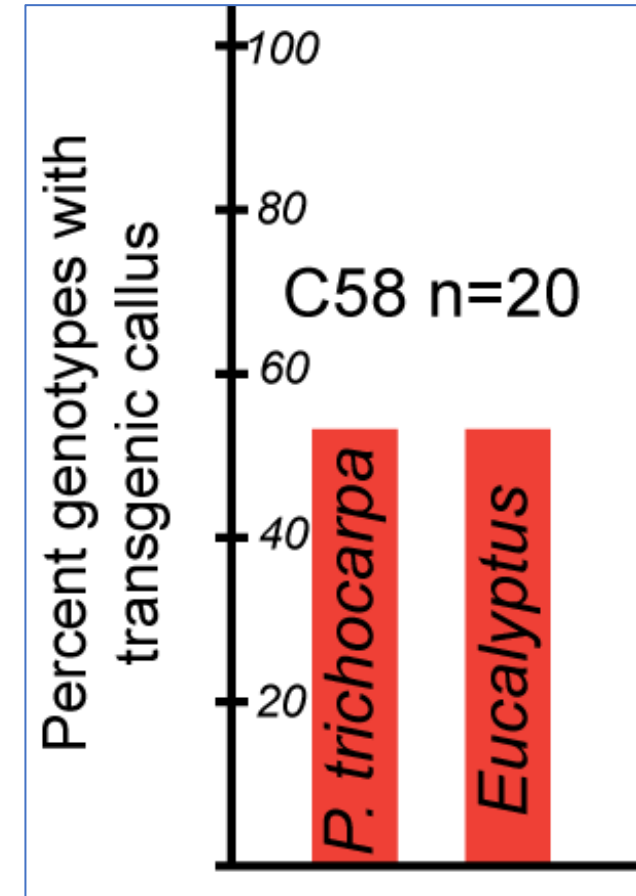
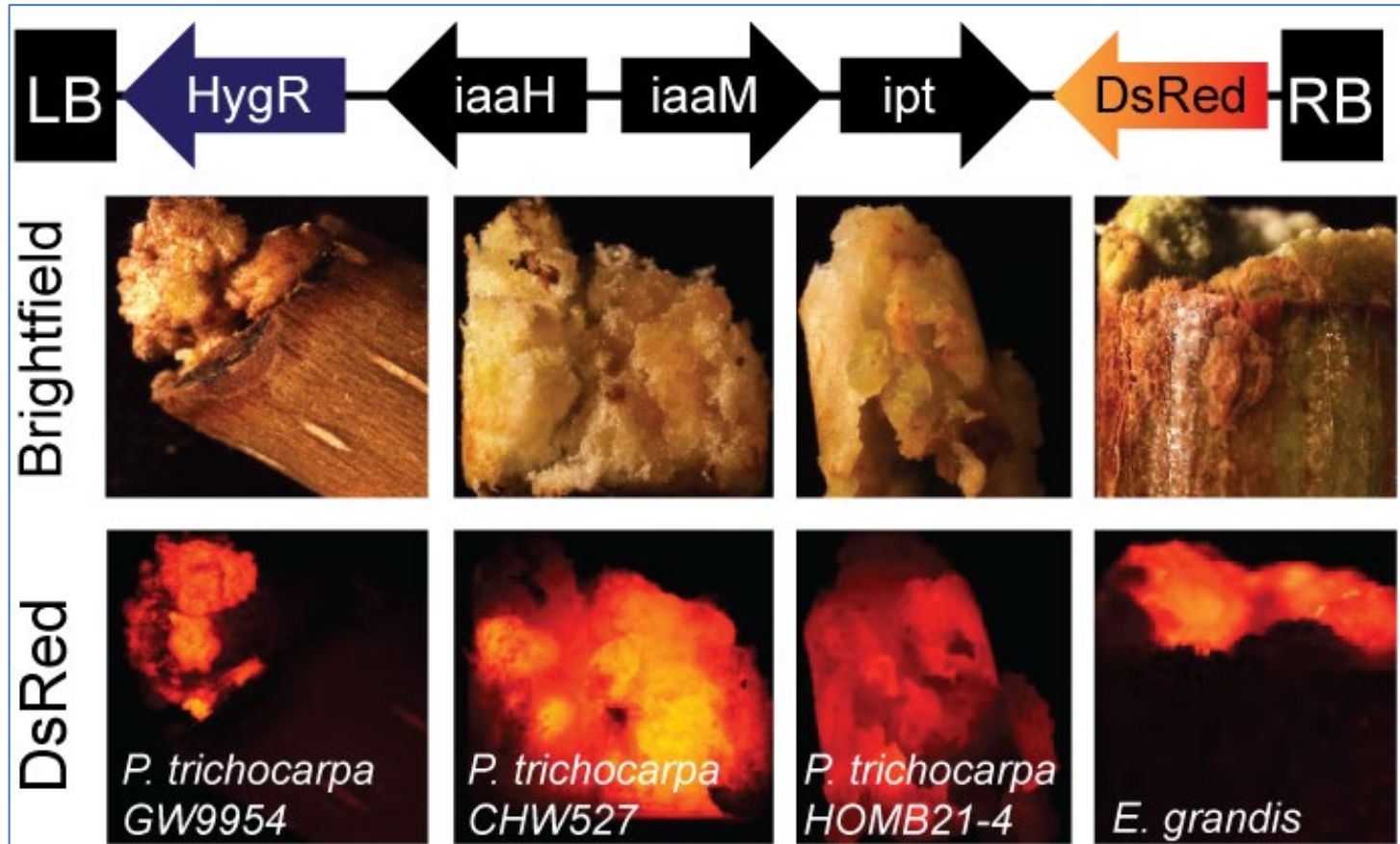


A. tumefaciens hormone genes promote regeneration
useful for *in planta* methods?



iaa/ipt genes form a positive feedback loop to reinforce undifferentiated cell growth

iaaH/M and *ipt* genes from *Agrobacterium* were effective *in planta* inducers of transgenic cells in diverse genotypes



Can we find more useful, developmentally flexible Agro genes?

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An alternative approach for gene transfer in trees using wild-type *Agrobacterium* strains[†]

Ana Cristina Miranda Brasileiro¹, Jean-Charles Leplé², Joris Muzzin^{2,3}, Dalila Ounnoughi², Marie-France Michel^{2†} and Lise Jouanin^{1*}

¹Laboratoire de Biologie Cellulaire, INRA, route de Saint-Cyr, F-78026 Versailles Cedex, France (*author for correspondence); ²Station d'Amélioration des Arbres Forestiers, INRA, Ardon, F-45160 Olivet, France; ³present address: Piccoplant Mikrovermehrungen, Brockhauser Weg 75, D-2900 Oldenburg, Germany

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Key words: *Agrobacterium*, crown gall, poplar, tree transformation, wild cherry

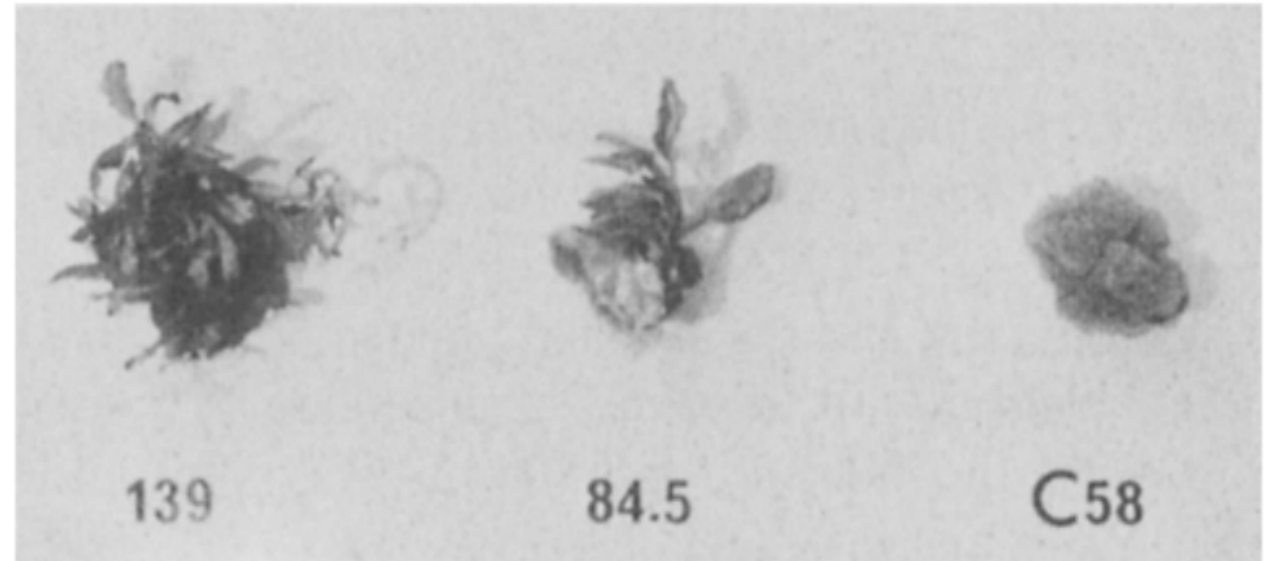
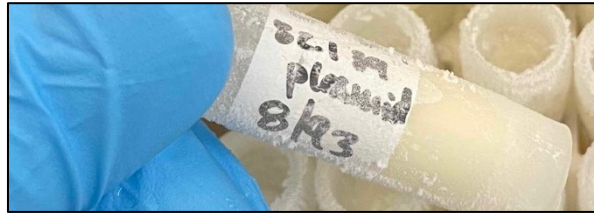
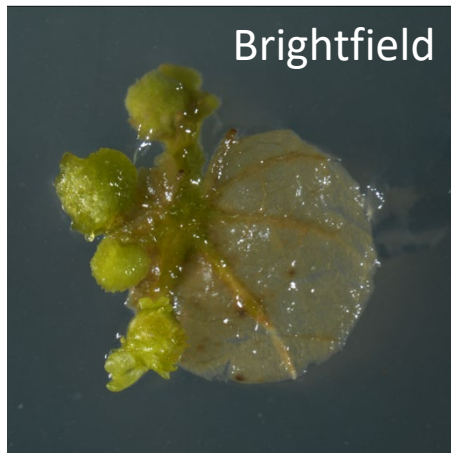


Fig. 1. Tumors and shoot differentiation from poplar tumors induced by *A. tumefaciens* strains 82.139, 84.5 and C58 and cultivated on MS medium, 6 weeks after inoculation.

