



## Synthetic Induction of 22nt tasiRNAs

### OVERVIEW

Potato Virus Y (PVY) is the main virus associated with potato viral disease, causing decreased yield and quality of crops, and is the most economically damaging potato virus, causing up to 100% yield loss.

This technology uses synthetic tasiRNAs to degrade RNA produced by PVY. The modification of potato plants to produce tasiRNAs against PVY (tasiPVYs) generates potatoes resistance to the four epidemiologically important PVY strains that affect North American potato crops.

### KEY ADVANTAGES

- This technology uses plant gene regulation mechanisms to generate potato plants which can suppress and degrade PVY genes, producing potato plants resistant to the virus
- Non-toxic to the plant
- Better efficacy and distribution throughout the plants than current RNA-based methods to control PVY infection.

### APPLICATIONS

This technology can be used to produce potato plants which are resistant to PVY disease, and has potential to be used against other potato viruses such as *Potato mop-top virus*, and *Tobacco rattle virus*.

### DETAILS

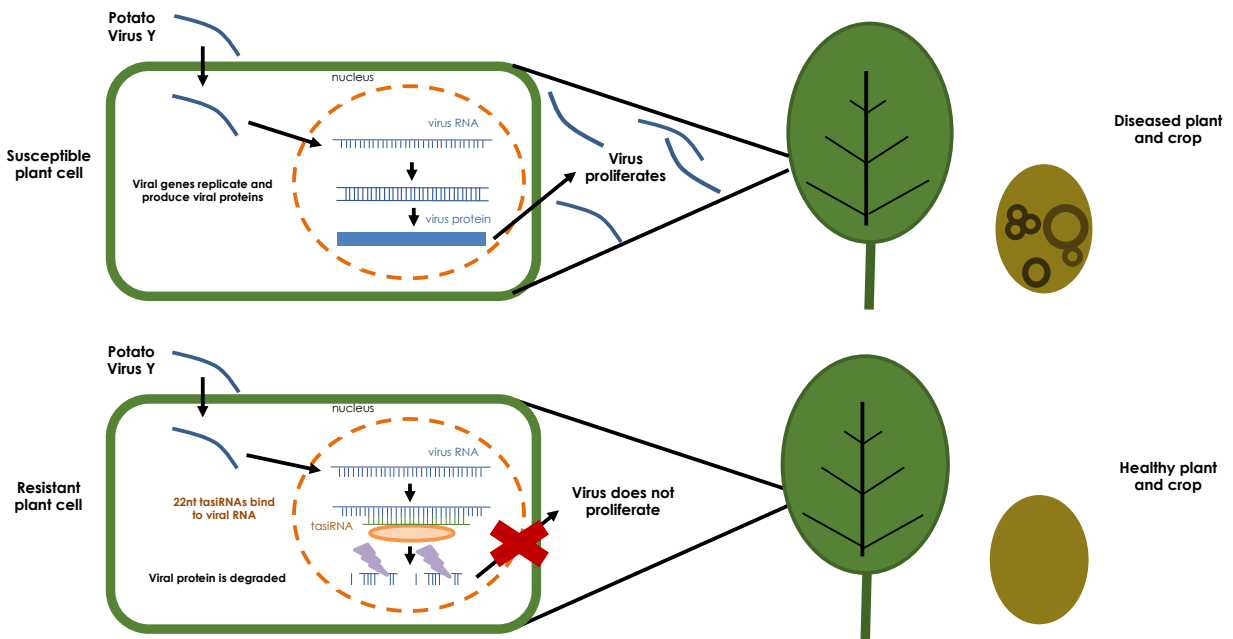
**Tech ID:**  
DDPSC0092

**Status:**  
Patent Filed

**Stage:**  
Proof of Concept

**Inventors:**  
Patricia Baldrich, Ph.D.  
Rui Xia, Ph.D.  
Blake Meyers, Ph.D.







## Inventor Background

### BLAKE MEYERS, PH.D.

Research in the Meyers lab focuses on utilizing genome-scale RNA studies to elucidate RNA function and silencing pathways in a range of plants. The Meyers group characterizes small RNAs to determine both their function and synthesis, which will lead to a greater understanding of plant gene expression. This approach is currently being used by the Meyers lab to determine how microRNAs against disease resistance genes are used in plant defenses against pathogens.

### RUI XIA, PH.D.

Rui researches regulations of RNA in a variety of plants, with a focus on small RNAs.

### PATRICIA BALDRICH, PH.D.

Patricia's work aims to identify plant gene regulation by microRNAs. She uses RNA sequencing data to determine the abundance of microRNAs in plants, and deep sequencing to identify RNA modifications such as uridylation and methylation.

