

# Innovative Control of *Phragmites* and Other Invasive Species: Species Specific Gene Silencing

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# Targeting *Phragmites* Success As Invasive Species

- *Ph*



ion



# Managers: Where (Who) are We?

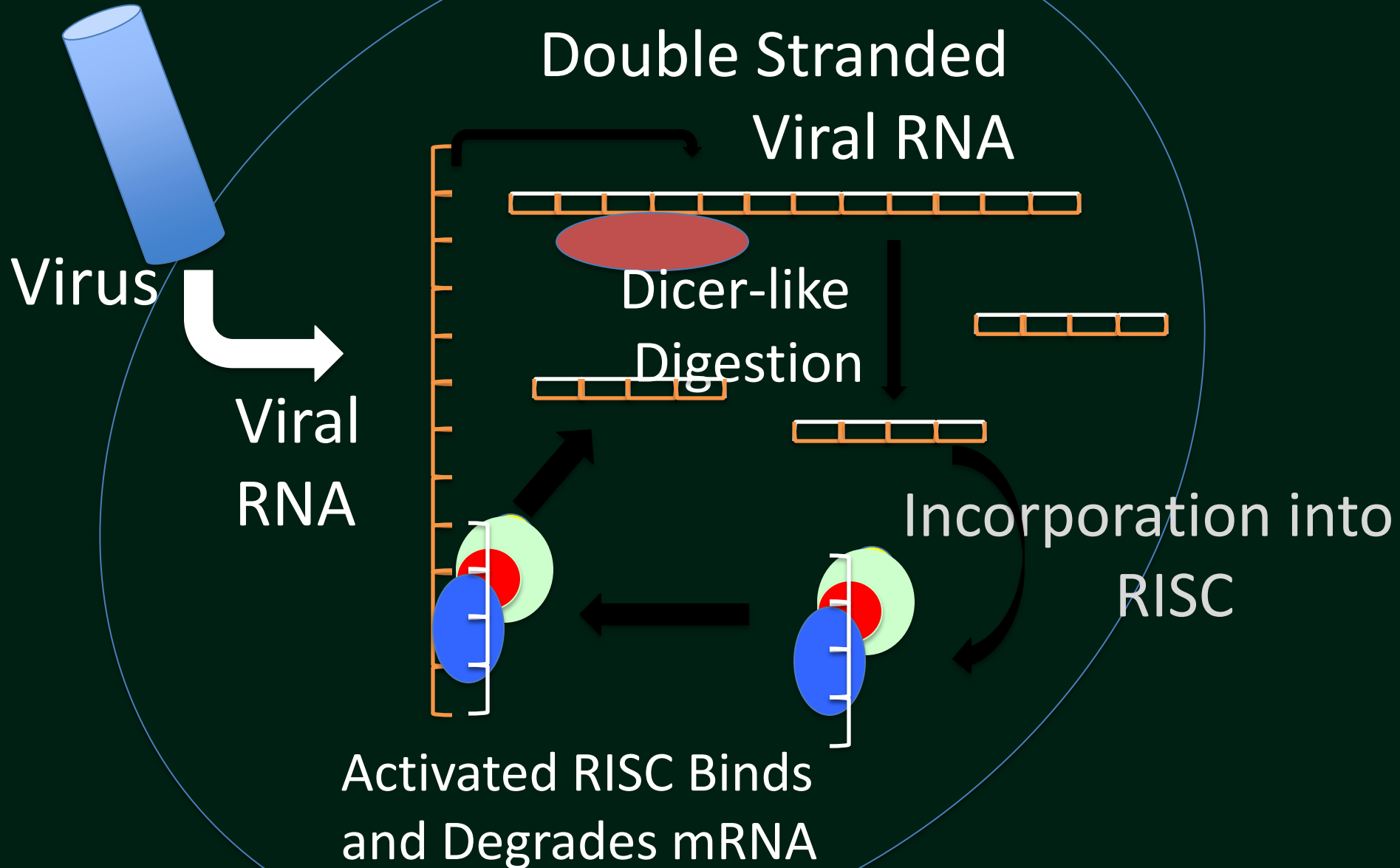


# Developing a New Arsenal

## Gene Silencing

- What is gene silencing?
  - PTGS- Post Transcriptional Gene Silencing
  - RNAi- RNA interference
- Triggered by double stranded RNA
  - siRNA
  - miRNA
- Natural and common mechanisms in organisms
  - Viral defense
  - Gene regulation (development)

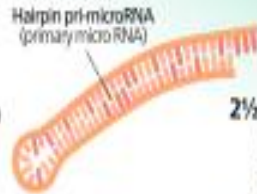
# siRNA and Viral Defense





nucleus

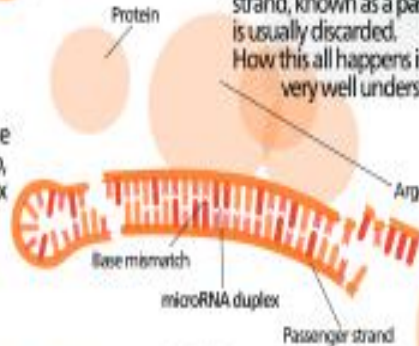
1 A protein called exportin-5 transports a hairpin primary microRNA (pri-miRNA) out of the nucleus.



Exportin-5

2½ Meanwhile, one of the strands joins a group of proteins, forming an microRNA-protein complex. The other strand, known as a passenger strand is usually discarded. How this all happens is still not very well understood.