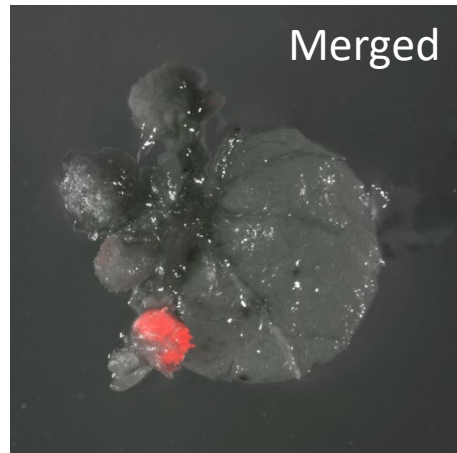
We cloned out the DEV genes from our resurrected clone in deep freeze



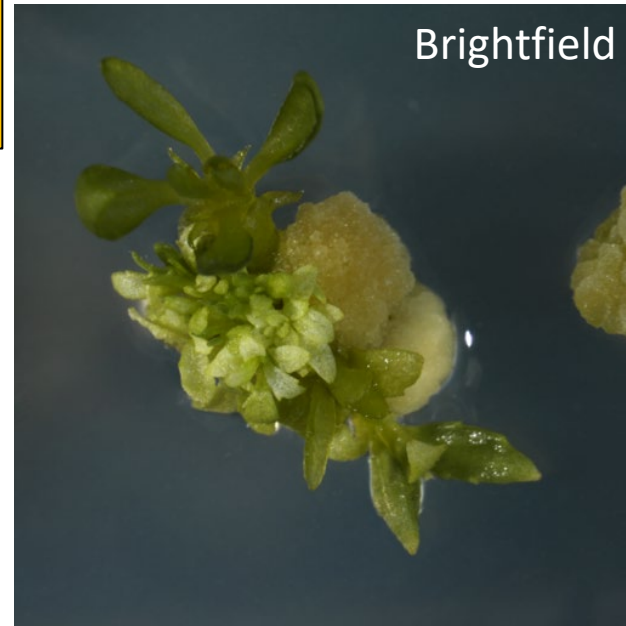
Agro transformed tissues promoted regeneration of shoots



