FLP to the Future: Methylation-Insensitive Gene Excision System for **Clean Gene Editing**

ZACHARY HEINHOLD

HEINHOLZ@OREGONSTATE.EDU

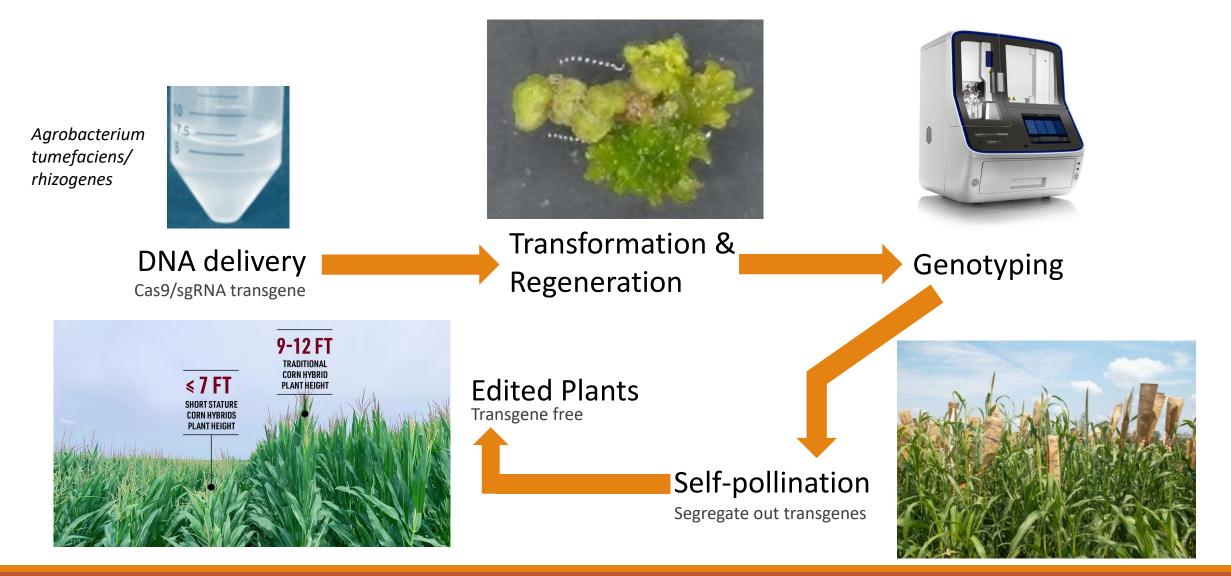
FOREST BIOTECHNOLOGY LABORATORY

FOREST ECOSYSTEMS & SOCIETY (FES), COLLEGE OF FORESTRY



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Typical Gene Editing Workflow for Row Crops



Problems in Clonally Propagated Tree Systems

- Time constraint to floral onset (years)
- Loss of phenotype characteristics through selfpollination (hybrid trees)



Stanton et al. 2010 *Populus* Breeding: From the Classical to the Genomic Approach

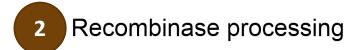


Excising Transgenes with Site-Specific Recombinases

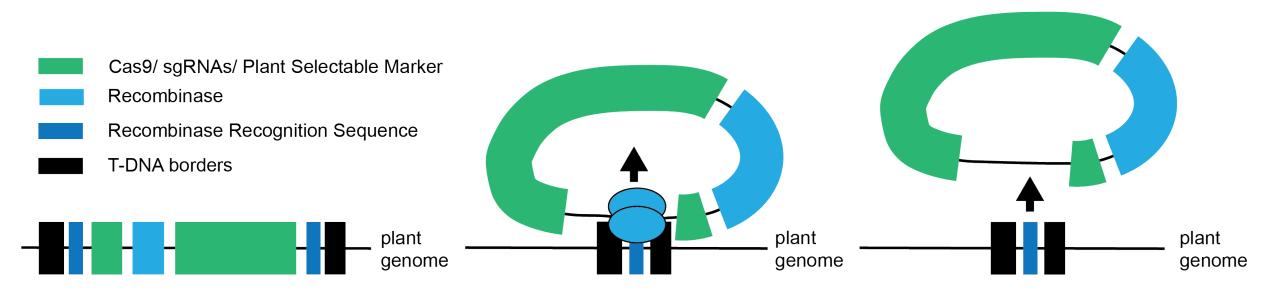
Reduces off-target gene edits

Deregulation? (RSR-trait-MOA regulation may allow for footprint approval – potential USDA-SECURE simple edit exceptions)