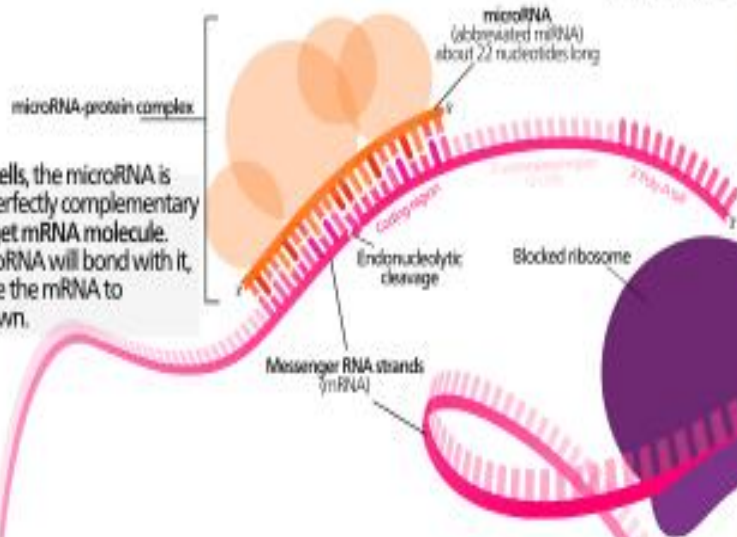
2 An enzyme called dicer (not shown) trims the pri-miRNA and removes the hairpin loop, leaving a double stranded microRNA duplex molecule.



Argonaute proteins

4 In animal cells, the microRNA nucleotides typically don't pair up with the mRNA nucleotides as well. Their base pairing often follows a pattern though.

3 In plant cells, the microRNA is usually perfectly complementary to its target mRNA molecule. The microRNA will bond with it, and cause the mRNA to break down.



Base mismatches

microRNA

Nucleotide 1

Has an A across from it

Deadenylation

3' Poly-A tail

Seed Region (Nucleotides 2-8)  
Perfect base pairing

Nucleotide 9

Has an A or U across from it

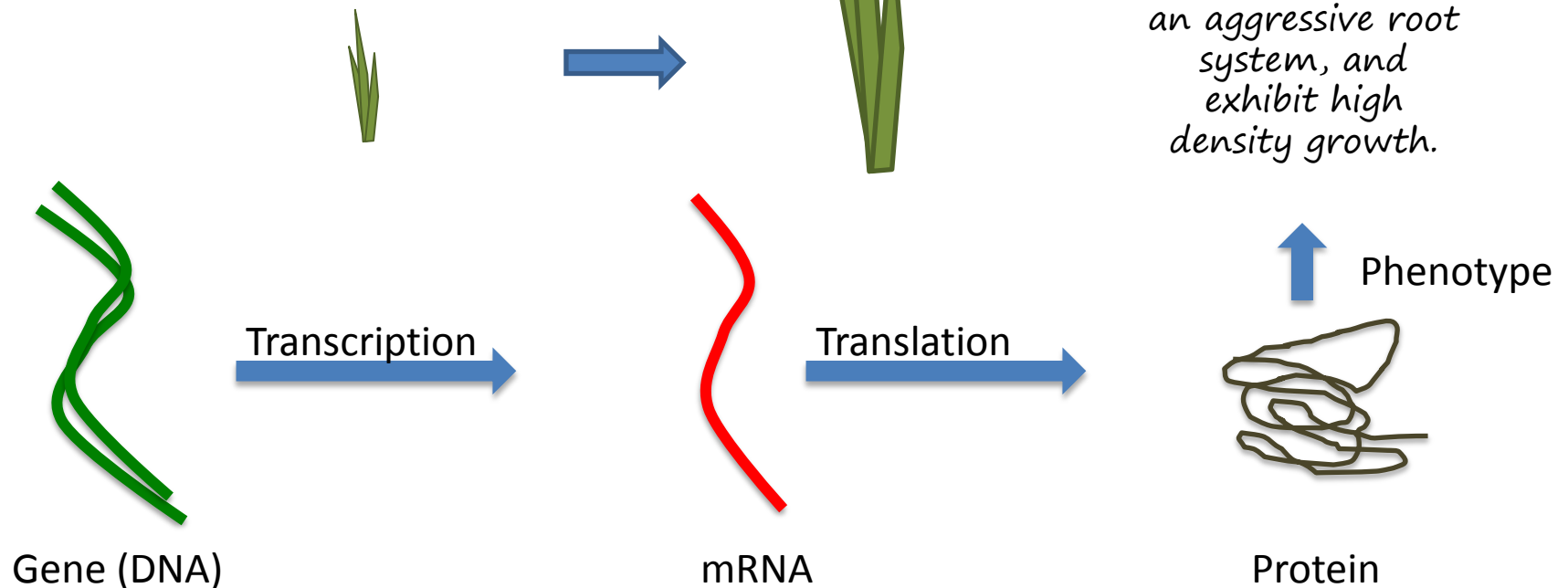
Nucleotides 13-16  
Good base pairing

5 The microRNA-protein complex's presence blocks translation as well as speeding up deadenylation (breakdown of the Poly-A tail), which causes the mRNA to be degraded sooner and translated less.