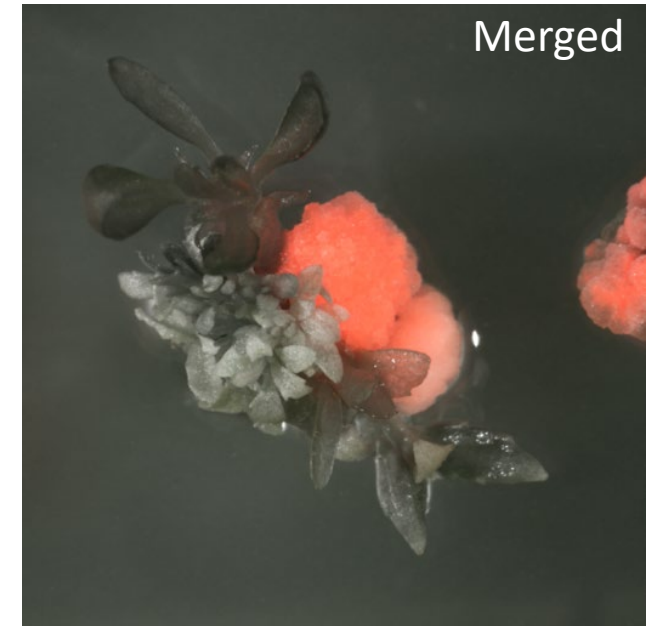
Brightfield



Merged

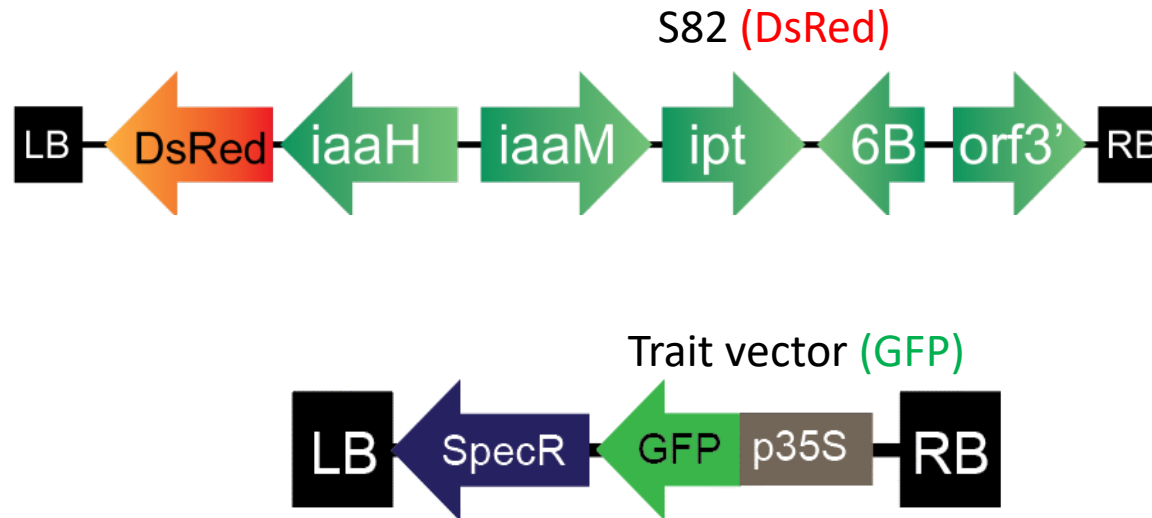


Brightfield



Merged

Mixed co-transformation with *Agrobacterium* genes

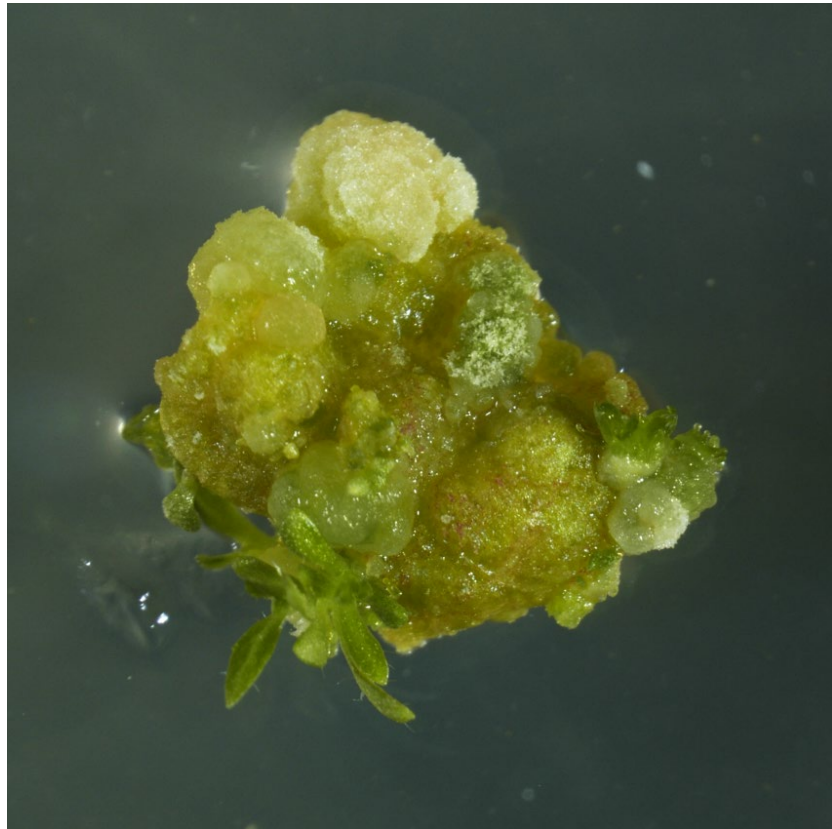


No hormones to induce regeneration

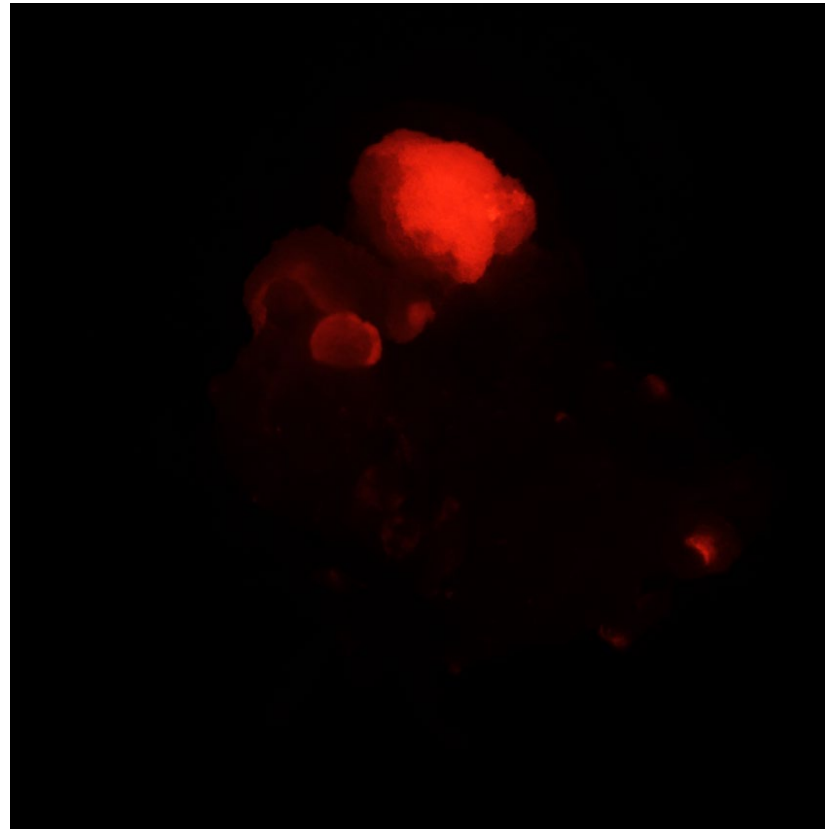
Only spec selection

82.139 DEV genes spur the regeneration of trait vector cells

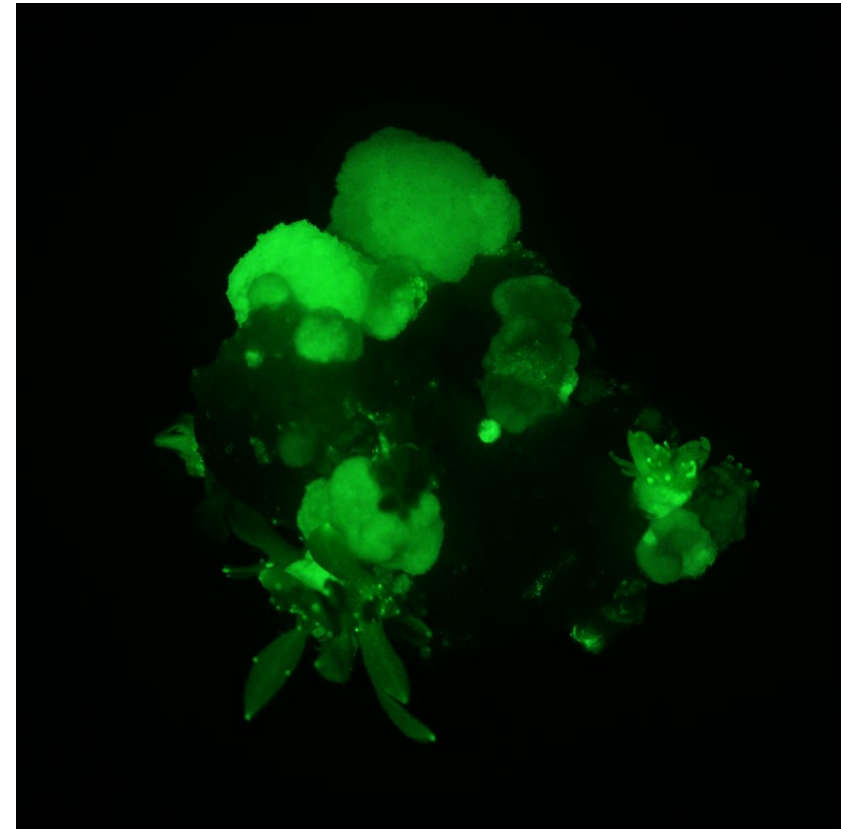
Bright-field



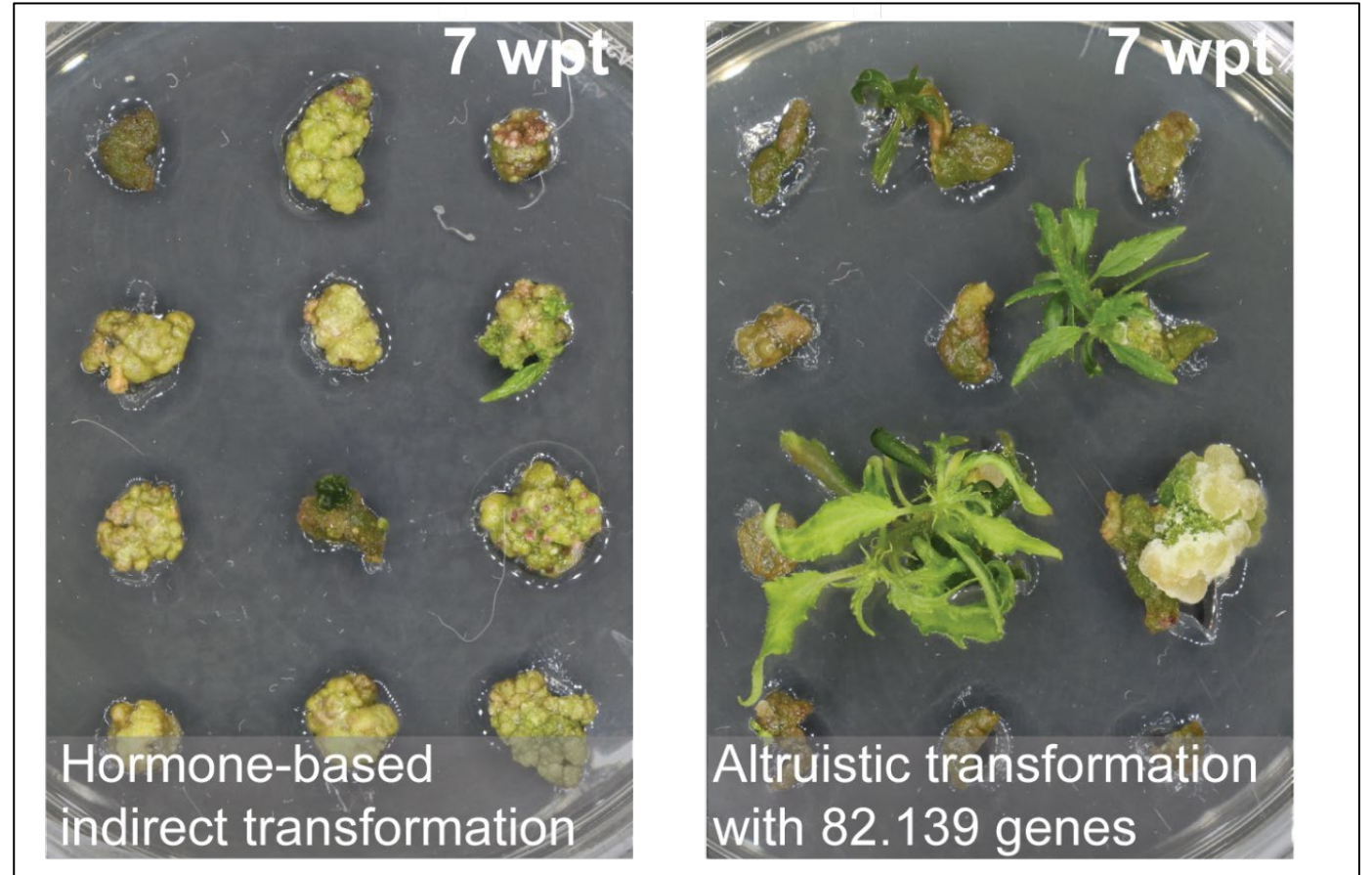
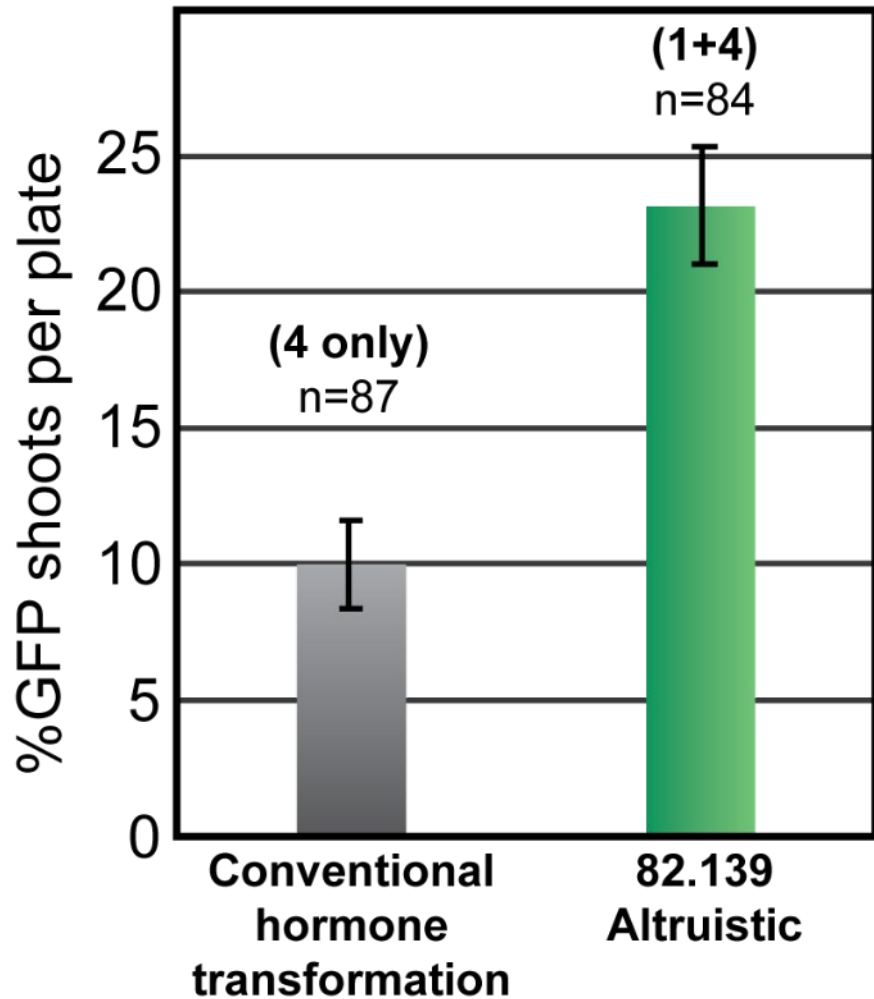
DsRed (82.139)

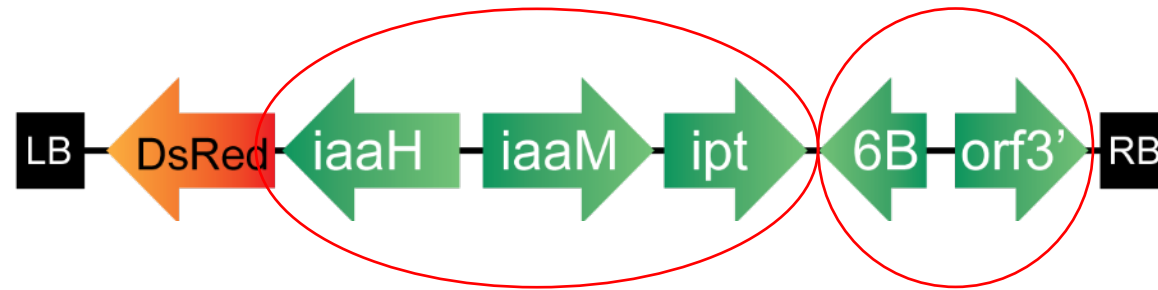


GFP (SpecR trait)



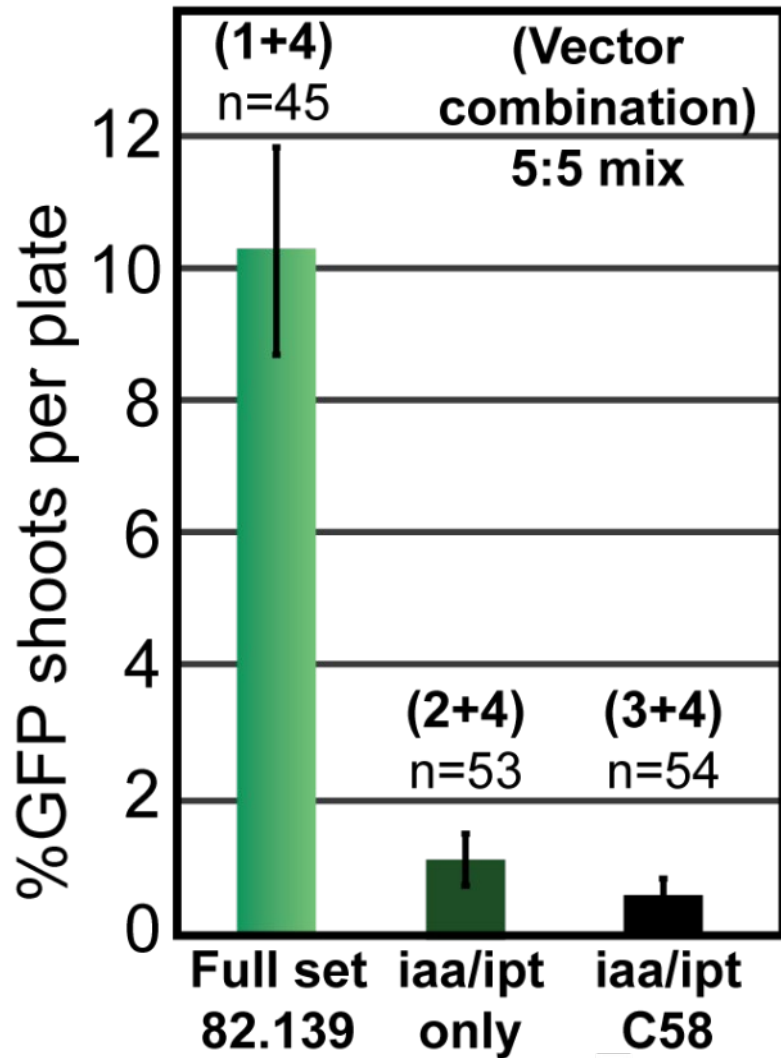
82.139 altruistic transformation was superior to routine hormone-based indirect transformation



