

Finding the known and unknown, plant waterborne virus in Oklahoma water

**Jon Daniels,
Suat Kaimak,
Francisco Ochoa Corona**

Oklahoma State University

**National Institute for Microbial Forensics
& Food and Agricultural Biosecurity**

Dept. of Entomology & Plant Pathology



The predicament...

**U.S. imports ~ 40 million tons
of agricultural products**



**Only 2% inspected:
> 39 million tons uninspected**

**Plus:
Tourism, immigration,
weather**

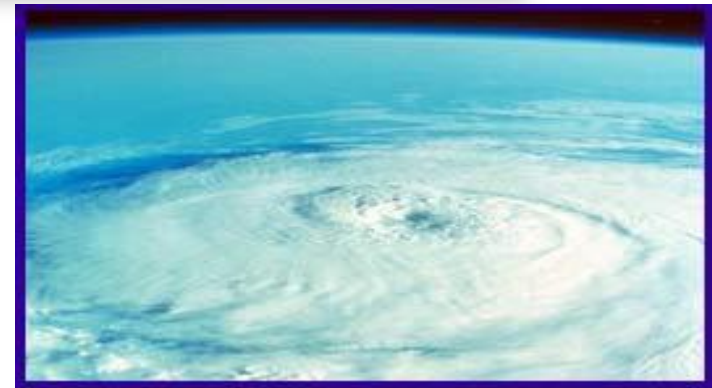


photo: ArtToday.com

The result



**Citrus
Greening**



**Plum Pox
Virus**



**Citrus
Leprosis**



**Soybean
Rust**



**Canna
Yellow
Mosaic Virus**



**Brown
spot**



**Lethal Yellowing of
Palm**

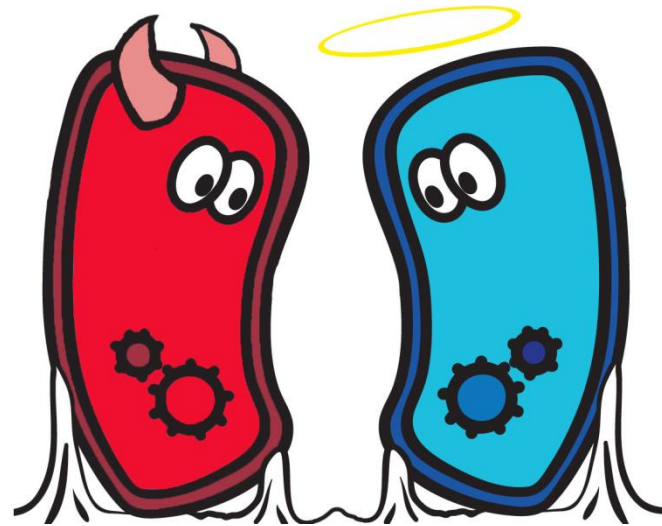


Southern Wilt

Challenges in plant pathogen diagnostics

- **Multiple types of plant pathogens**

- Viral
- Bacterial
- Fungal
- Phytoplasma
- Nematodes

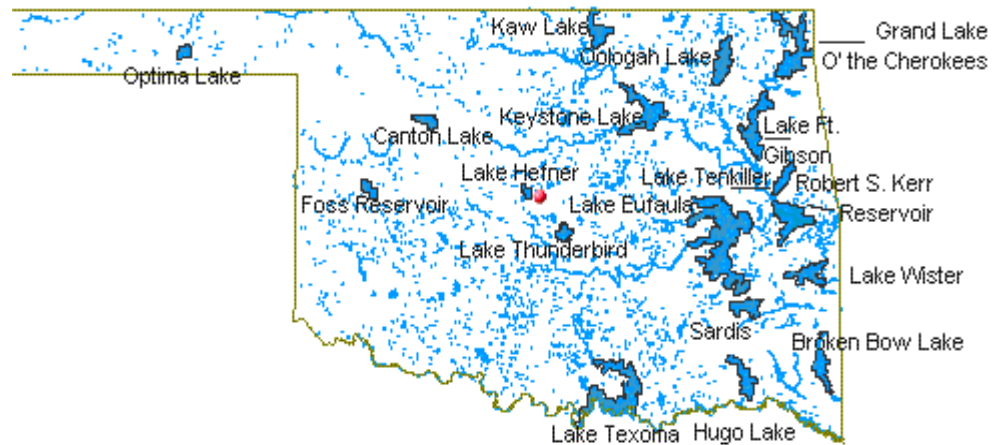


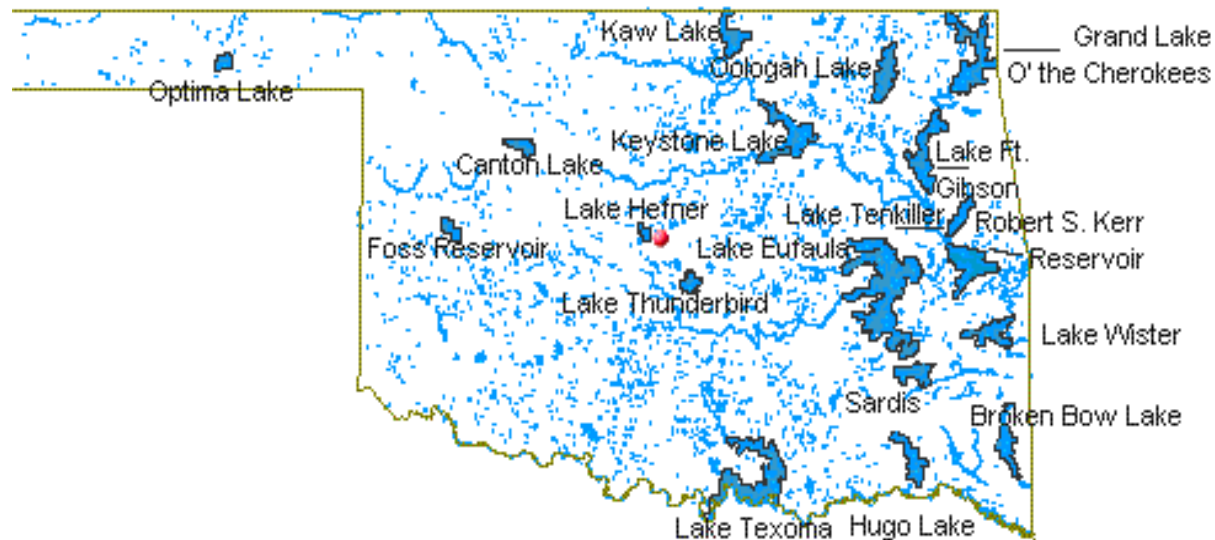
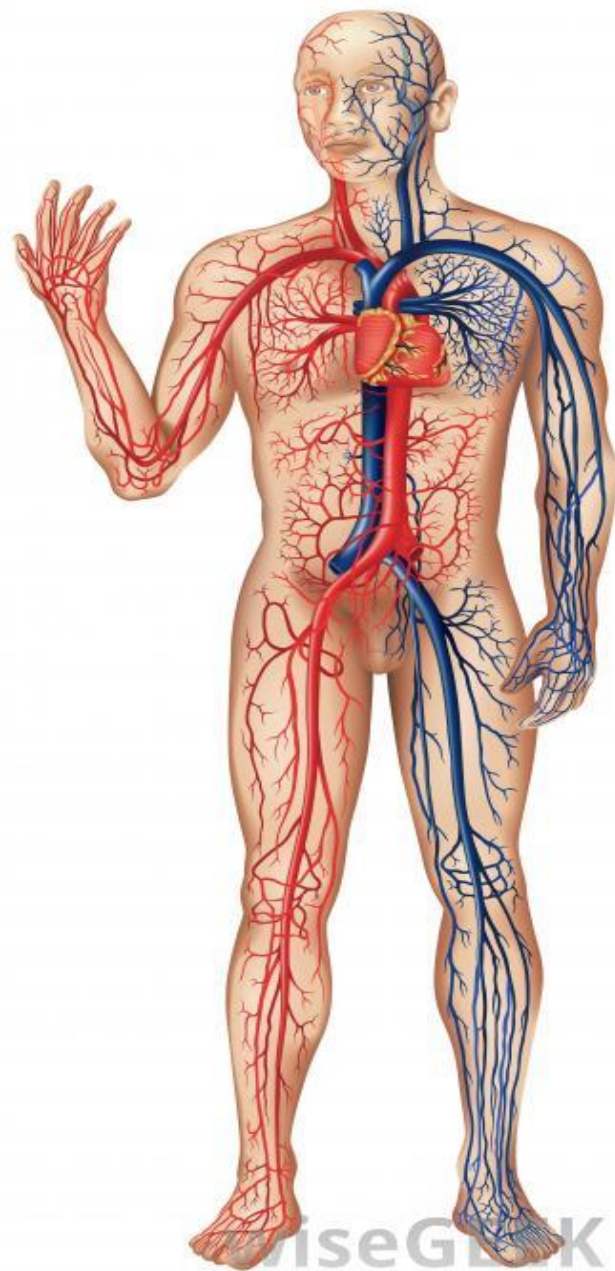
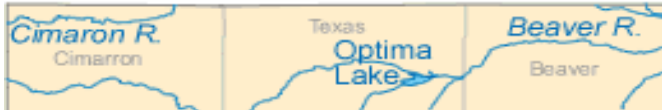
- **Non-pathogenic microbes living in the environment**

- Who are the good guys and who are the bad guys?