# the formation and function of micro RNAs

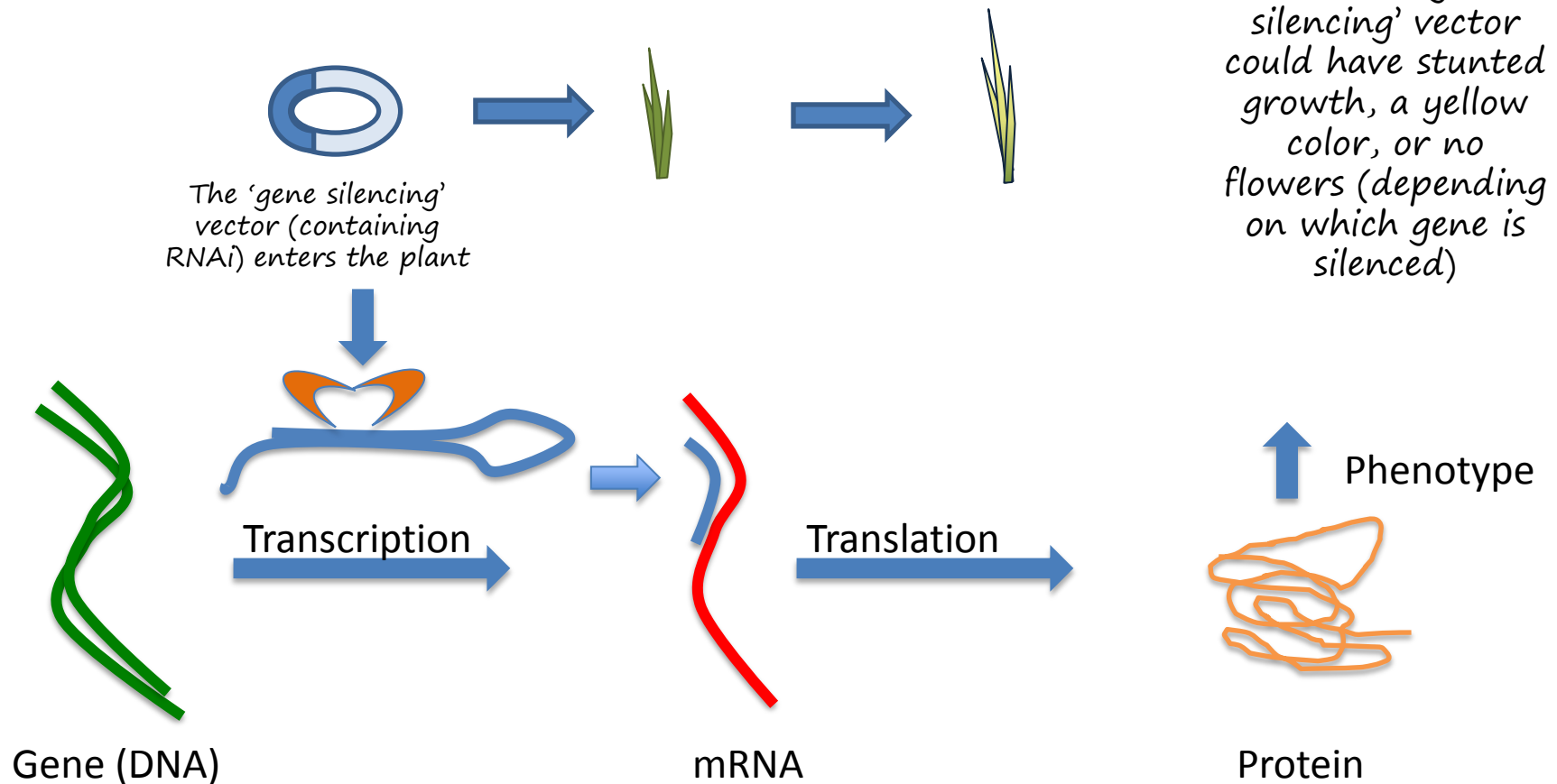
# What is Gene Silencing?

Plant processes, such as photosynthesis, are controlled by genetic material within the plant cells



# What is Gene Silencing?

Gene Silencing inhibits these intracellular processes resulting in muted trait expression





# Goal: Establish Gene Silencing for Control of Invasive Species

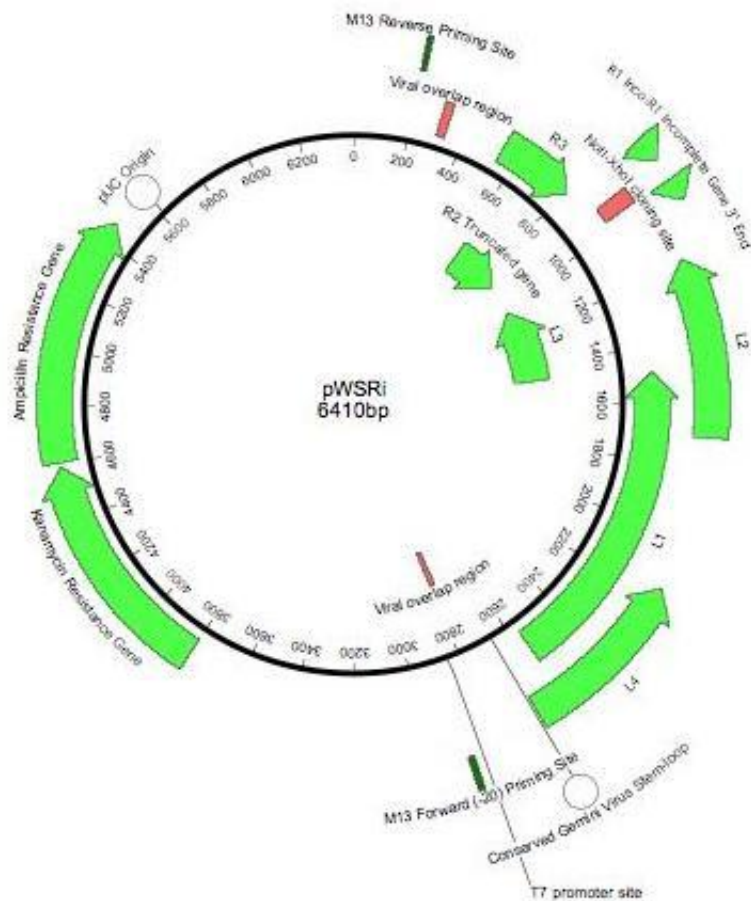
- Develop robust mode for the transient generation of dsRNA in *Phragmites*
- Develop efficient means of application to *Phragmites*
- Target genes involved in:
  - photosynthesis (biomass production)
  - flower development (sexual reproduction)
  - root development (asexual reproduction)
- Demonstrate reliable and effective gene silencing in *Phragmites*
- Test for reduction in competitive dominance of *Phragmites*