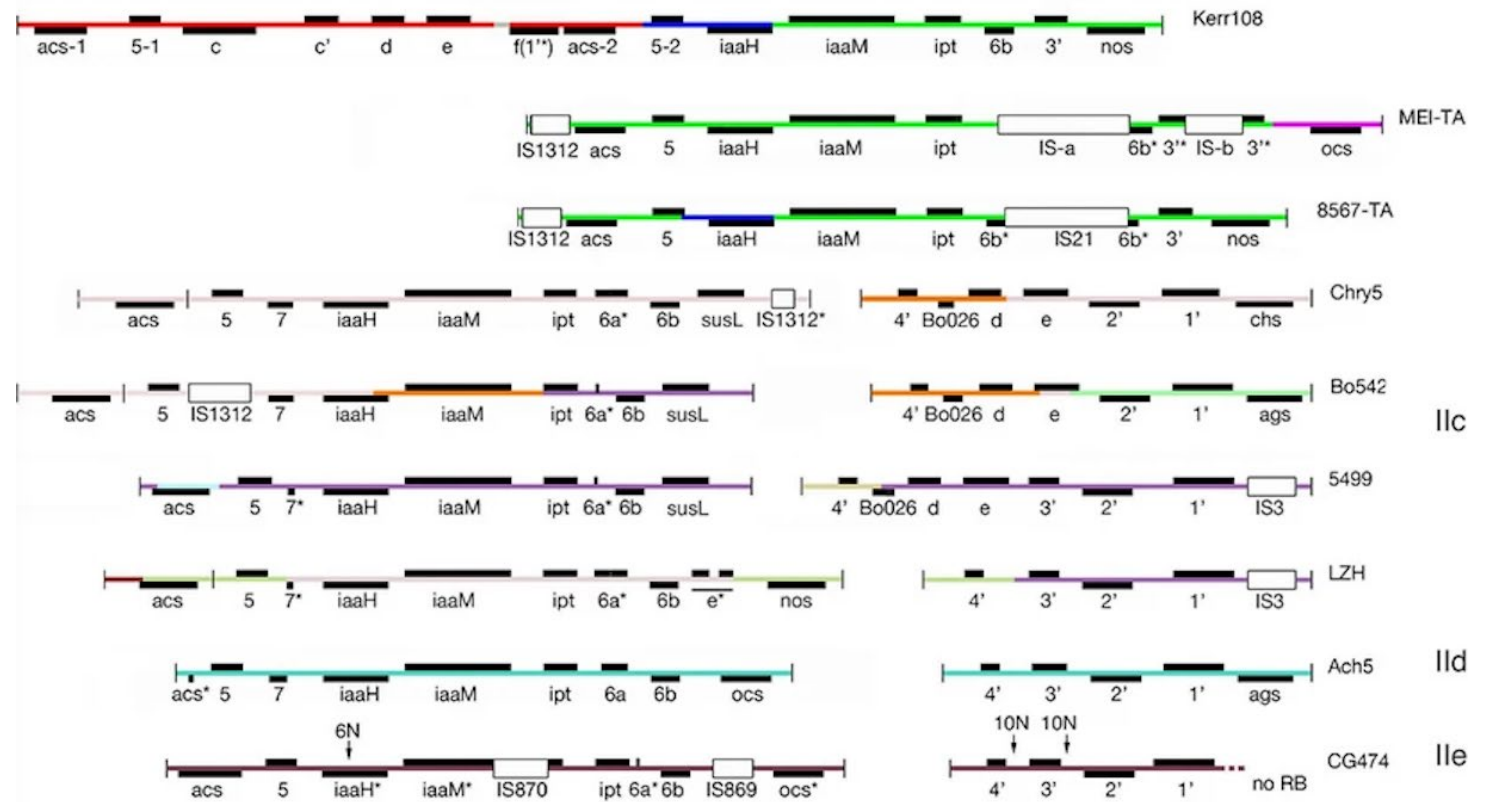


Which genes are most important for non-cell autonomous shoot promotion?

iaa/ipt genes alone did not support high rates of altruistic shoot induction



Many T-DNA genes and structures, most completely unexplored



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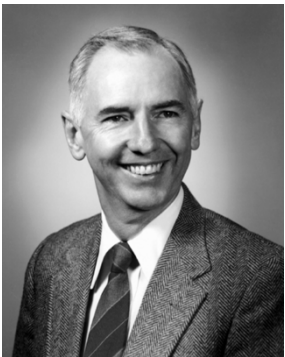
Are there other useful DEV genes? Agro diversity hardly studied

RESEARCH ARTICLE SUMMARY

PLASMID EVOLUTION

Unexpected conservation and global transmission of agrobacterial virulence plasmids

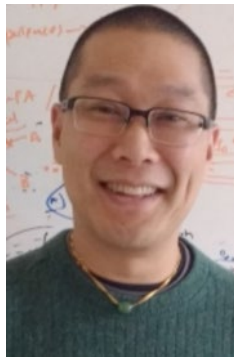
Alexandra J. Weisberg, Edward W. Davis II, Javier Tabima, Michael S. Belcher, Marilyn Miller, Chih-Horng Kuo, Joyce E. Loper, Niklaus J. Grünwald, Melodie L. Putnam, Jeff H. Chang*



Larry Moore



Alexandra Weisberg (BPP)



Jeff Chang (BPP)