Oklahoma water

- Over 200 lakes
- Over 1 million surface acres of water
- Numerous rivers, streams & ponds
- Boating & swimming





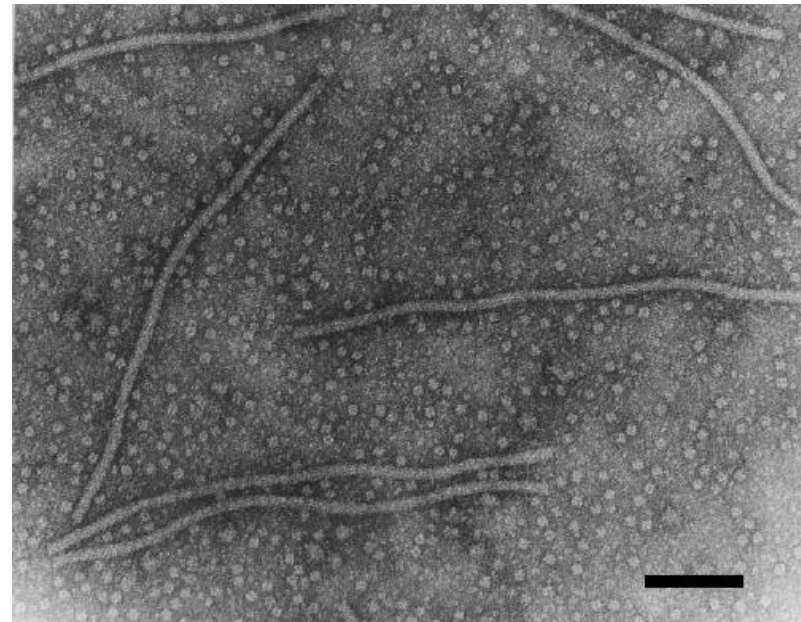
Waterborne viruses

- What do we mean by waterborne pathogens?
 - A ~~organism~~ virus capable of causing disease that can be transmitted via water
- ***Potexviruses***
- ***Tobamovirus***
- ***Tombusviridae***

Waterborne viruses

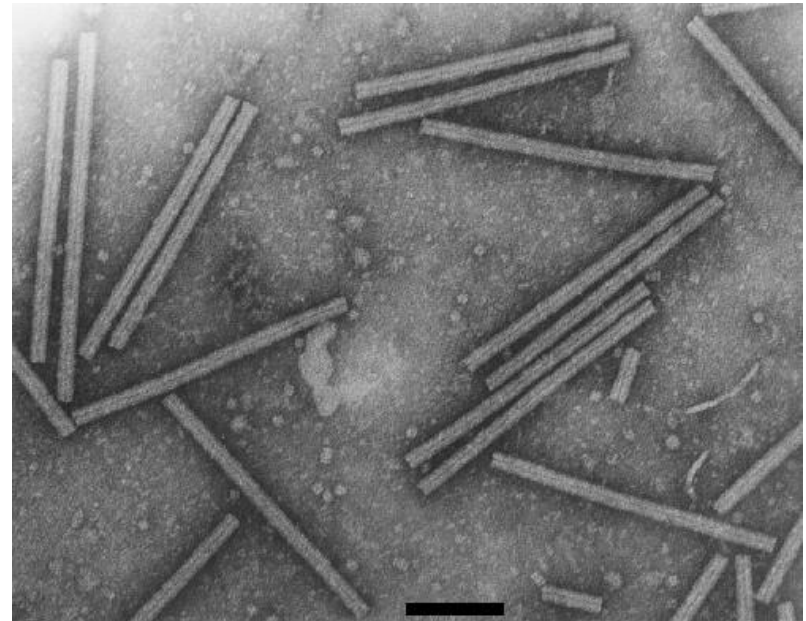
- What do we mean by waterborne pathogens?
 - A ~~organism~~ virus capable of causing disease that can be transmitted via water
- ***Potexviruses***

- *Tobamovirus*
- *Tombusviridae*



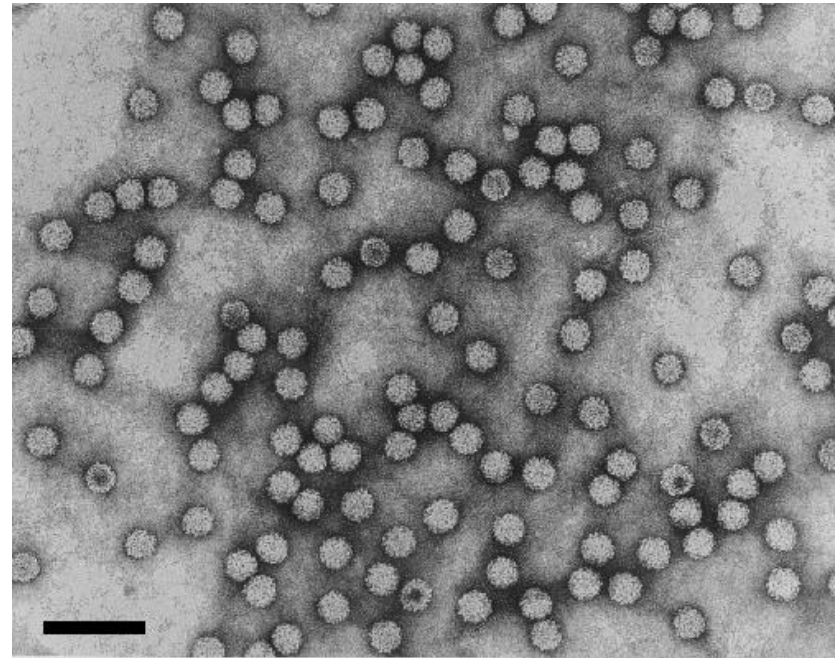
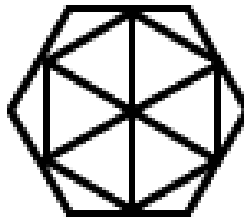
Waterborne viruses

- What do we mean by waterborne pathogens?
 - A ~~organism~~ virus capable of causing disease that can be transmitted via water
- *Potexviruses*
- *Tobamovirus*
- *Tombusviridae*



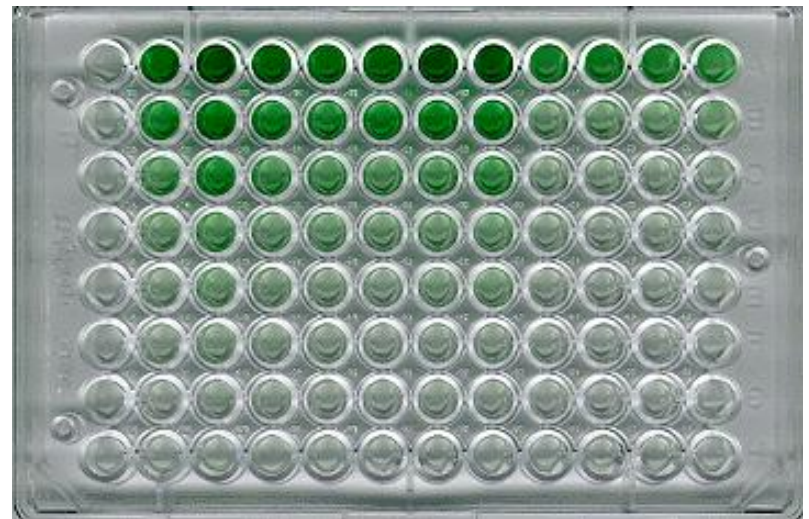
Waterborne viruses

- What do we mean by waterborne pathogens?
 - A ~~organism~~ virus capable of causing disease that can be transmitted via water
- *Potexviruses*
- *Tobamovirus*
- *Tombusviridae*



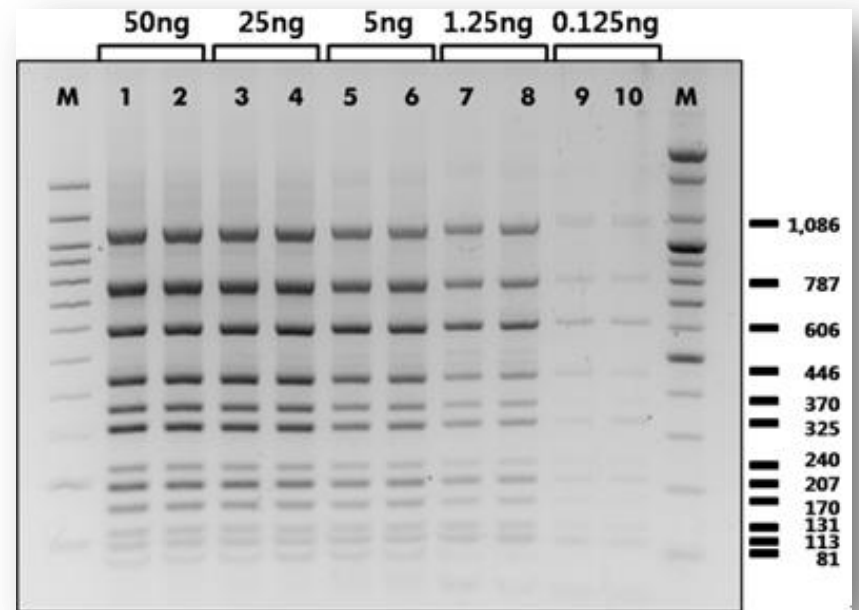
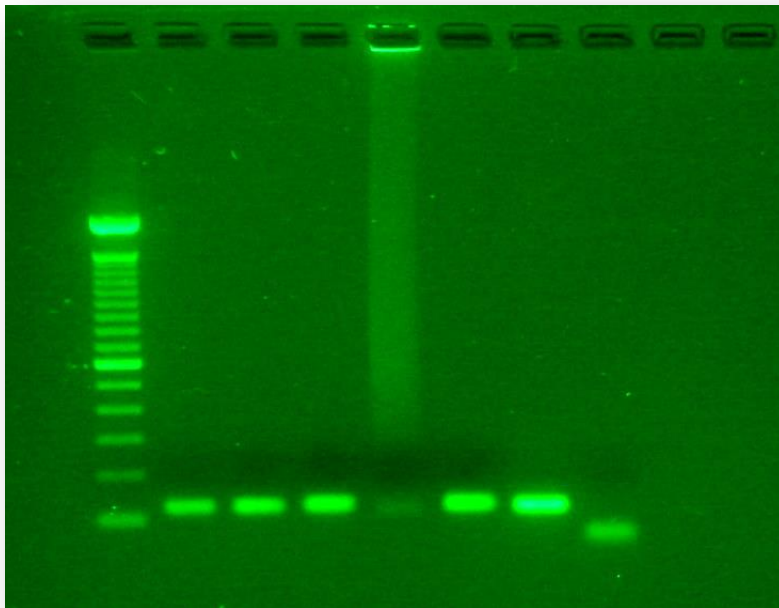
Current plant pathogen detection technologies