1 Genomic integration



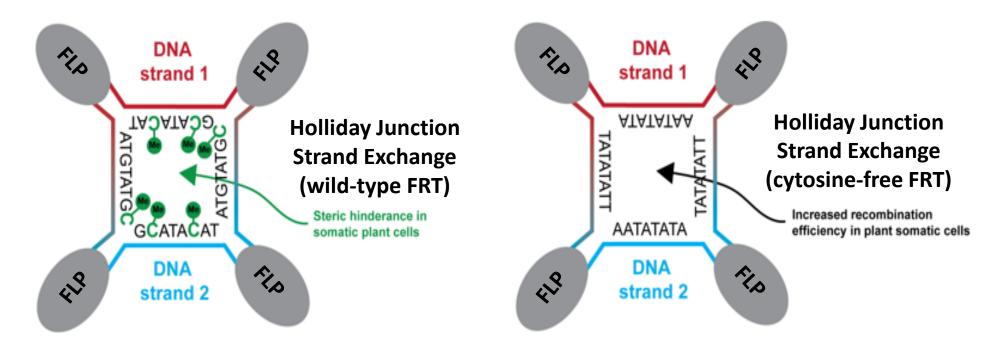
3 Excised transgene



Recombinase Challenges in Plant Systems

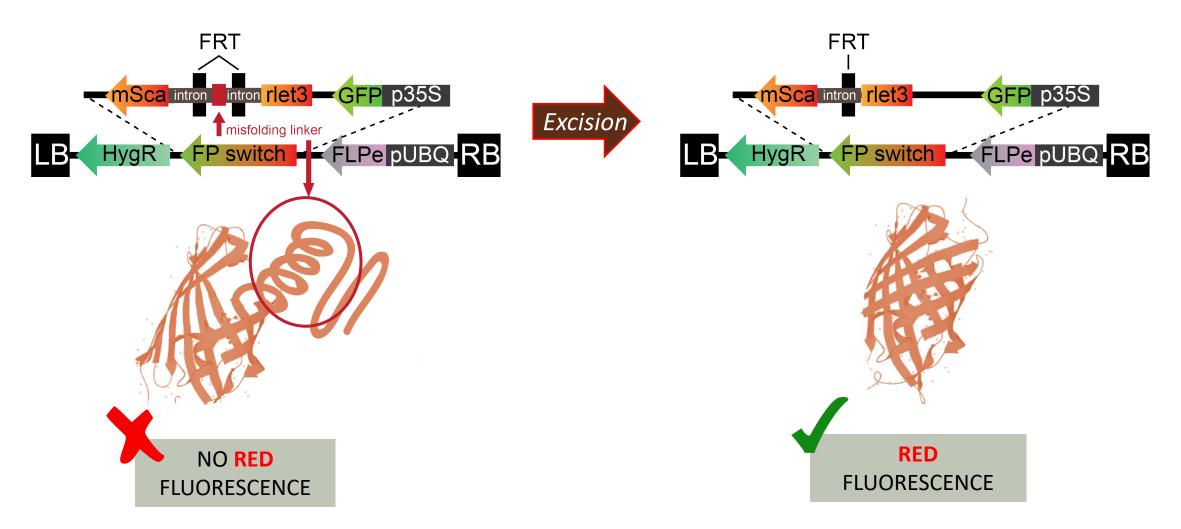
DNA methylation occurring in Cre-expressing cells inhibits loxP recombination and silences loxP-sandwiched genes