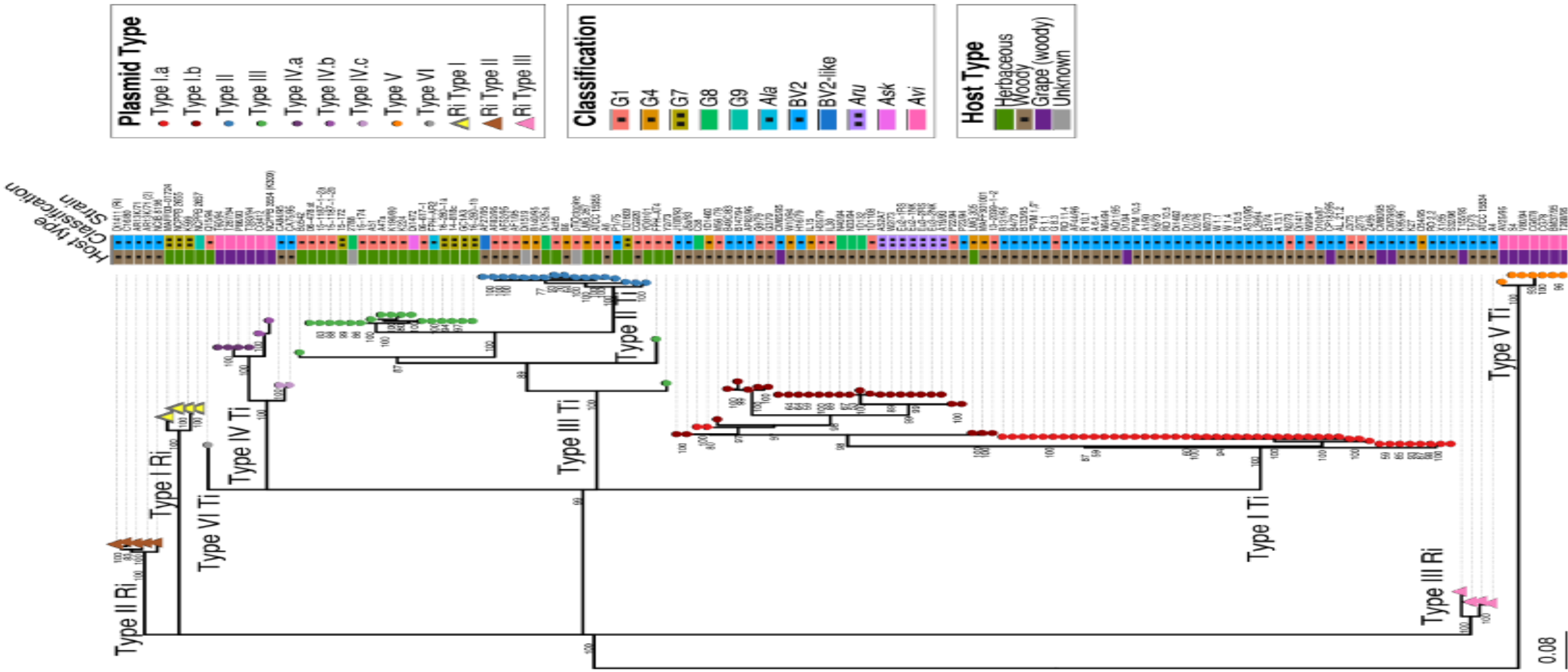


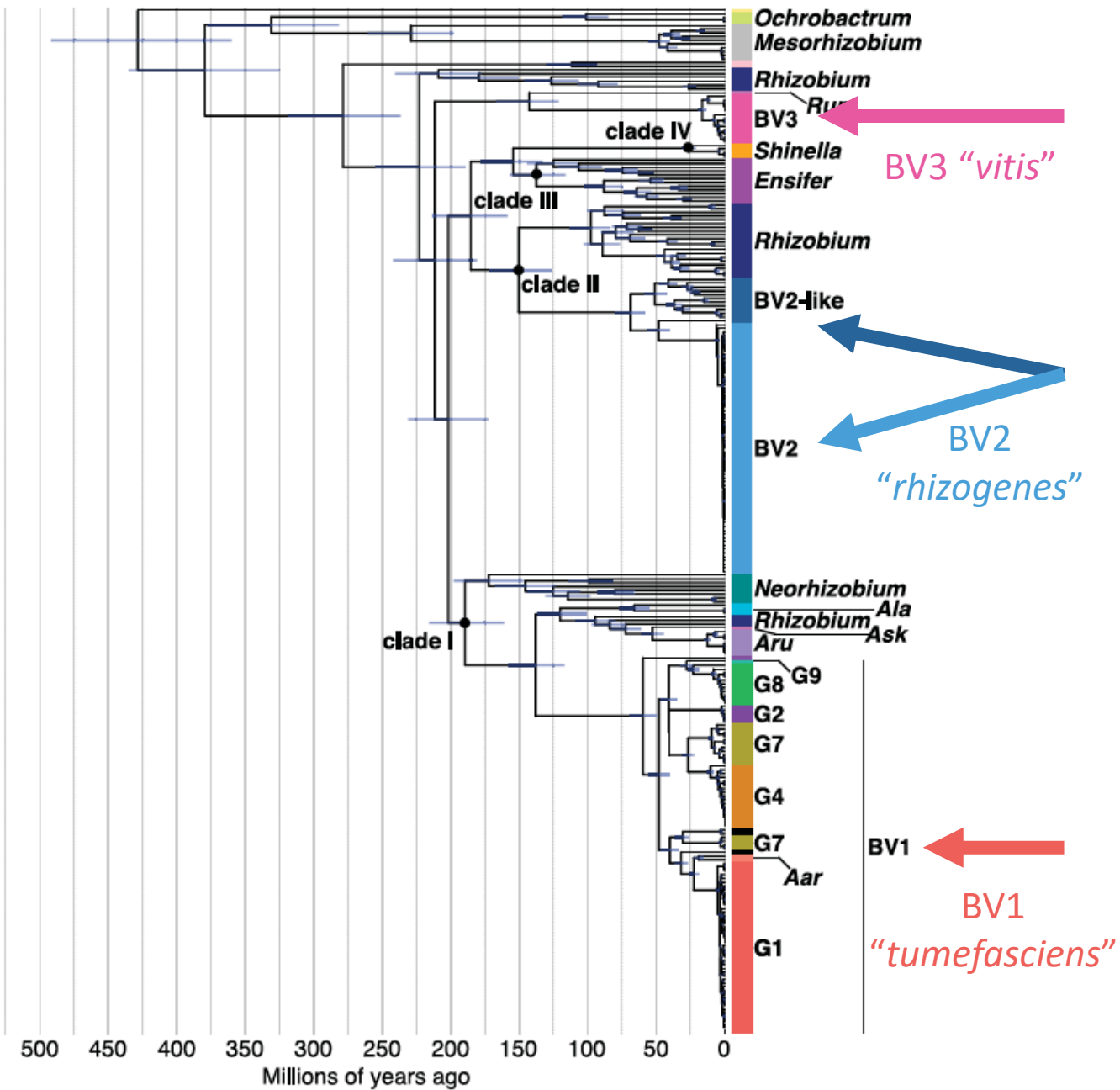
Disarmed lab strain



“Shooty” relative of 82.139

What does the Ti/Ri plasmid diversity look like?



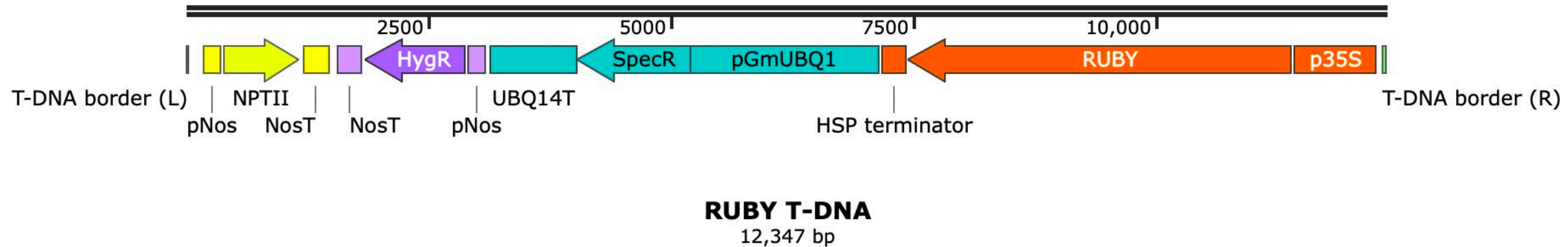


What about chromosomal diversity?

.....Three independent chromosomal lineages

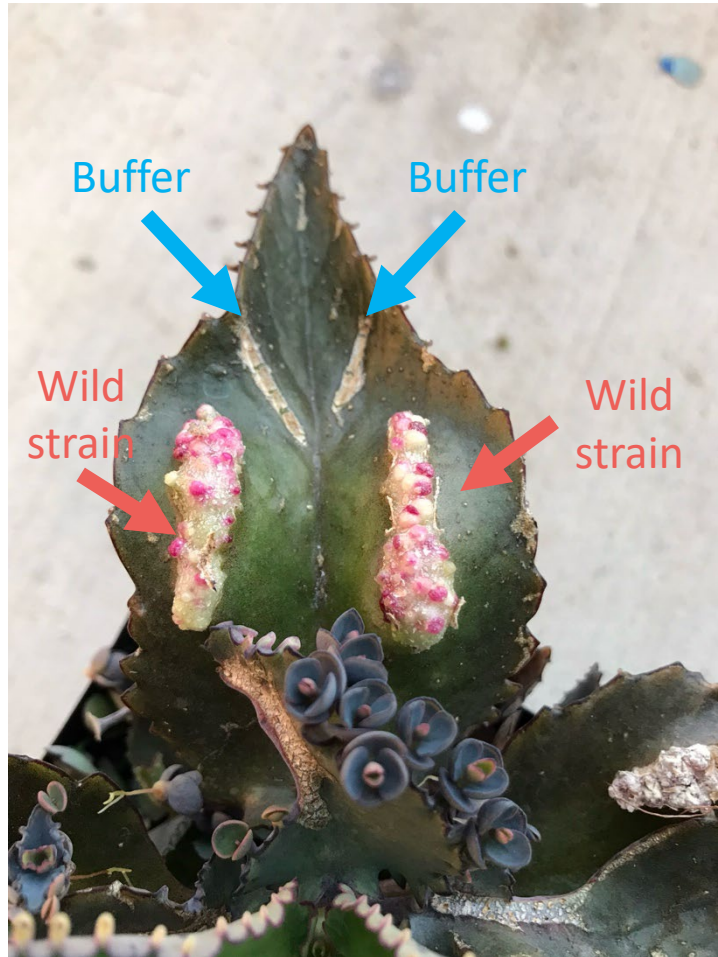
Fig. 1. Time-calibrated phylogenetic tree of the agrobacteria-rhizobia complex. Blue horizontal bars

To see transgenic tissues and try a variety of selection systems, we adopted a universal binary vector to place into wild strains



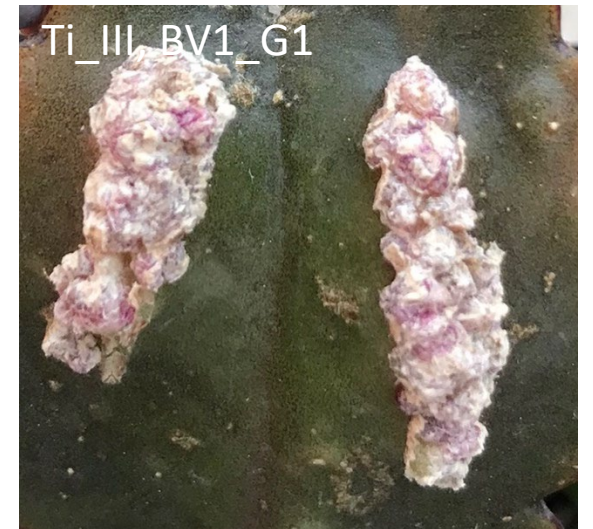
- Selected 10 strains with widely varied Ti/Ri lineages, gene content, chromosomal background
- Testing *in vitro* and *in planta* in several species

Kalanchoe as a simple system to assess strain characteristics



- Rapid callus/gall development
- Easy to propagate
- Simple to wound and apply Agro
- Flat surface for imaging
(hyperspectral / machine vision)

In kalanchoe TG tissue tended to be discrete amongst regenerating non-TG tissue



How about woody plants like poplar?

How should we approach *in planta* transformation?

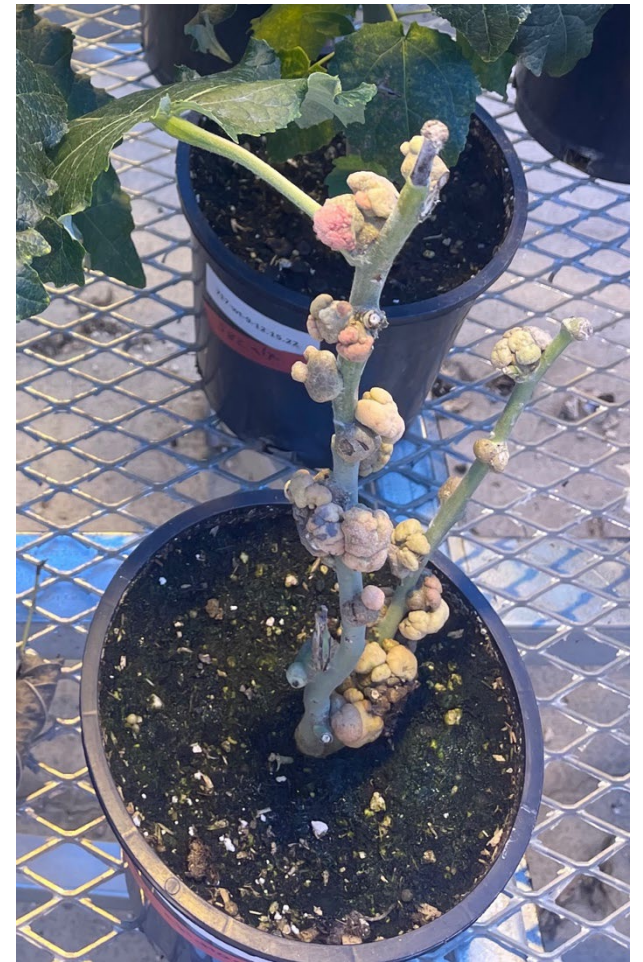
In planta methods are still changing rapidly, require a different way of thinking about transformation



***Populus tremula x alba* 717-1B4**



Apical decapitation



Axillary bud injection

We transformed two poplar genotypes with three treatments using apical decapitation