- **Protein based immunological assays**
 - Immunostrip test
 - ELISA



Current plant pathogen detection technologies

- **Nucleic acid based assays**
 - Polymerase chain reaction (PCR)
 - qPCR
 - Multiplex PCR

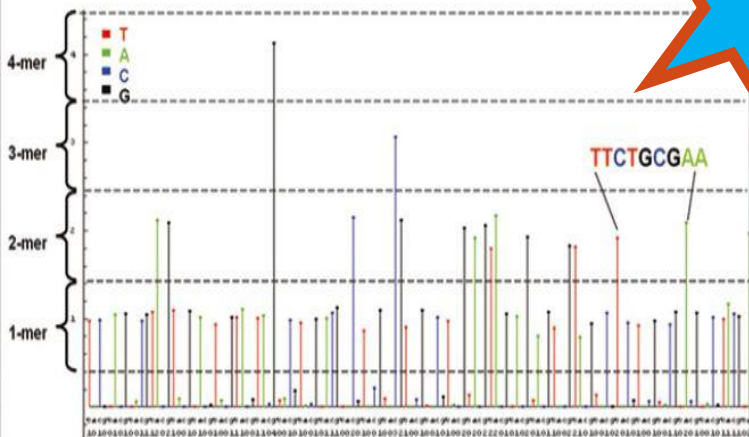
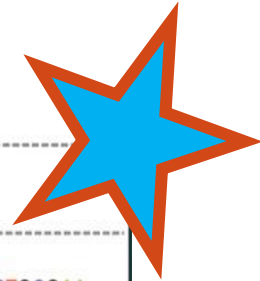
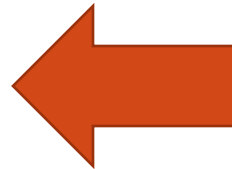
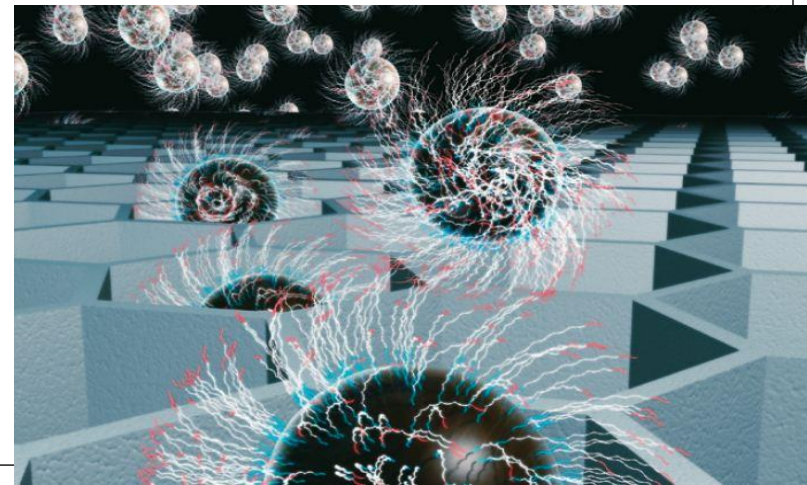
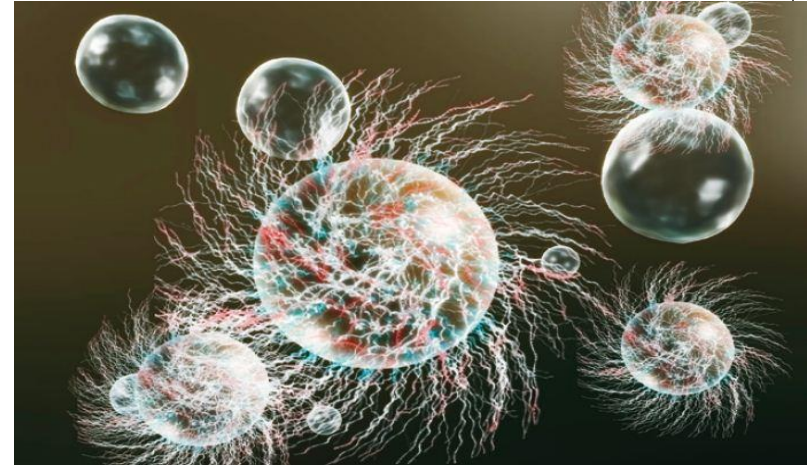
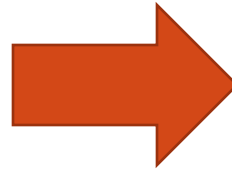
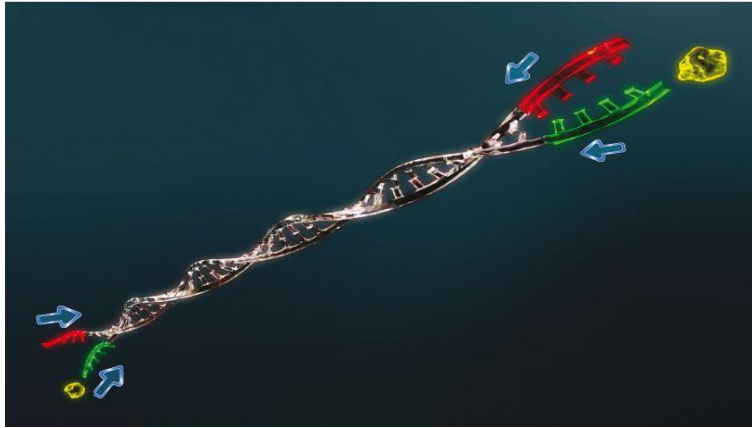


Current plant pathogen detection technologies

- **Protein based immunological assays**
 - Immunostrip test
 - ELISA
- **Nucleic acid based assays**
 - Polymerase chain reaction (PCR)
 - qPCR
 - Multiplex PCR
- **Can only detect a few pathogens at a time**
- **Prior characterization of the pathogen is required for all**

Next generation sequencing technology

- 454 Pyrosequencing

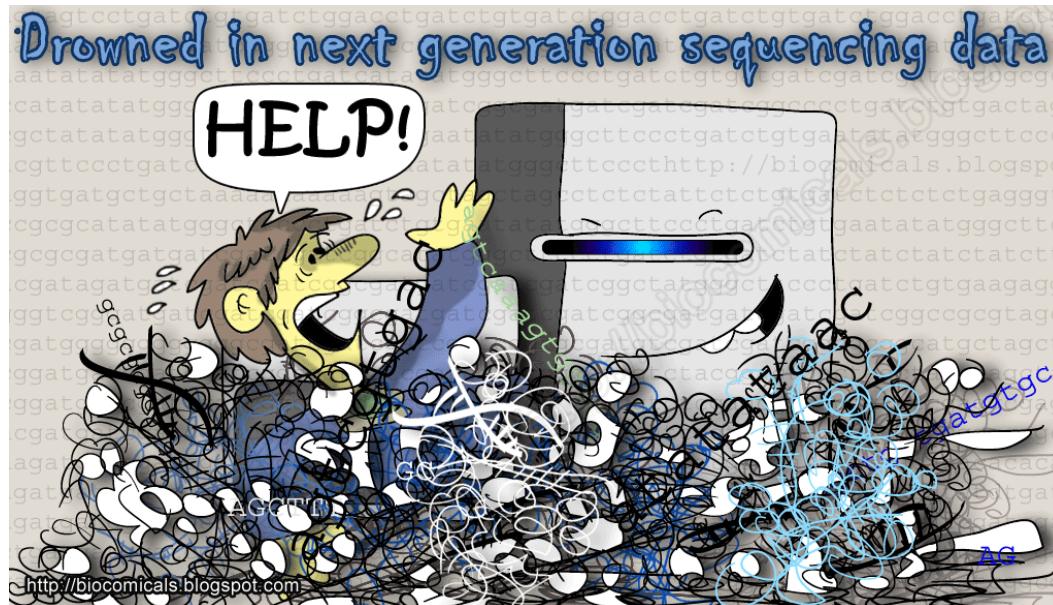


Next generation sequencing technology

- **454 Junior Pyrosequencing Power**
 - **Generates 35 million bases (Roche)**
 - OSU Core facility over 61million bases
 - Read length ~400 bp
 - **100,000 shotgun reads**
- **Roche 454**
- **SOLiD**
- **Illumina**
- **Ion Torrent**

Why use next generation sequencing?