# Develop robust mode for generation of dsRNA in *Phragmites*

- Viral Induced Gene Silencing-VIGS
- Hairpin generating vectors
- Artificial microRNA- amiR

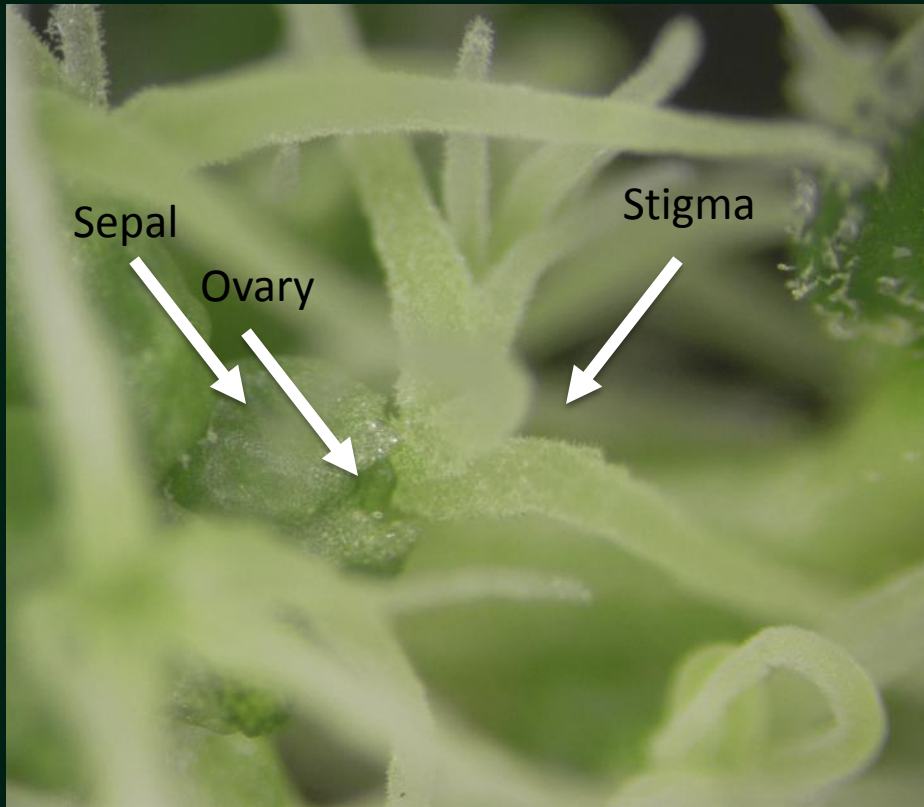
# VIGS- Viral Induced Gene Silencing

pWSRi is a Beet curly top virus (BCTV) based vector system (Golenberg et al 2009)