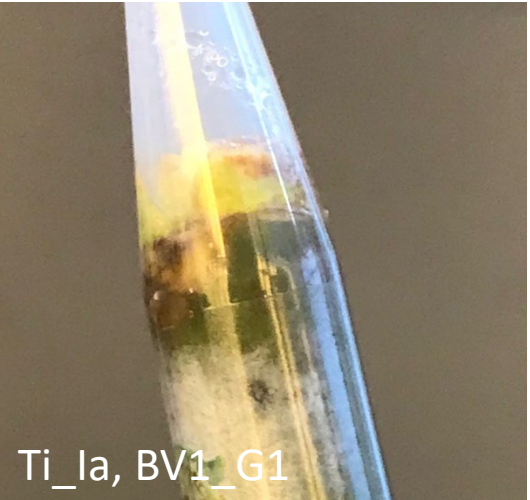
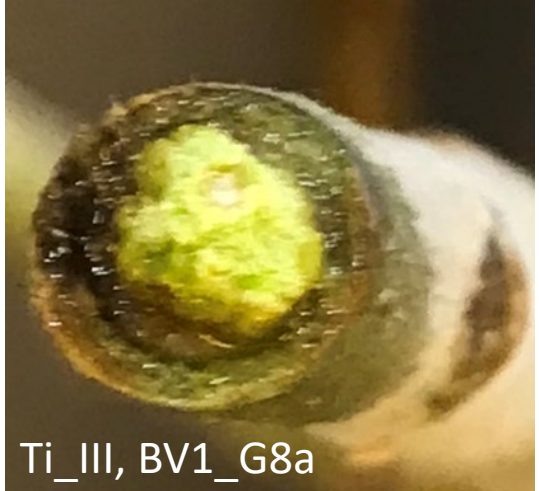
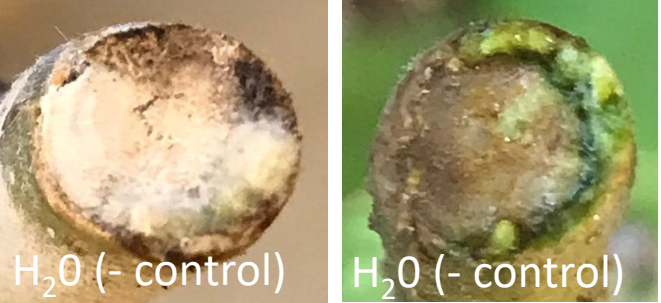
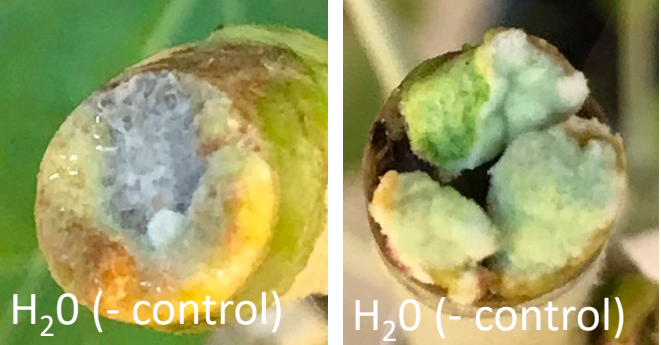
Genotypes:

- *Populus tremula x alba* 717-1B4 – transformable hybrid aspen
- *Populus trichocarpa* SKWB-22 (“T10”) –more challenging

Treatments:

1. No selection or hormones, moisture control with inverted epp. Tube
2. Selection only 1/week (100mg/L kanamycin)
3. Selection + weak cytokinin (tests whether galls are developmentally labile)

No selection or hormones, in 717 hybrid aspen



Kanamycin treatment in 717 hybrid aspen

C58 (+ control)



Ti_Ia, BV1_G1



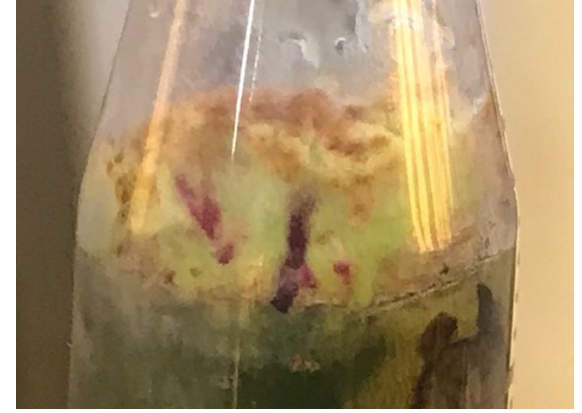
Ti_III, BV1_G8a



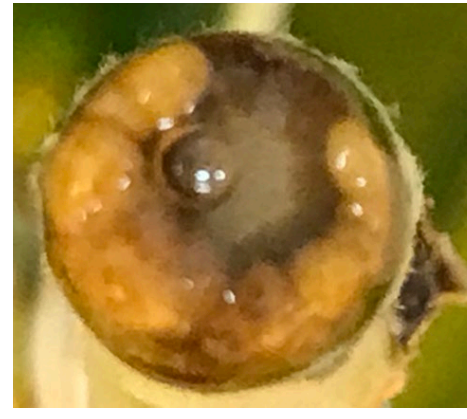
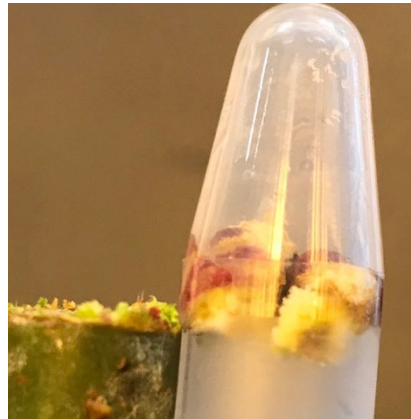
Ti_III, BV1_G1



Ti_Ib, BV1_G4

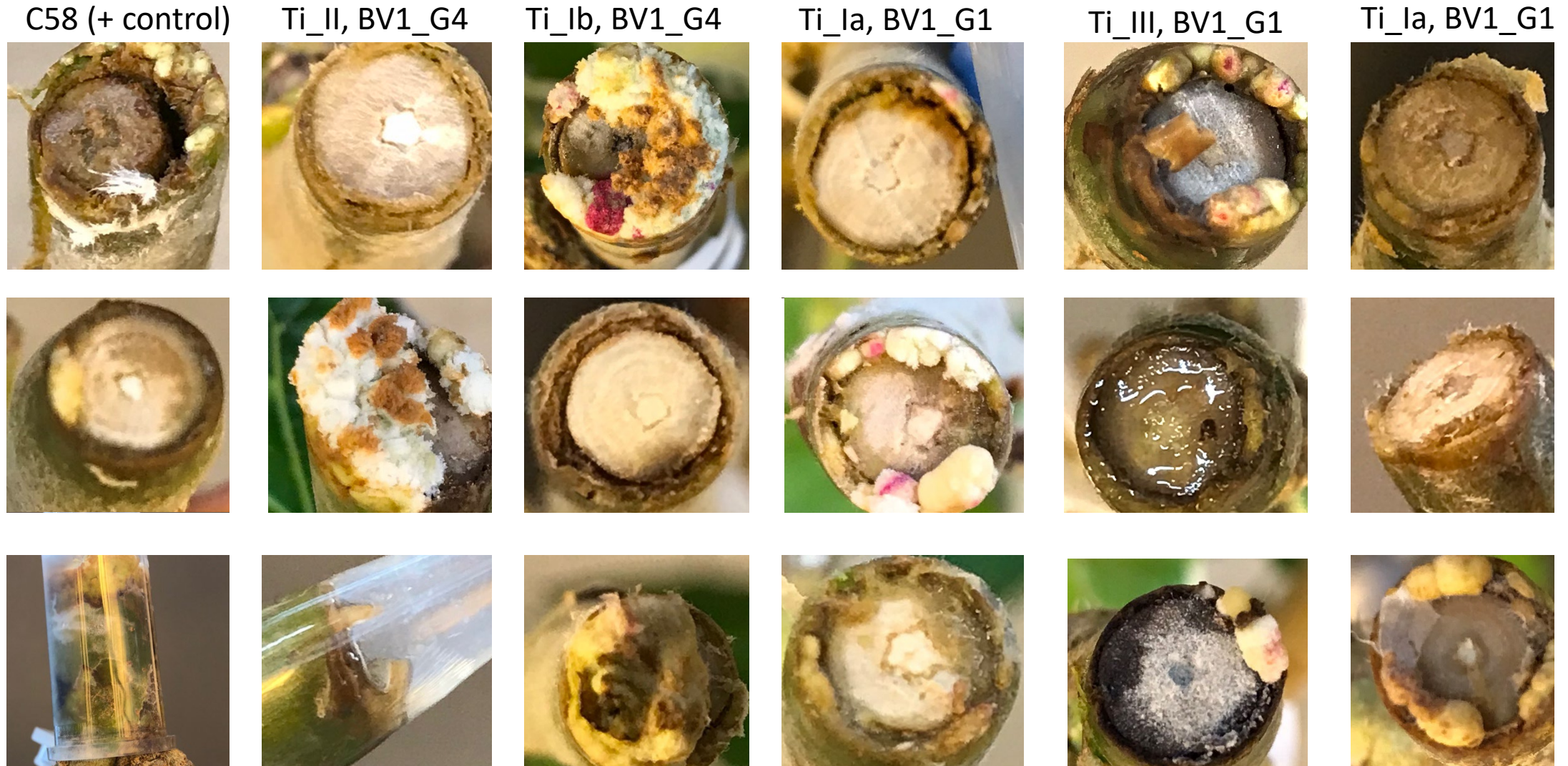


Different trees treated with wild strains

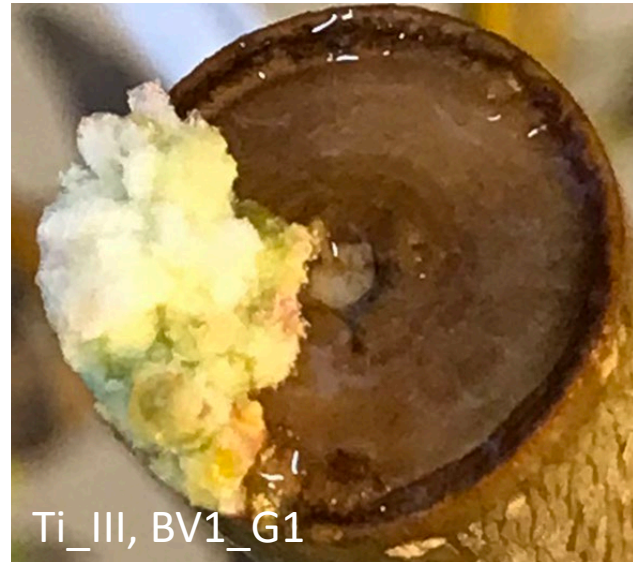


kanamycin + TDZ treatment in 717 hybrid aspen

Different trees treated with wild strains



No selection or hormones in T10 black cottonwood



Kanamycin treatment in T10 black cottonwood

Different trees treated with wild strains

C58 (+ control)



Ti_Ib, BV1_G4



Ti_Ia, BV1_G1



Ti_II, BV1_G1



Ti_Ia, BV1_G4



Genotypes and existing kill curves for antibiotic often need to be re-worked with *in planta* inoculation

kanamycin + TDZ treatment in T10 black cottonwood

C58 (+ control)



Ti_Ib, BV1_G4



Ti_II, BV1_G1



Ti_III, BV1_G1



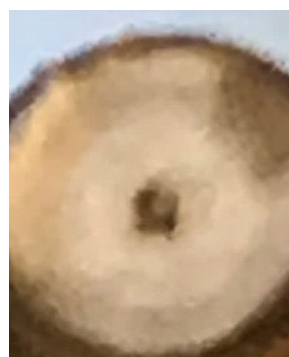
Ti_Ia, BV1_G1



Ti_Ia, BV1_G1



Ti_II, BV1_G4



How does *in vitro* differ from *in planta* when transforming with wild strains?