- We get an enormous amount of data
- What to do with all that sequence data?
- We do not need all of the data
- Eliminate all irrelevant sequence data and reduce the bioinformatic load

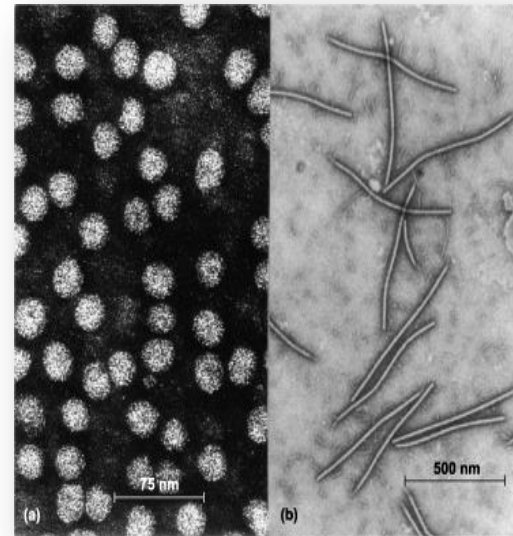
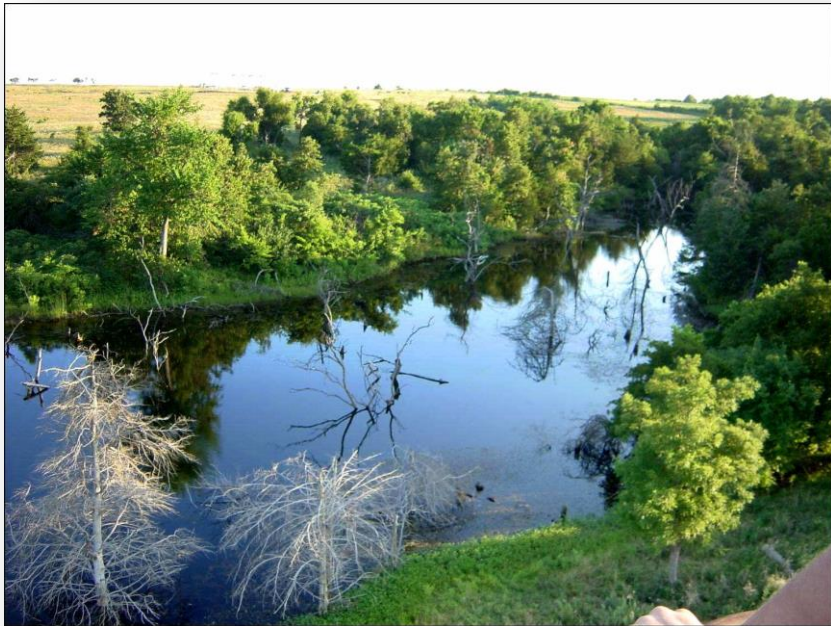


Justifications

- One-sixth of the GDP = \$1 trillion annually
- 1 in every 8 individuals is employed by the **total agricultural industry**
- \$50 billion in exports annually
- Single largest positive contributor to the U.S. economy
- In Oklahoma, ~\$1 billion annually (2005)
- NGS allows the possibility of simultaneously **detecting** and **identifying** unknown waterborne plant pathogens

Purpose

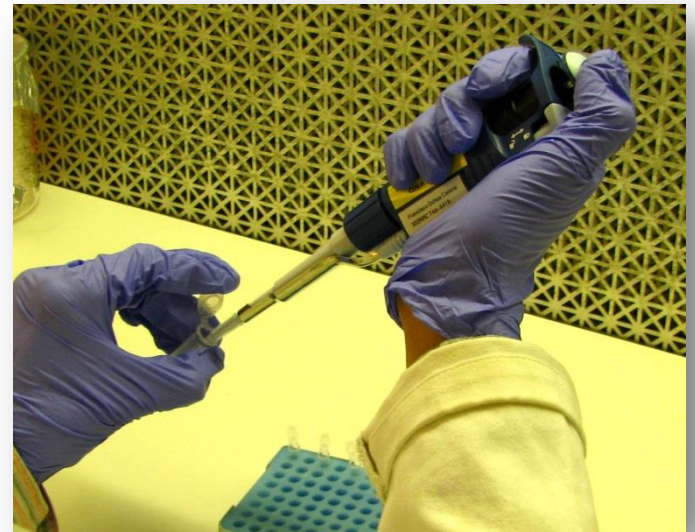
This study addresses the current need for detecting water borne viruses, in a single assay by combining metagenomics, NGS and bioinformatics. Our goal is to develop simple methods to facilitate the role of first detectors and managers monitoring water resources.



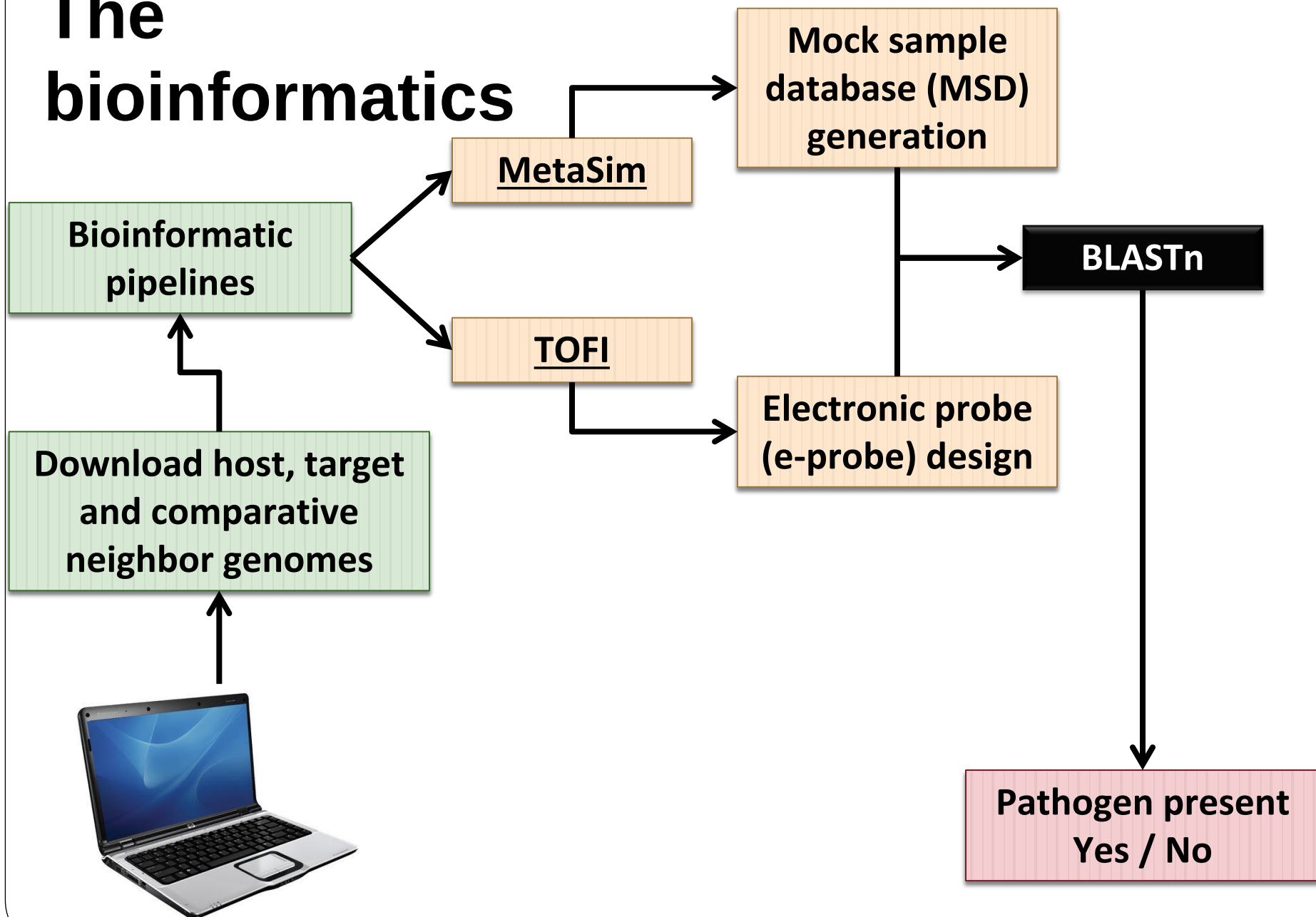
Virus

How can we detect waterborne viruses?

- Use tools/methods that combine **bioinformatics** with **plant pathology**

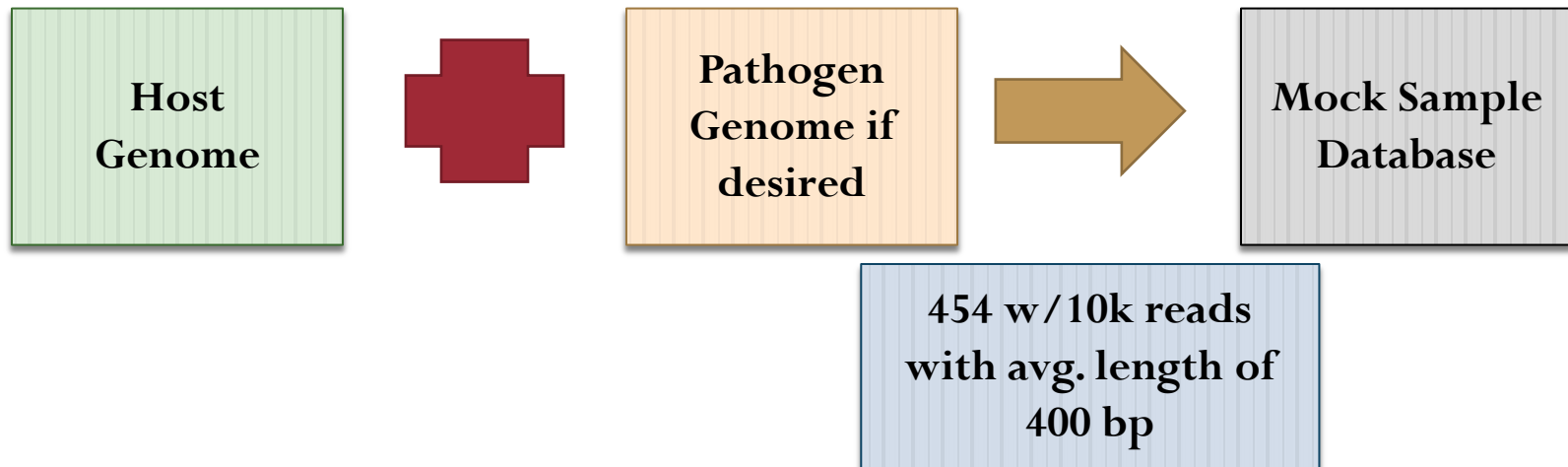
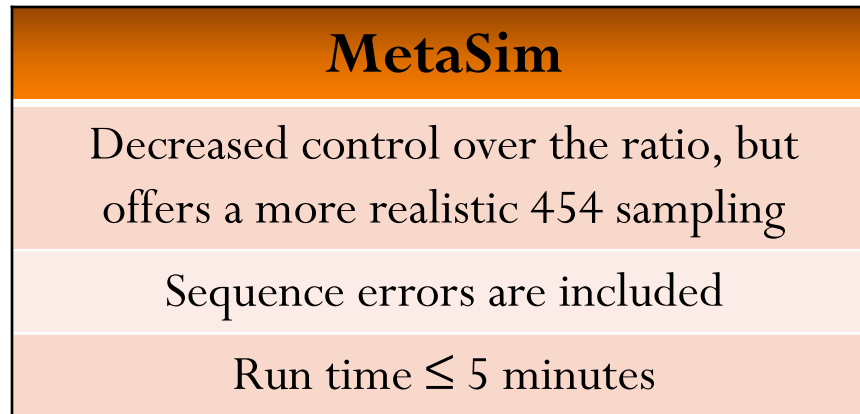