# Examples of Gene Silencing

## Sterilizing a Flower



Wildtype Spinach Female Flower

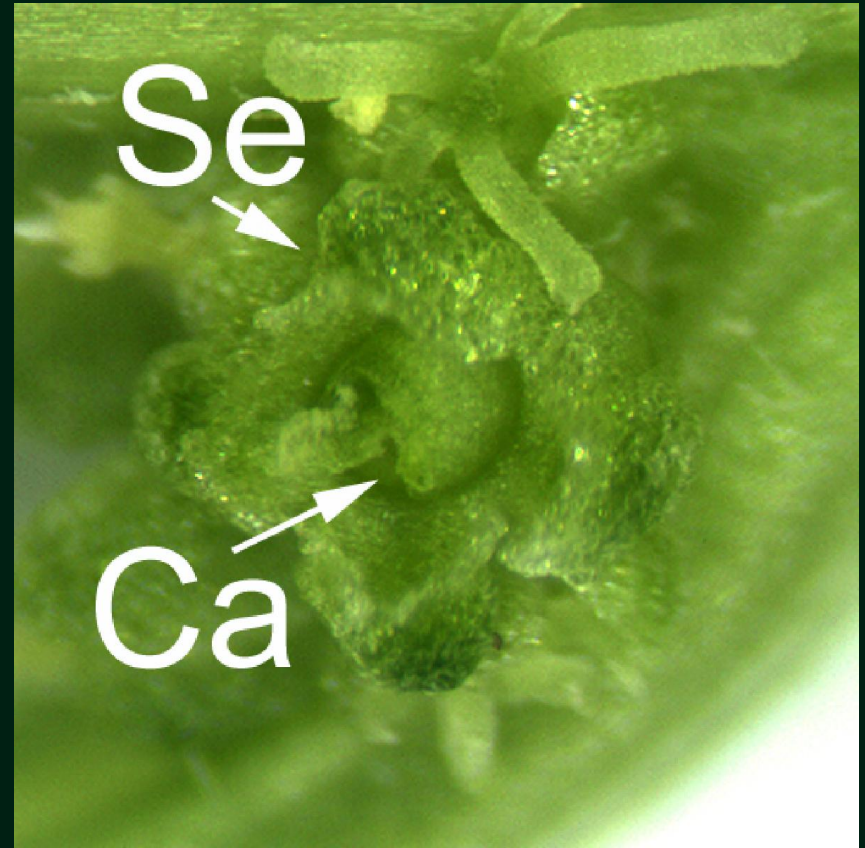


Sterile Silenced Female Flower

# Examples of Gene Silencing Changing Flower Gender



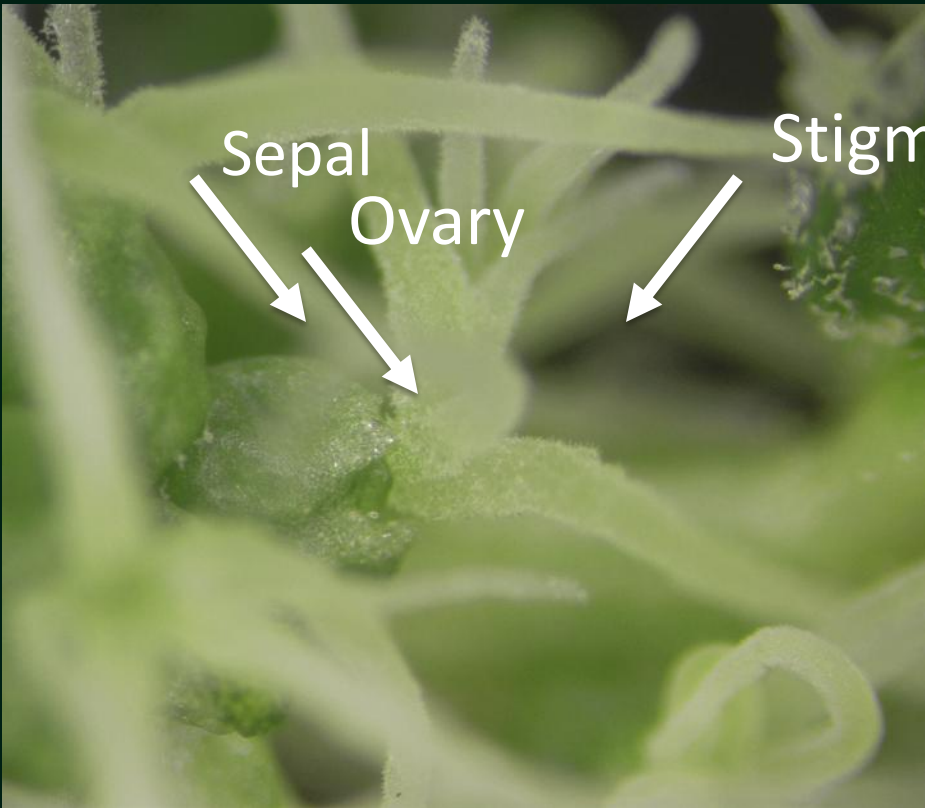
Wildtype Spinach Male Flower



Feminized Spinach Male Flower



# Examples of Gene Silencing Changing Flower Gender



Wildtype Spinach Female Flower



Masculinized Female Flower

# Examples of Gene Silencing Changing Flower Gender



Wildtype Spinach Male Flower

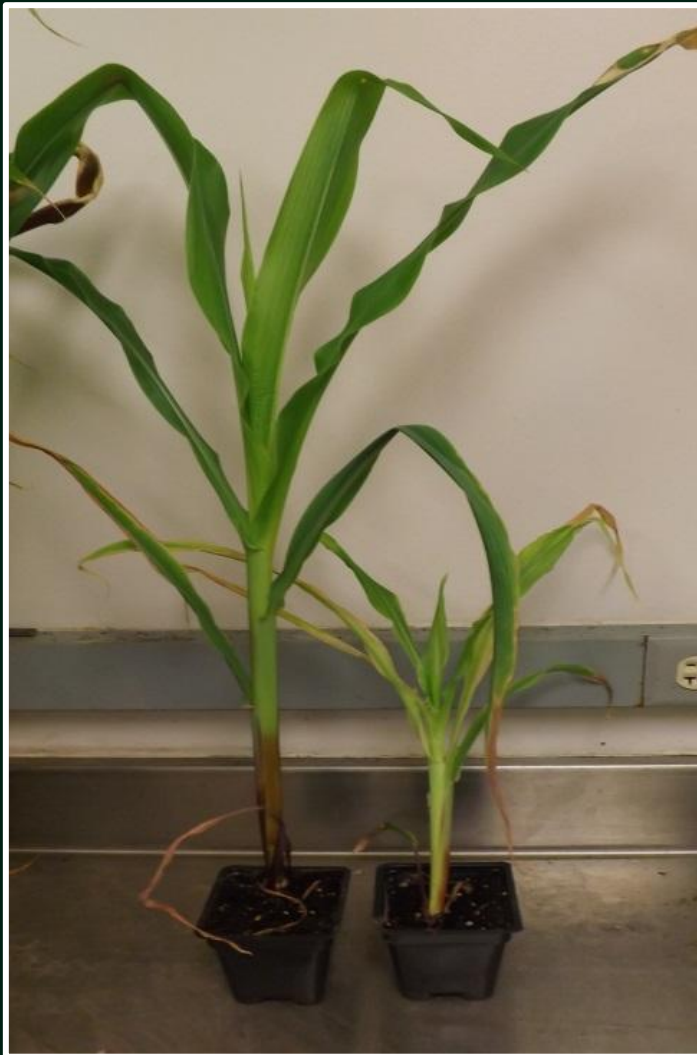


Hermaphroditized Spinach Male Flower

*pWSRiMSV:ZmPDS*  
Agrobacterium infected