Pilot tests in hop showed strong variance in delivery and regeneration among strains

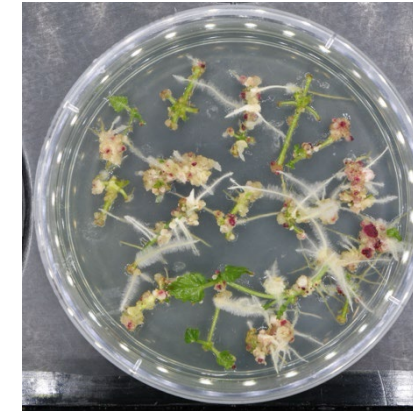
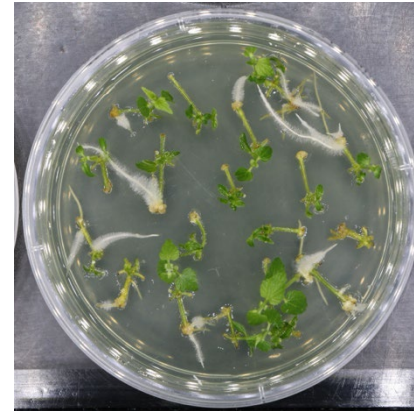
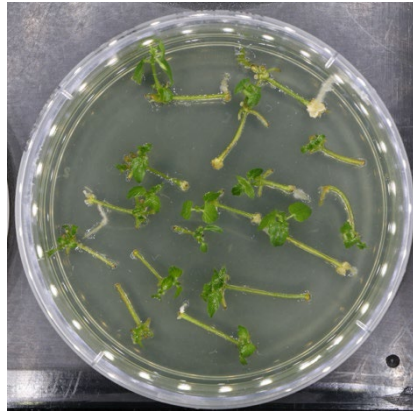
Ri_I, BV1_G7c

Ri_III, BV2

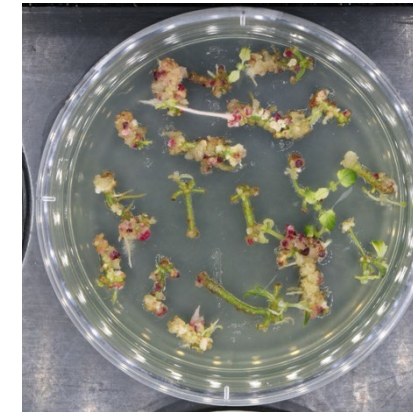
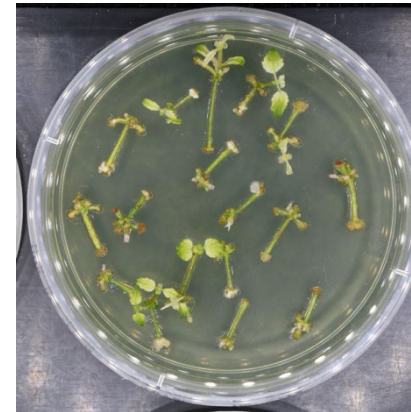
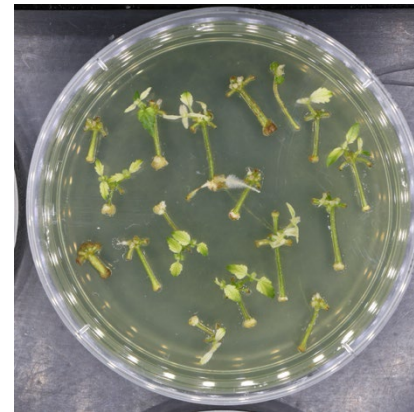
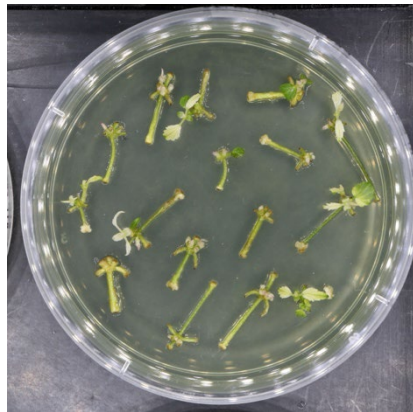
Ri_II, BV2

Ti_Ia/Ri_II, BV2

No selection



10 mg/L spec

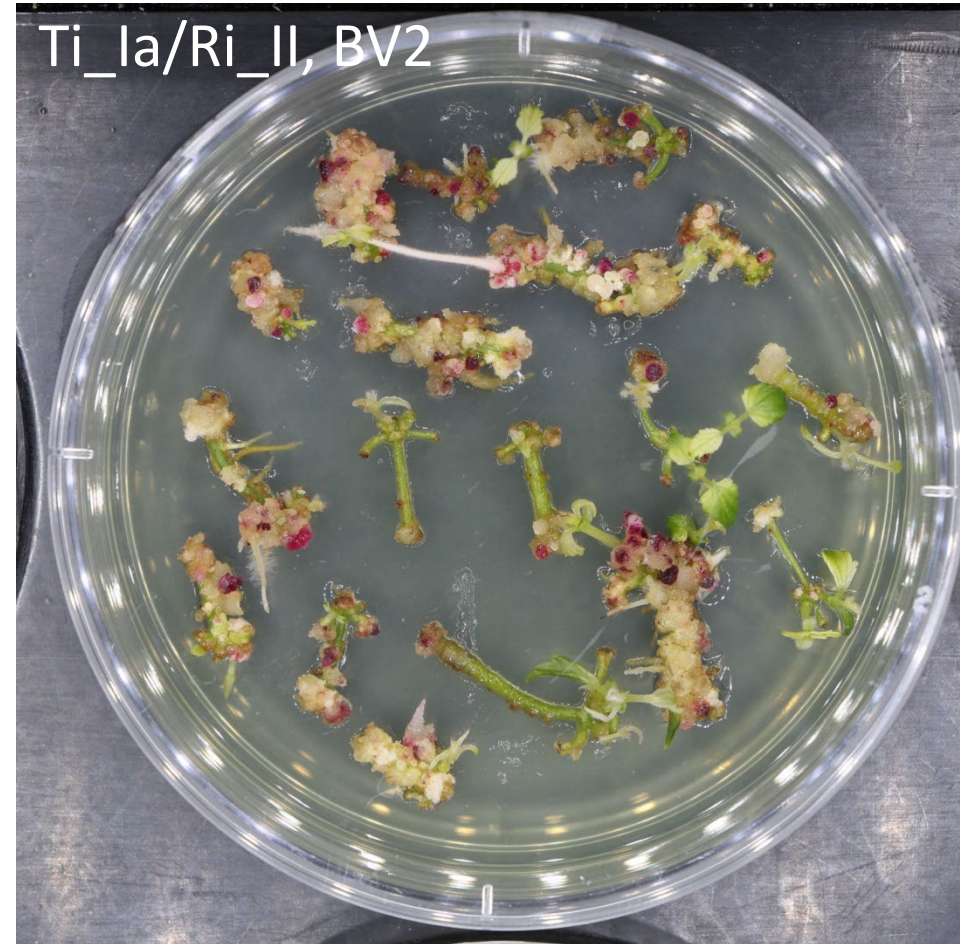
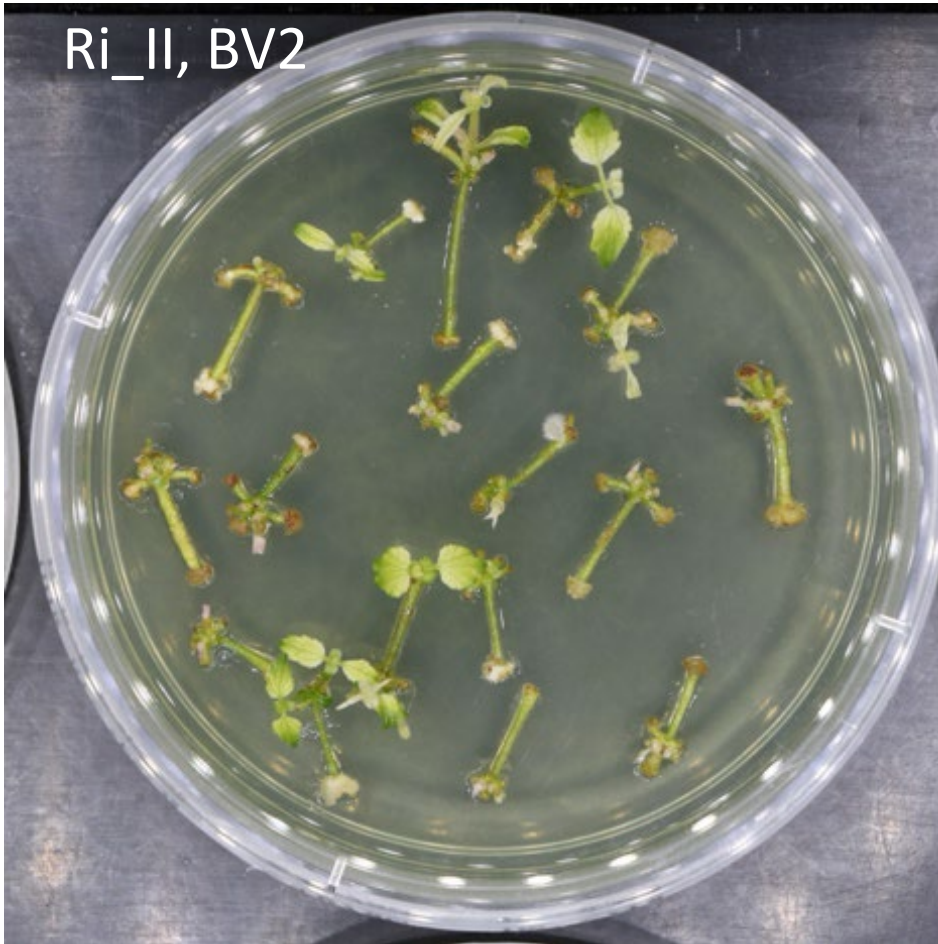


Chris Willig, OSU

Humulus lupulus cv. "Cascade"