The bioinformatics



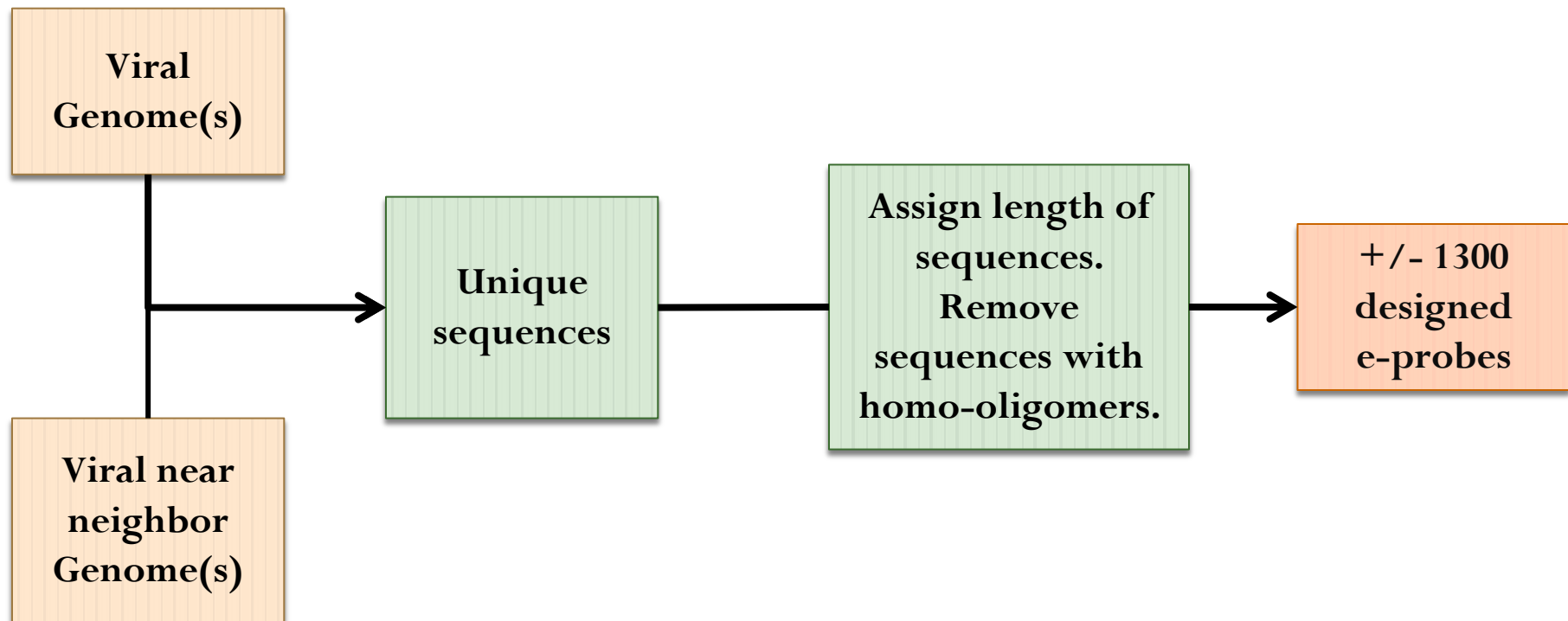
Mock Sample Database Generation

- Develop a Mock Sample Database for BLAST



Electronic probe (e-probe) design

- The pipeline for **e-probe** generation by using parts of **Tools for Oligo Fingerprint Identification (TOFI)**.



E-probe design

- Developed a pipeline for query generation by using parts of Tools for Oligo Fingerprint Identification (**TOFI**).

Target virus



Neighbor

E-probe design

- Developed a pipeline for query generation by using parts of Tools for Oligo Fingerprint Identification (**TOFI**).

Target virus

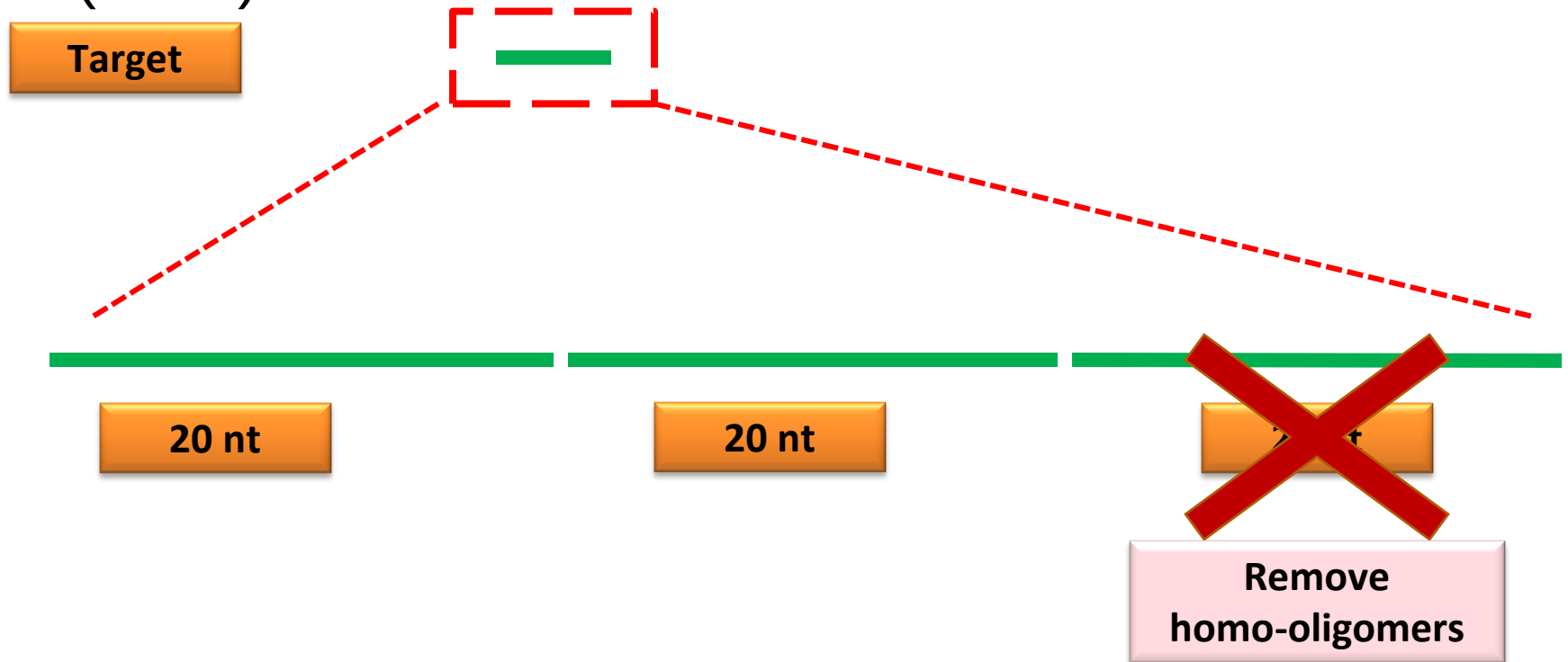


Neighbor



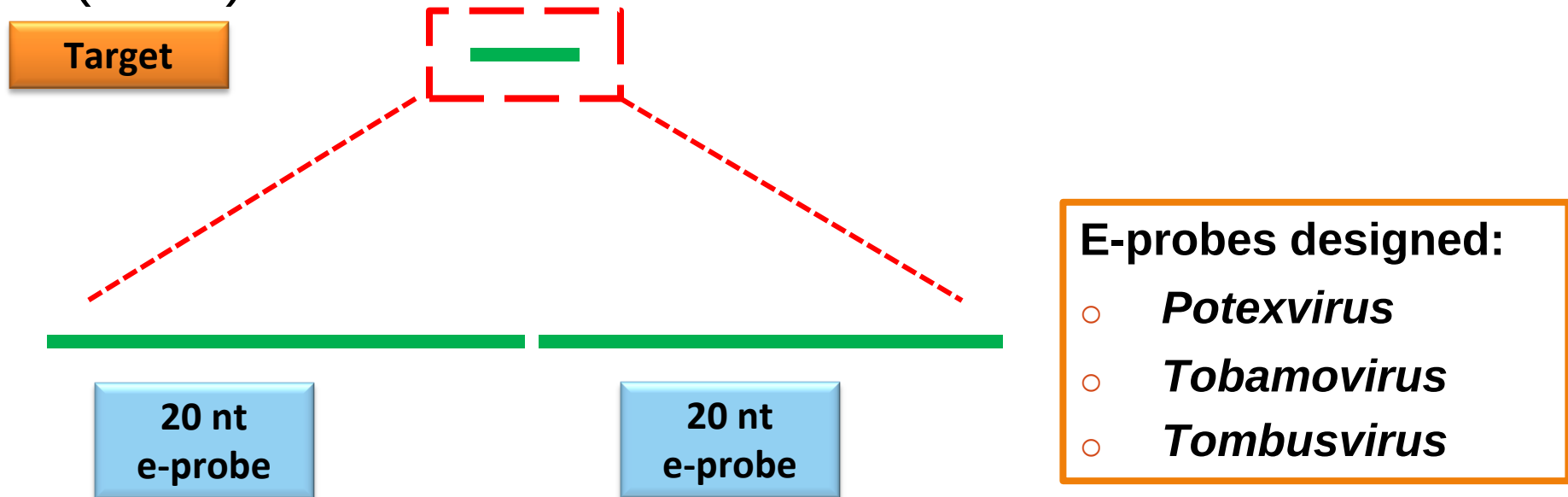
E-probe design

- Developed a pipeline for query generation by using parts of Tools for Oligo Fingerprint Identification (**TOFI**).