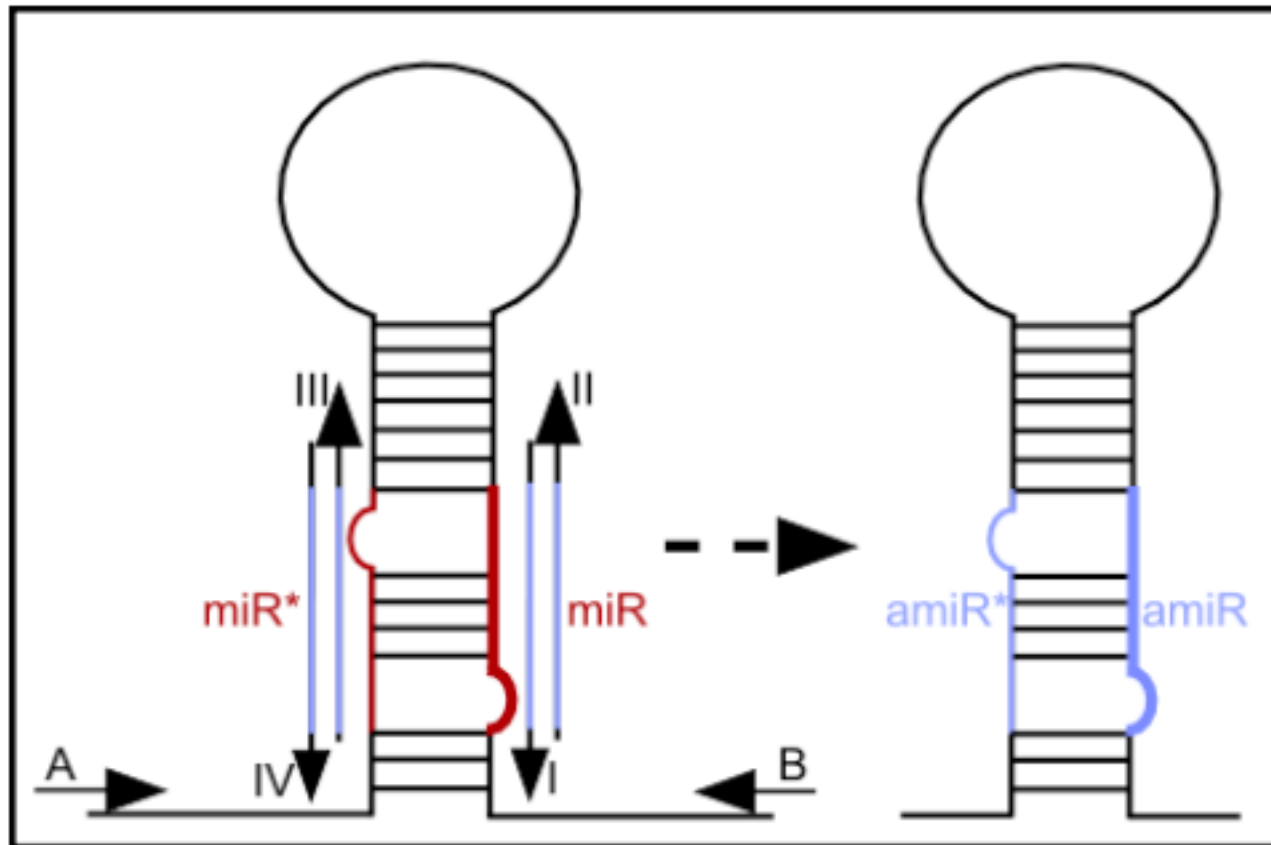


*pIPKb007:ZmPDS*  
*Agrobacterium* Infected



**Silenced Photosynthetic  
abilities in model grass  
species**

# amiR





# What's the advantage of switching to Artificial micro RNA (amiR)?

- Natural Micro RNA
  - Express genes in normal genomes
  - Used to regulate gene expression in development
  - Utilizes silencing machinery in the cell
- Artificial Micro RNA
  - Uses very small sequences for silencing
  - Gives the ability to design targets that are very specific
    - Can be species specific
    - Maybe even at the genotype level (i.e. native vs. invasive *Phragmites*)