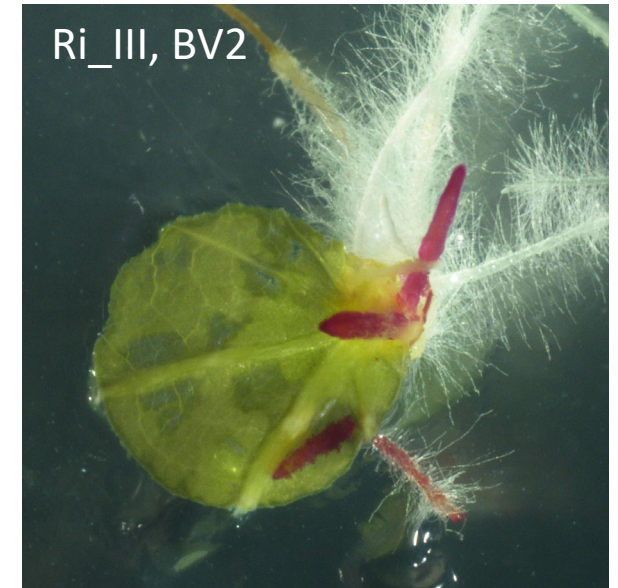
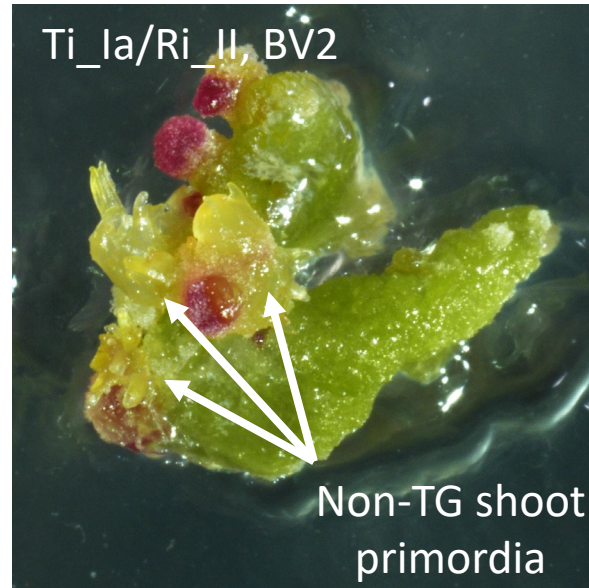
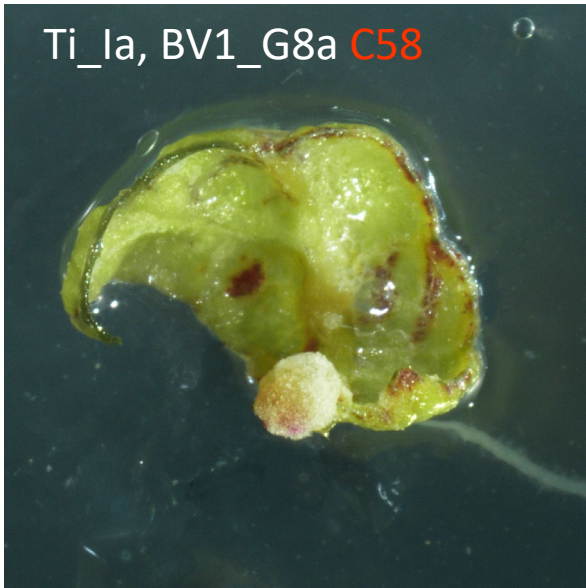
Domains of transgenic vs. non-transgenic regenerating tissue often distinct among strains

10 mg/L spec



Humulus lupulus cv. "Cascade"

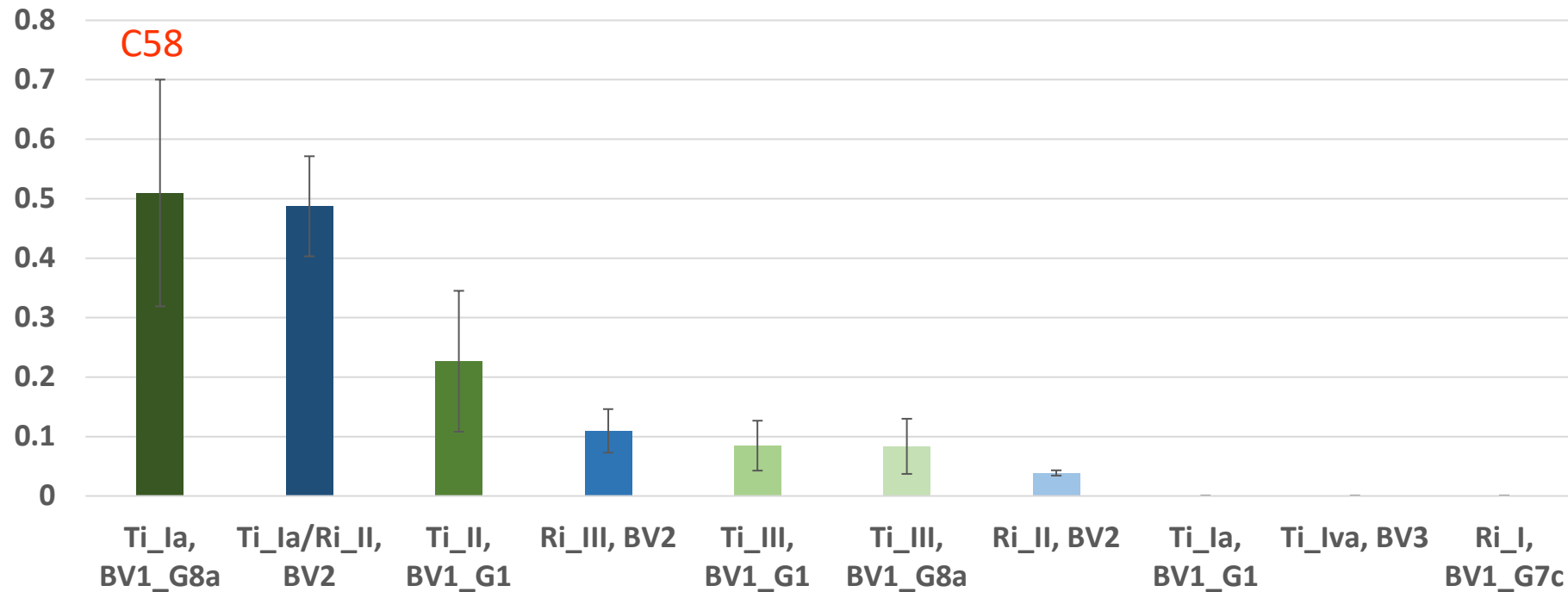
In vitro testing in poplar showed a wide range regeneration outcomes, TG vs. non-TG domains



- Transformable genotype 717-1B4 *P. tremula x alba*
- No selection in this experiment

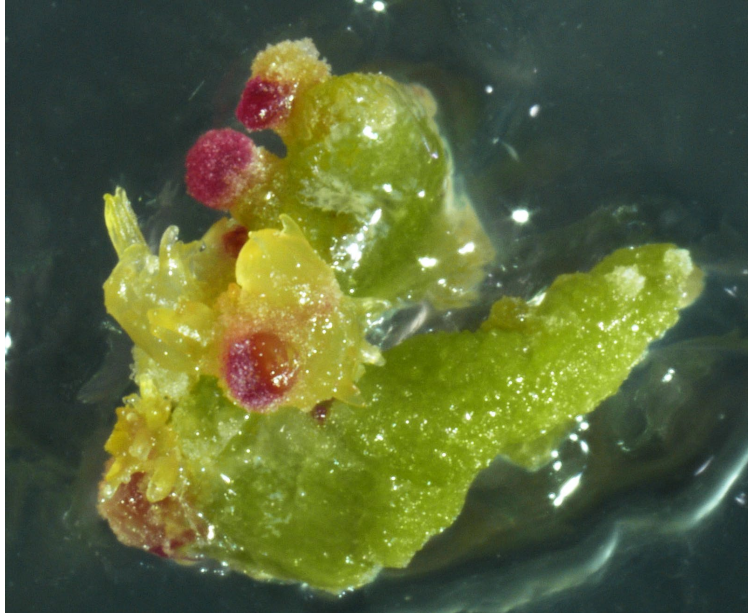
RUBY regenerating callus or hairy roots varied widely amongst strains in poplar

Ratio of explants with RUBY tissue



Ti strains = green bars, Ri strains = blue bars

Transforming greenhouse plants is tough, but we are learning!



- Things we take for granted like *Agrobacterium* preparation methods, selection strength, media composition all need to be re-calibrated *in planta*
- So far our wild strains exhibit potent morphogenic outcomes *in vitro*, highlighting many for further study

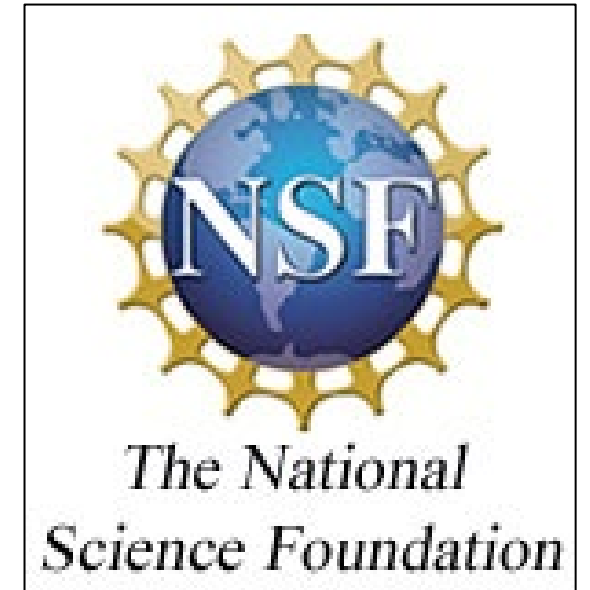
Summary

- Agro genes have impressive morphogenic potential for transformation
- Many Agro genes are unexplored mechanistically in the ways they change plant development
- Binary vectors using RUBY are effective tools to assess strain characteristics
- Agro strains have wide variability in transgene delivery and regeneration outcomes on different hosts

Going forward

- *Agrobacterium* diversity, both in terms of transgene delivery and regeneration outcomes warrants further study
- Screening population of sequenced strains will highlight unexplored T-DNA genes for further mechanistic study or careful combination
- *In planta*, tissue culture-free systems have many technical challenges in vegetatively propagated crops –co-transformation with Agro genes could be a path forward
- Strain “domestication” a priority in cases where lab strains (C58/Ach5) are inadequate for the desired plant species

Thanks to our funders and collaborators

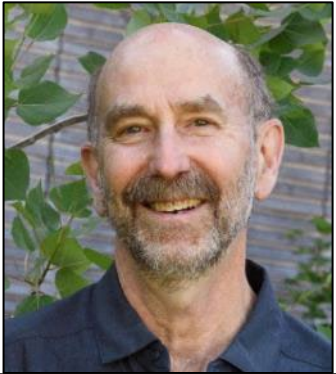


GREAT TREES Consortium

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



Thank you to all the people in the lab who contributed!



Steve Strauss
Director TBGRC, Professor



Cathleen Ma
Transformation &
Greenhouse
Experiments



Lisa Hargest
Biotechnology
Program
Manager



**Greg
Goralogia**
Postdoc,
Flowering &
Gene Editing



Victoria Conrad
Undergraduate
Gene Editing



Kate Peremyslova
GWAS,
Transformation
Experiments



Chaney Hart
PhD Fellow
Ecophysiology/genetics



Michael Gordon
PhD Candidate, HIGS



Michael Nagle
Postdoc: GWAS,
Phenomic systems



Chris Willig
Postdoc: Hop
transformation



Tanner Whiting
Undergraduate
Hop transformation



Anthony Marroquin
Greenhouse Manager



Xavier Tacker
Undergraduate
Researcher