E-probe design

- Developed a pipeline for query generation by using parts of Tools for Oligo Fingerprint Identification (TOFI).



In silico results from a 100-year agricultural field metagenomic database

NGS Simulator MetaSim	Total # of viral genomes	Avg. individual virus load	Total viral load	Total matches	Pathogenic virus present yes/no
NGS simulator (non-spiked)	unknown	unknown	unknown	1	Yes
NGS simulator (spiked)	27	0.14%	3.76%	343	Yes

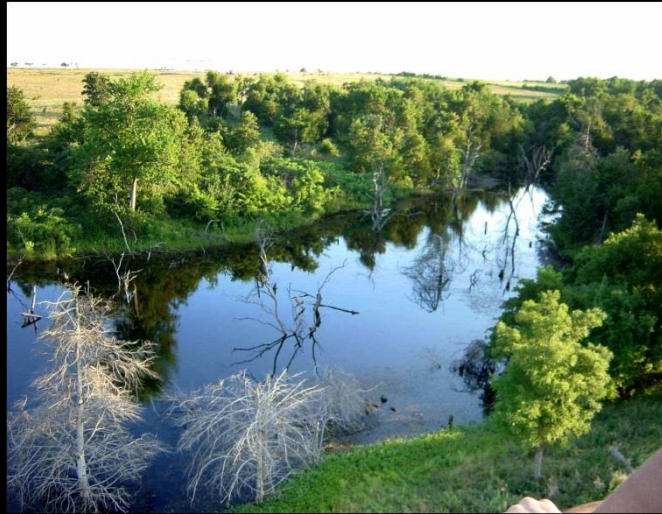
E-probes used:

- *Potexviruses*
- *Tobamovirus*
- *Tombusviridae*

Odontoglossum ringspot virus (ORSV)

- ssRNA
- Plant pathogenic virus affecting orchids

Experiment Collection sites



1



2



3



Experiment:

Basic procedures



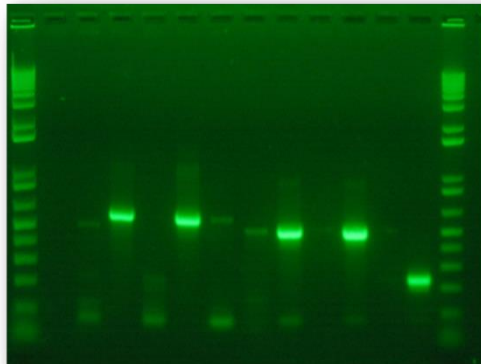
Collection



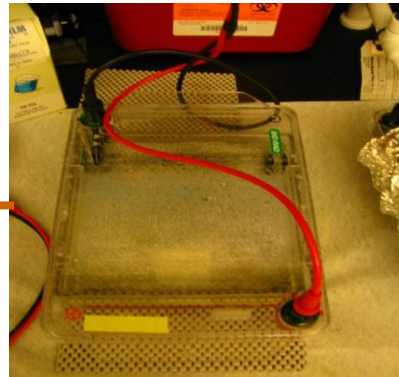
Extraction



PCR amplification



Products

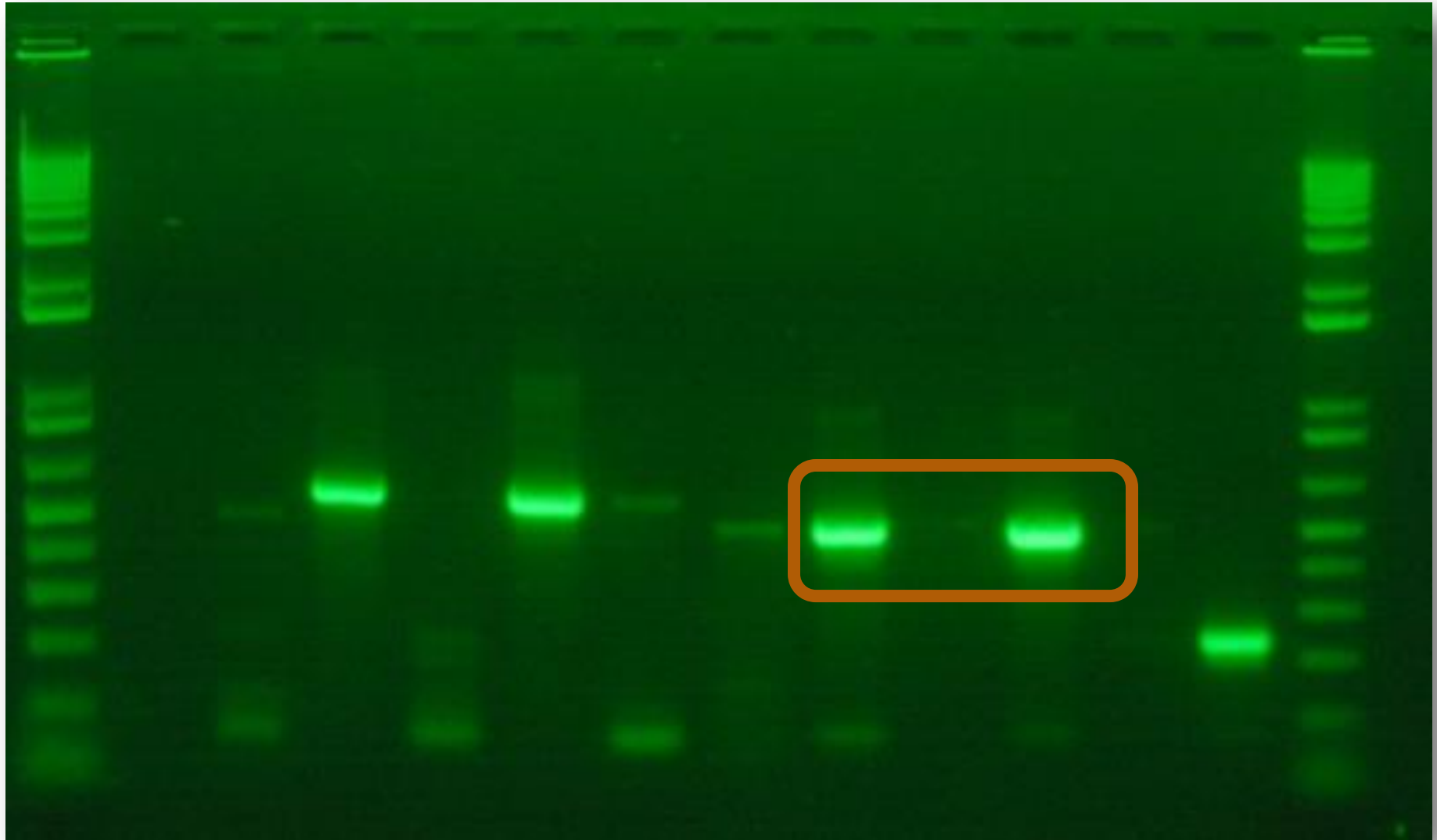


Gel electrophoresis



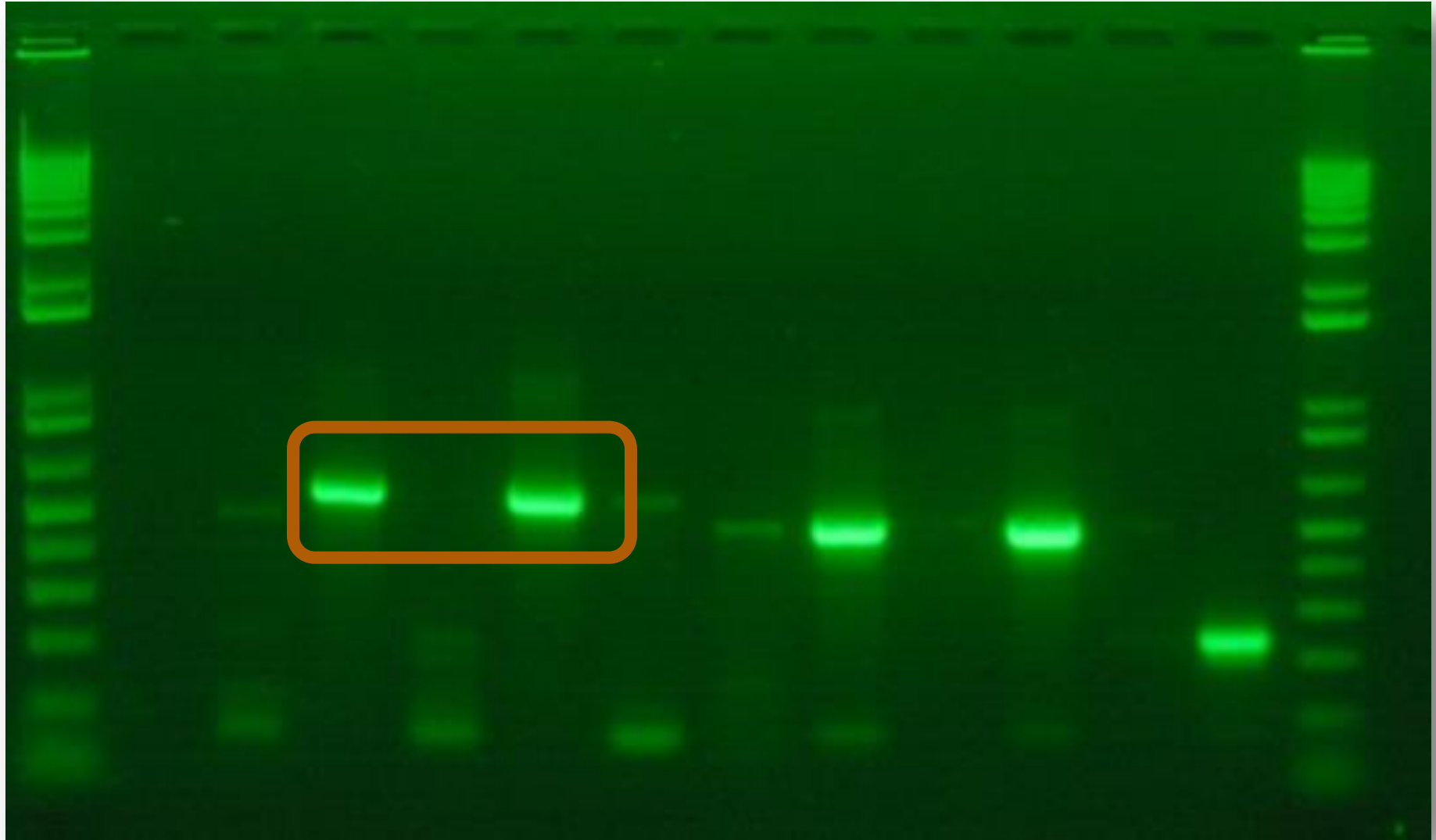
Experiment

Gel electrophoresis: *Tombusvirus*?



Experiment

Gel electrophoresis: *Potexvirus*?



Sequencing the bands

- **>*Tombusvirus***

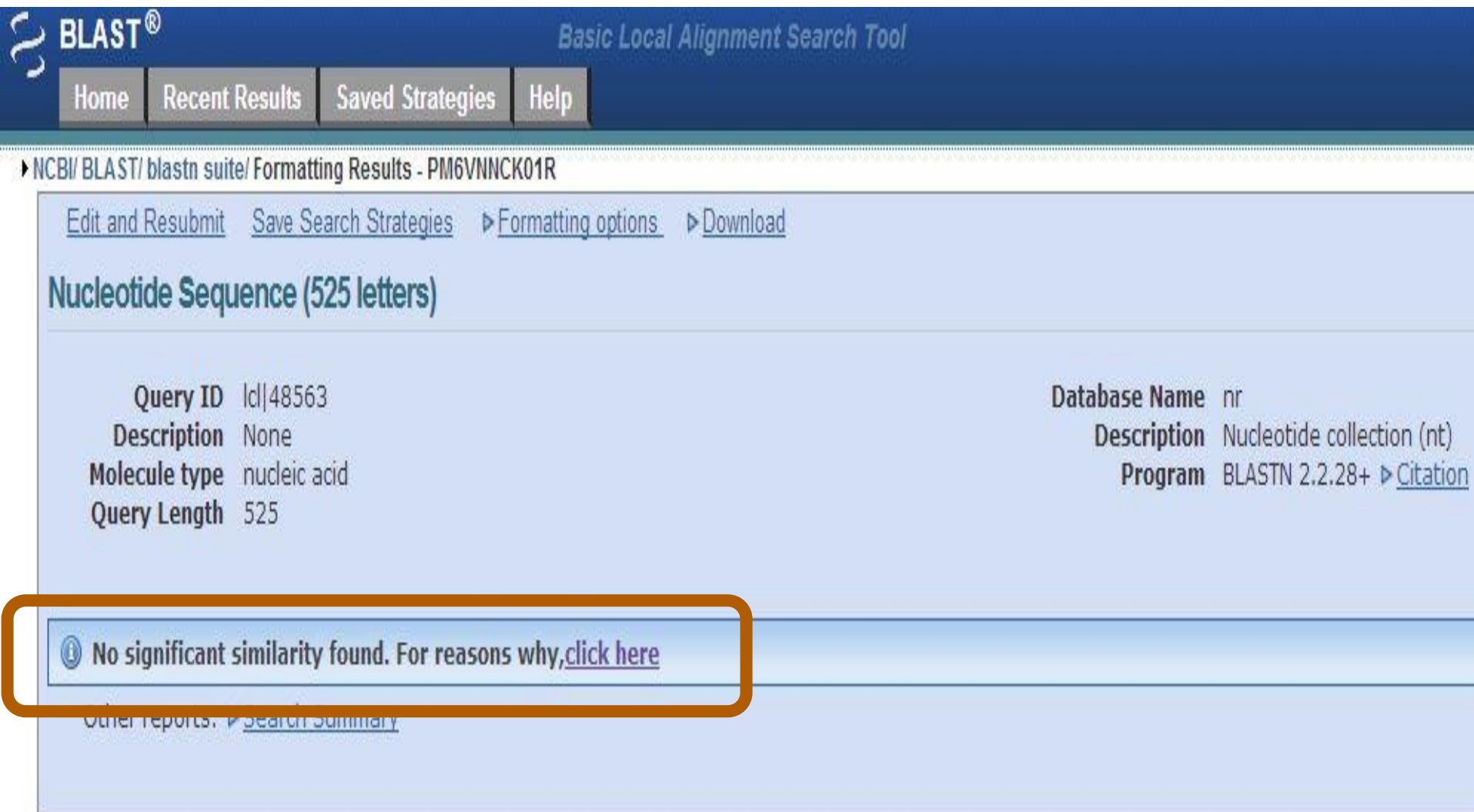
- AAGGGTAAAAGGATGGTGAGGTATTCCGTTTTGACCATGTCGCCTGCGATCCAGGCATTGAGGGATA
GGCATTGAGGGATCGCTTGTCCAACAAGGATTGGCGGATGCGGAACCTTTACCTCATCCTCGACGA
GGAGGGTAGGACCGTTCCGTTTGTATGCGGGGCGAGCAGGAGCAGTTCCTGCGGGAGAGGCACA
ACCGGAATTTTCATCCCCAAAGCTCGGAAGCTTGGGATGTCTACTGCCATCGTGCTAGCCAACCTCGA
TGACTGCATTTTCAACGGCAATCTCGCGGCAGGGATCATCGACCTCACCAAGGACGATGCCTTCGC
GAAACTGTCGATGGCGAGGTTTCGCATGGGCATCTGGGCCGCTCCATCCAGATCCCGCTATCGGCGC
ACTTTGGAAGTCACTGCACAAGGCCAATCCGCTTGAGAAGGATGCCGGGGGCGAGATGGTCTGGC
GCAACGGATCAAGGATCACCGCAGGTGTAGCCTTCACGGGCCGCACTCCACACCCCTACCAA

- **>*Potexvirus***

- GGGGCACCCGACTATCGAGATCGGATGACTTGTGACCCACCGAGTCGACACGGCTGACTCGCCC
GGCAGCCGGAAAGCCAACGGTGGCTTGCTGCCACCTGCCAGCTGATGCAGCTGGGTTTCTAGCCC
ACGAGTCGTTTTATCGATCGAACCAAGCGCCGGCCGAACCAAGTGCCTTCCAATCCGACTCGACCTT
CTCCTTCTGAGCTCGCAGAGATGCGATTTCCGTCGCTTGGGGTCCTTTTCCAGCGAAGCAATTCGC
TTTCGGGAGTTCTGATAATCCTGGATGTCCTTCGACCACTGAGCGTAGATCGAATCGATTTGGTCGAT
CGCCTTATTGGCCAGCTTGTCGGCTTCCTGCTTGTTCTCGAATCCATAGTAGGTCGAGGCCTGCGCG
ACATAGTCGCCGATGACCTGAGCCATCTTGTCGCGGTCTAAGCGGATCGTCCCATCCTGGTCCGGG
ATCAACGCCTGGAAGTGCCTCCGAGCGGCCCTTTGGCAGCCTGCAGAAAGCCAATCGAGGAAAA
CTTGCCGTCCCGAACCTTCGACCCAA

BLAST the sequences

- *>Tombusvirus*



The screenshot displays the NCBI BLAST web interface. At the top, the BLAST logo and the text "Basic Local Alignment Search Tool" are visible. Below this is a navigation bar with links: Home, Recent Results, Saved Strategies, and Help. The main content area shows the search results for a nucleotide sequence (525 letters). The results are summarized in a table with two columns: Query ID, Description, Molecule type, Query Length, Database Name, Description, and Program. The query ID is 1d|48563, description is None, molecule type is nucleic acid, and query length is 525. The database name is nr, description is Nucleotide collection (nt), and the program is BLASTN 2.2.28+. A message at the bottom states: "No significant similarity found. For reasons why, click here".