pPEARLEYGATE100:ZmPDS<sup>mir-1</sup>











# amiR Trials in Sunflower



pPEARLEYGATE100:HaKOA1miR2



# GS Trials in *Phragmites*



# Construct Development

Species	Gene	System/Function	Name
<i>Helianthus annua</i> (Sunflower)	<i>rbcS</i>	Photosynthesis	<b>HarbcSmiR</b>
<i>Helianthus annua</i> (Sunflower)	<i>ent-kaurenoic acid oxidase (KA01 gene), dwarf2 mutant</i>	Gibberellin Production	<b>HaKOAmiR1</b>
<i>Helianthus annua</i> (Sunflower)	<i>ent-kaurenoic acid oxidase (KA01 gene), dwarf2 mutant</i>	Gibberellin Production	<b>HaKOAmiR2</b>
<i>Helianthus annua</i> (Sunflower)	<i>ent-kaurenoic acid oxidase (KA01 gene), dwarf2 mutant</i>	Gibberellin Production	<b>HaKOAmiR3</b>
<i>Zea mays</i> (Maize)	<i>rbcS</i>	Photosynthesis	<b>ZmrbcSmiR1</b>
<i>Zea mays</i> (Maize)	<i>rbcS</i>	Photosynthesis	<b>ZmrbcSmiR2</b>
<i>Zea mays</i> (Maize)	<i>GA 3-oxidase 1 (D1)</i>	Gibberellin Production	<b>ZmGA3OxmiR1</b>
<i>Zea mays</i> (Maize)	<i>phytoene desaturase (pds1)</i>	Photosynthesis	<b>ZmPDStasiR</b>
<i>Zea mays</i> (Maize)	<i>phytoene desaturase (pds1)</i>	Photosynthesis	<b>ZmPDSmiR1</b>
<i>Zea mays</i> (Maize)	<i>phytoene desaturase (pds1)</i>	Photosynthesis	<b>ZmPDSmiR2</b>
<i>Zea mays</i> (Maize)	<i>phytoene desaturase (pds1)</i>	Photosynthesis	<b>ZmPDSmiR3</b>
<i>Zea mays</i> (Maize)	<i>phytoene desaturase (pds1)</i>	Photosynthesis	<b>ZmPDSmiR4</b>
<i>Zea mays</i> (Maize)	<i>magnesium chelatase subunit I precursor (ChlI), oil yellow</i>	Photosynthesis	<b>ZmY01ImiR1</b>
<i>Zea mays</i> (Maize)	<i>magnesium chelatase subunit I precursor (ChlI), oil yellow</i>	Photosynthesis	<b>ZmY01ImiR2</b>
<i>Phragmites australis</i>	<i>phytoene desaturase</i> –derived from transcriptome	Photosynthesis	<b>PaPDSmiR</b>
<i>Phragmites australis</i>	<i>phytoene desaturase</i> –derived from transcriptome	Photosynthesis	<b>PaPDSmiR</b>
<i>Phragmites australis</i>	<i>phytoene desaturase</i> –derived from transcriptome	Photosynthesis	<b>PaPDStasiR</b>
<i>Phragmites australis</i>	<i>GA 3-oxidase 1</i> - derived from transcriptome	Gibberellin Production	<b>PaGA3OxmiR1</b>
<i>Phragmites australis</i>	<i>GA 3-oxidase 1</i> - derived from transcriptome	Gibberellin Production	<b>PaGA3OxmiR2</b>



How do we transfer from model  
species to *Phragmites*?



# Building *Phragmites* Data Base

- Identify genetic code for particular traits in *Phragmites*
  - *Phragmites* transcriptome sequenced
    - Generated 4 RNAseq libraries: Inflorescence, Leaf, Root, Ramet meristem
    - Pair-end sequences for each library
    - Sequences each direction per library: Inflorescence and leaf 35 million each , Root and meristem 25 million each
  - Target traits Identified

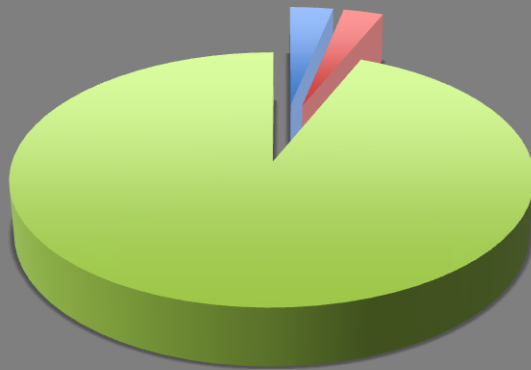
# *Phragmites* Transcriptome

Tissue	Transcriptome Length	Proportion of total
Inflorescence	32826103	0.262
Leaf	146724	0.001
Root	151693	0.001
Shoot tip	22670484	0.181
Shared	69294171	0.554



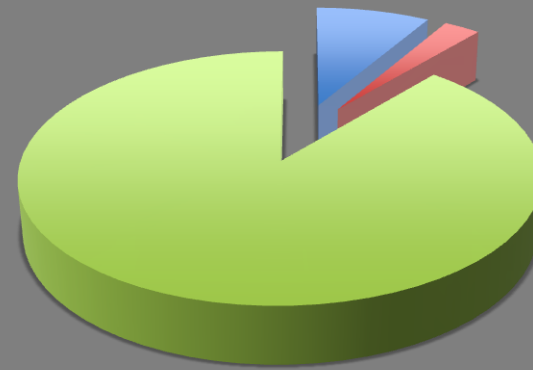
# *Phragmites* Transcriptome Transcript Distribution by Tissue

Flower



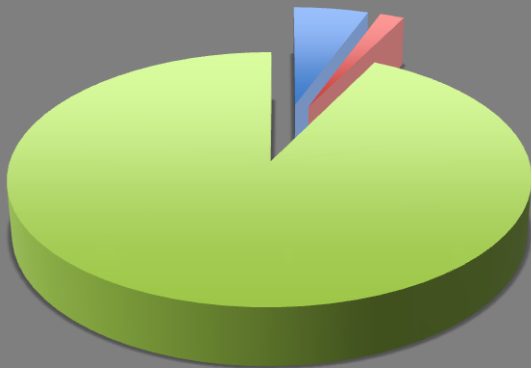
■ mt % of total  
■ cp % of total  
■ other % of total

Root



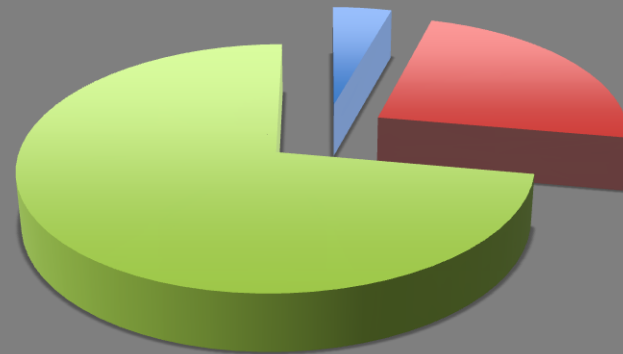
■ mt % of total  
■ cp % of total  
■ other % of total