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

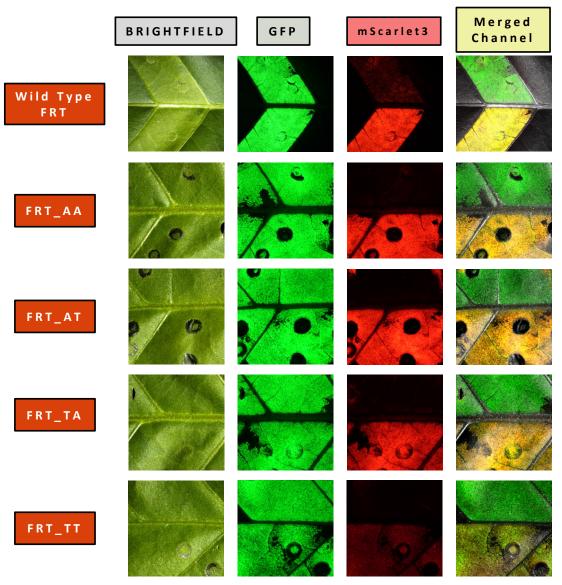


Methylation at recognition site spacer sequence causes steric hindrance at Holliday junction during recombination

Quantify Excision Efficiency – Active Excision Reporter



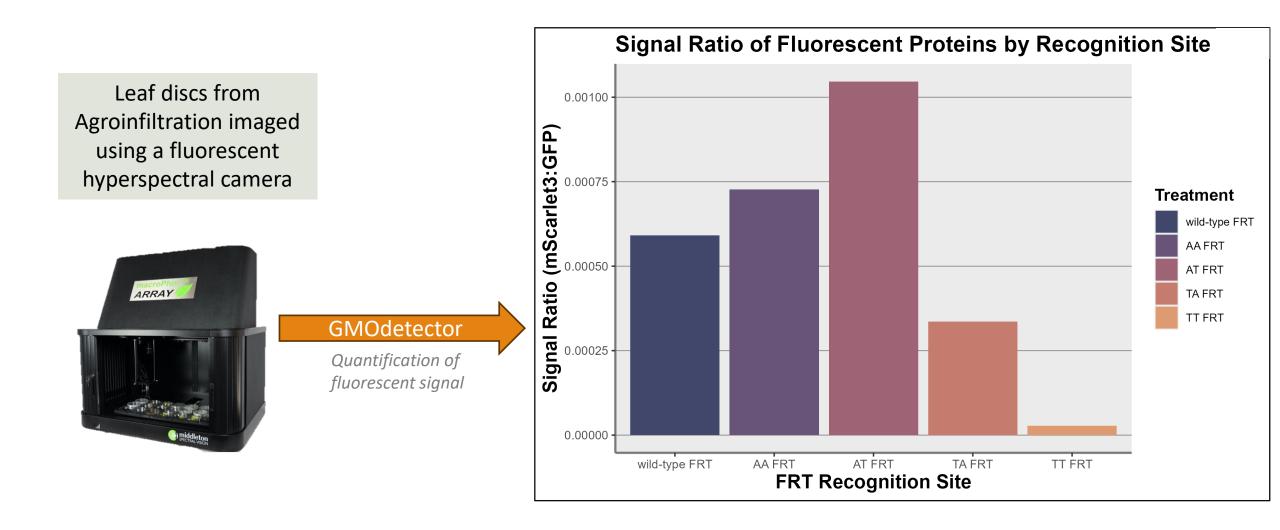
Site Efficiency Screen - Agroinfiltration



Top no FLP recombinase

<u>Bottom</u> with FLP recombinase

Analysis Using GMOdetector Phenomics Pipeline



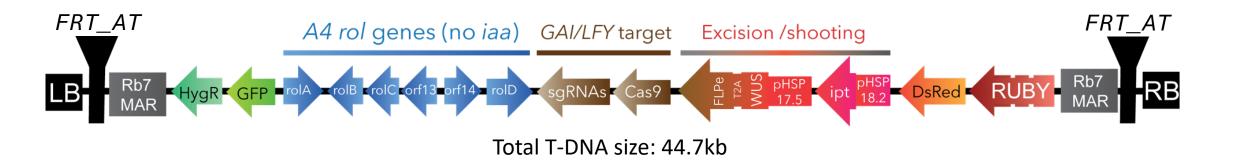
Summary & Future

"AA" and "AT" FRT sites showed promise in this construct with transient expression
Other sites lower-performing, still saw some excision

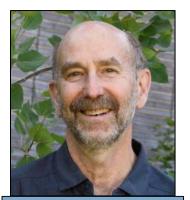
➢Future Goals:

> Test this construct in stable transformation for hybrid poplar

>Head-to-head of top-performing cytosine-free FRT site against wild-type FRT site in root-to-shoot construct (below)



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