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite/ Formatting Results - PM6VNNCK01R

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (525 letters)

Query ID	1d 48563	Database Name	nr
Description	None	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.2.28+ Citation
Query Length	525		

No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#)

BLAST the sequences

- **>Potexvirus**



The screenshot displays the NCBI BLAST web interface. At the top, the BLAST logo and the text "Basic Local Alignment Search Tool" are visible. Below this is a navigation bar with buttons for "Home", "Recent Results", "Saved Strategies", and "Help". The main content area shows the search results for a nucleotide sequence (555 letters). The results are summarized in a table with two columns: "Query ID" and "Database Name". The "Query ID" column contains "Id|27431", "Description" is "None", "Molecule type" is "nucleic acid", and "Query Length" is "555". The "Database Name" column contains "nr", "Description" is "Nucleotide collection (nt)", and "Program" is "BLASTN 2.2.28+". A message at the bottom states "No significant similarity found. For reasons why, click here". The "click here" link is highlighted with an orange box. Below the message, there is a link for "Search Summary".

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite/ Formatting Results - PM739WSJ014

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

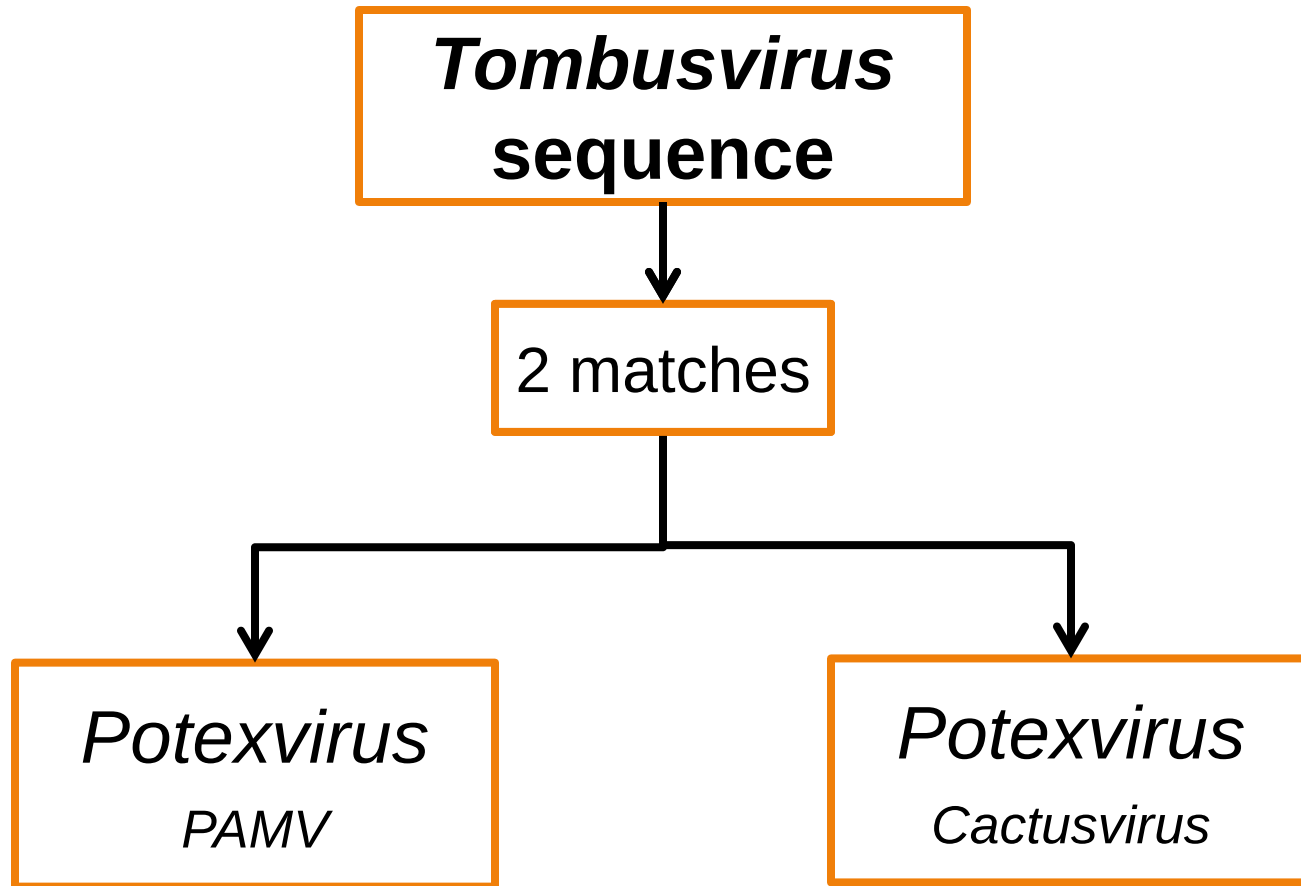
Nucleotide Sequence (555 letters)

Query ID	Id 27431	Database Name	nr
Description	None	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.2.28+ Citation
Query Length	555		

No significant similarity found. For reasons why, [click here](#)

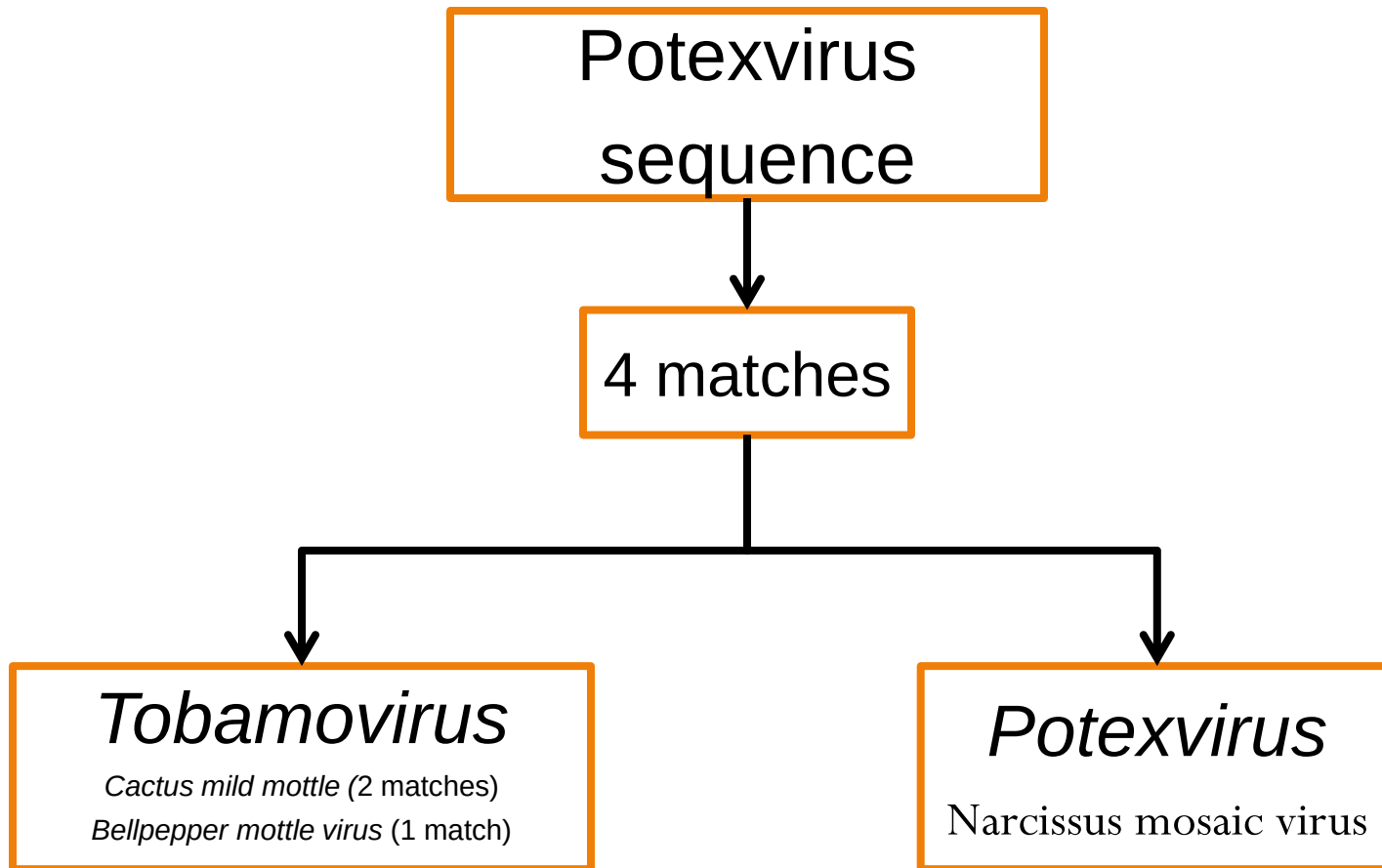
Other reports: [Search Summary](#)

Using e-probes to BLAST the sequences



Both are plant pathogens!

Using e-probes to BLAST the sequences



All are plant pathogens!

Validation



Validation



Conclusion

- Using bioinformatic tools in combination with molecular tools enables to detect waterborne viruses.
- Positive detection is possible from 100 ml samples.
- Because of the volume, dilution and putative water dynamics of water as virus pathway, finding known and unknown plant pathogenic viruses is a very difficult specially for unknowns.
- The proposed database of waterborne viruses is dynamic and can be updated periodically.

Acknowledgements



AFRI Plant
Biosecurity
Program
2009-2013

Massively Parallel Sequencing (MPS) as a diagnostic
and forensic analysis tool for plant pathogens



Division of
Agricultural Sciences
and Natural Resources



Celebrating 50 Years

Funding Industry Solutions Through Research and Education

National Institute for Microbial Forensics &
Food and Agricultural Biosecurity



RESEARCH

Vice President for
Research and
Technology
Transfer

Please feel free to contact anytime!

Webpage:

<http://entoplp.okstate.edu/profiles/ochoa-corona.html>

Dr. Francisco Ochoa Corona:

ochoaco@okstate.edu

Jon Daniels: jon.daniels@okstate.edu