Meristem



■ mt % of total  
■ cp % of total  
■ other % of total

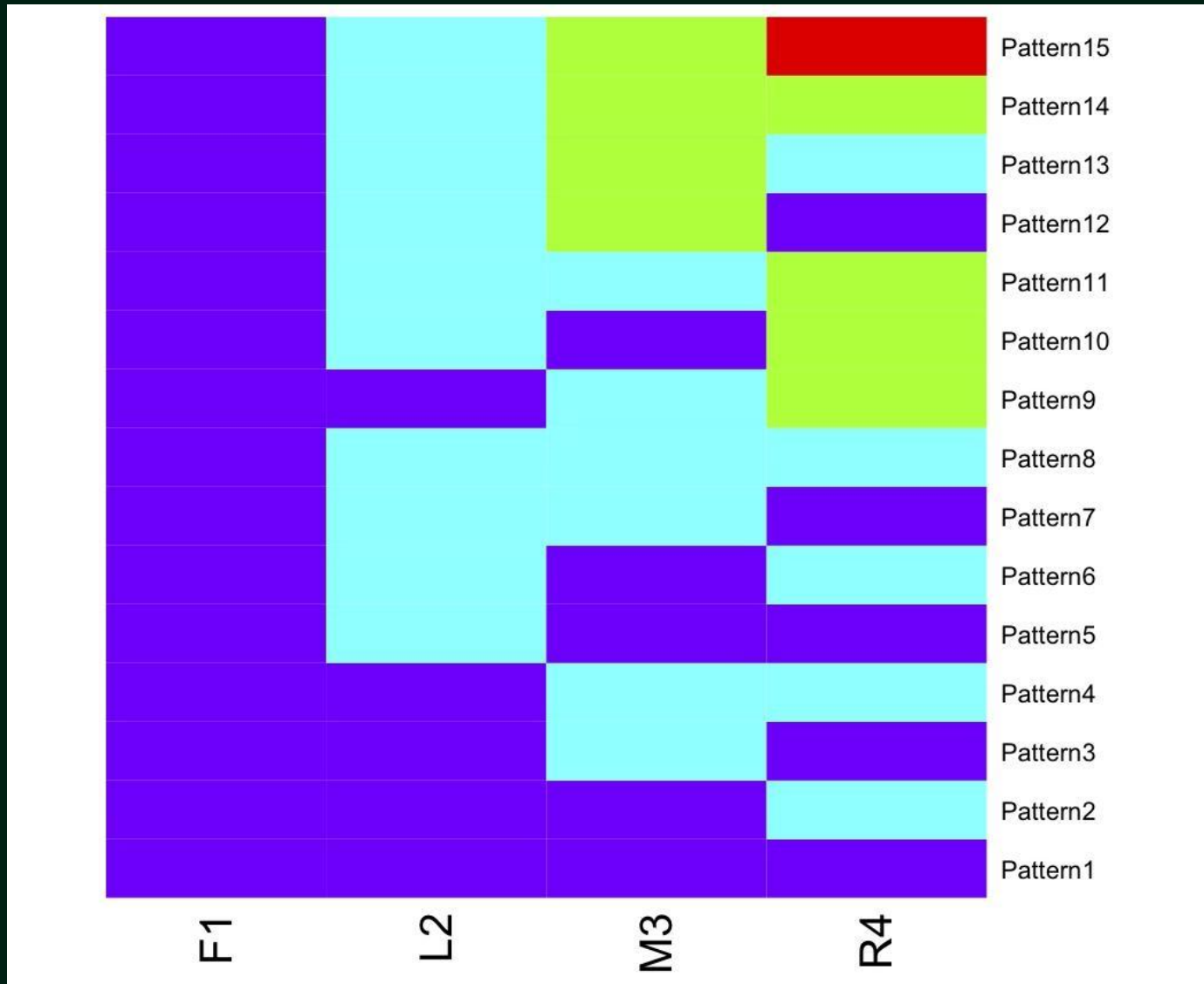
Leaf



■ mt % of total  
■ cp % of total  
■ other % of total

# Transcriptome Analysis

## *Phragmites* Differential Expression



# Transcriptome Analysis

## *Phragmites* Differential Expression

	0	1	2	3	4
#	184	135597	608	639	31155
5	6	7	8	9	10
17574	586	350	48574	455	317
11	12	13	14	15	
136	105	307	9983	330	

Pattern 1- All the same

Pattern 4- (FL)(MR)

Pattern 5- L(FMR)

Pattern 8- F(LMR)

Pattern 14- (F)(L)(MR)

# Why *Phragmites* Transcriptome is Important

- Once gene sequences are identified, specific traits can be targeted for silencing
- Differential expression patterns among strains of *Phragmites* (native vs. invasive) may identify specific targets
- Generates broad database for scientific community

# Why is Gene Silencing Important?

- The Holy Grail- This will show first real proof of gene silencing as a viable management/control option
- If silencing vector is effective in mixed plant compositions, widespread application in the field could be an option
- If invasive *Phragmites* is affected and native is not, that makes widespread application more ecologically viable



# Caveats and Concerns

- Penetrance and expressivity of miRs in *Phragmites*
- Persistence of silencing temporally
- Modes of applications
  - Mechanistically how to scale up
  - Environmentally are there unintended effects
- Development of management plans that includes guidelines for applications and reintroduction of native species

# This could be BIG

If gene silencing is effective in a field setting and proves to be species specific, it will represent a huge breakthrough in invasive species management



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# Thank you



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