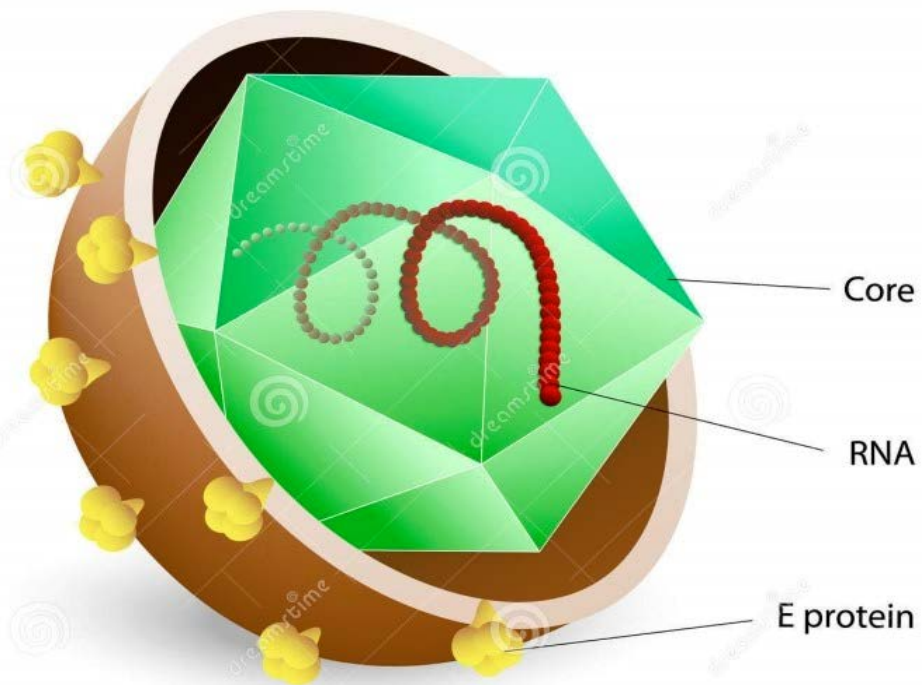




Application of Next Generation Sequencing for HCV

Kevin M. Rodeman
MDHHS Bureau of Laboratories

Hepatitis C virus



- ▶ HCV infects nearly 3% of the world's population.
- ▶ In the U.S. HCV is the most common chronic blood-borne infection and the leading cause of liver transplants.
- ▶ Since 2007 in U.S., HCV caused greater annual deaths than HIV infection.

- ▶ Estimated 3.9 Million Live with a Past or Current HCV Infection
- ▶ Estimated 101,200 People in Michigan Live with a Past or Current HCV Infection

Approximately, out of every 100 persons infected with HCV:

- ▶ 15–25 will clear the virus from their bodies
- ▶ 75–85 will go on to develop chronic infection
- ▶ 60–70 will go on to develop chronic liver disease
- ▶ 5–20 will go on to develop cirrhosis over a period of 20–30 years
- ▶ 1–5 will die from the consequences of chronic infection (liver cancer or cirrhosis)



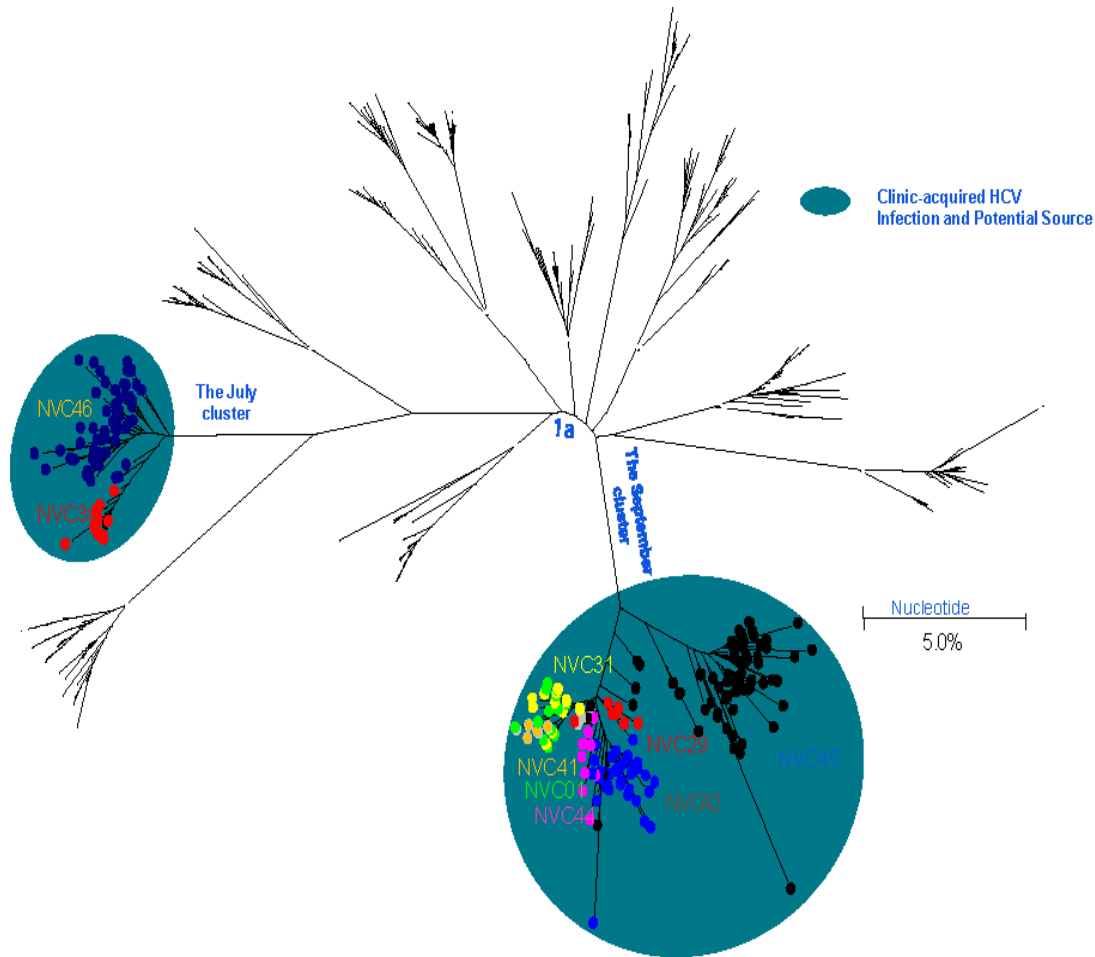
HCV Outbreaks Associated with the Following:

- ▶ Unsafe Injection Practices
- ▶ Drug Diversion
- ▶ Exposure to Blood and Blood Products
- ▶ MSM

How to Track Outbreaks?

- ▶ Sanger Sequencing of Each Infected Case to Yield a Consensus Sequence
- ▶ Consensus Sequences are not Satisfactory for accurate ID of viral strains–Quasispecies
- ▶ End–Point Limiting Dilution Technique
- ▶ Next Generation Sequencing
- ▶ Create a Phylogenetic Tree of Cases

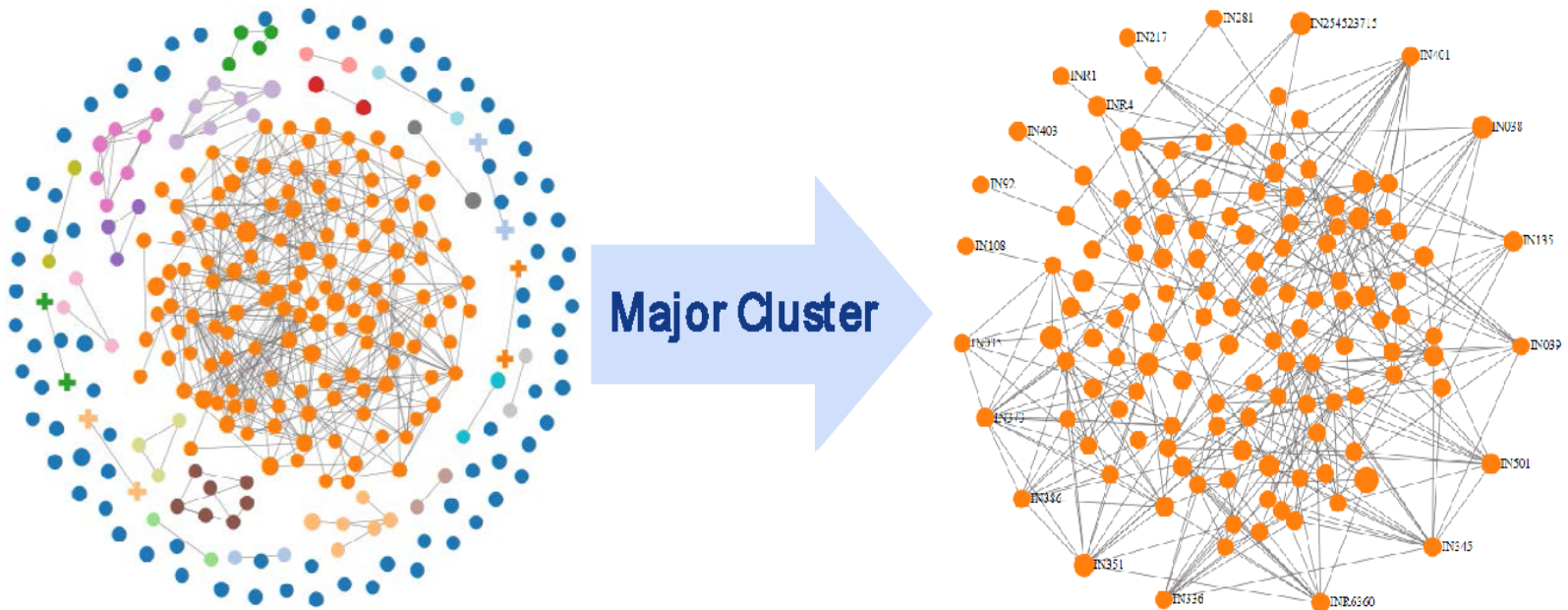
Traditional Phylogenetic Analysis



What is GHOST

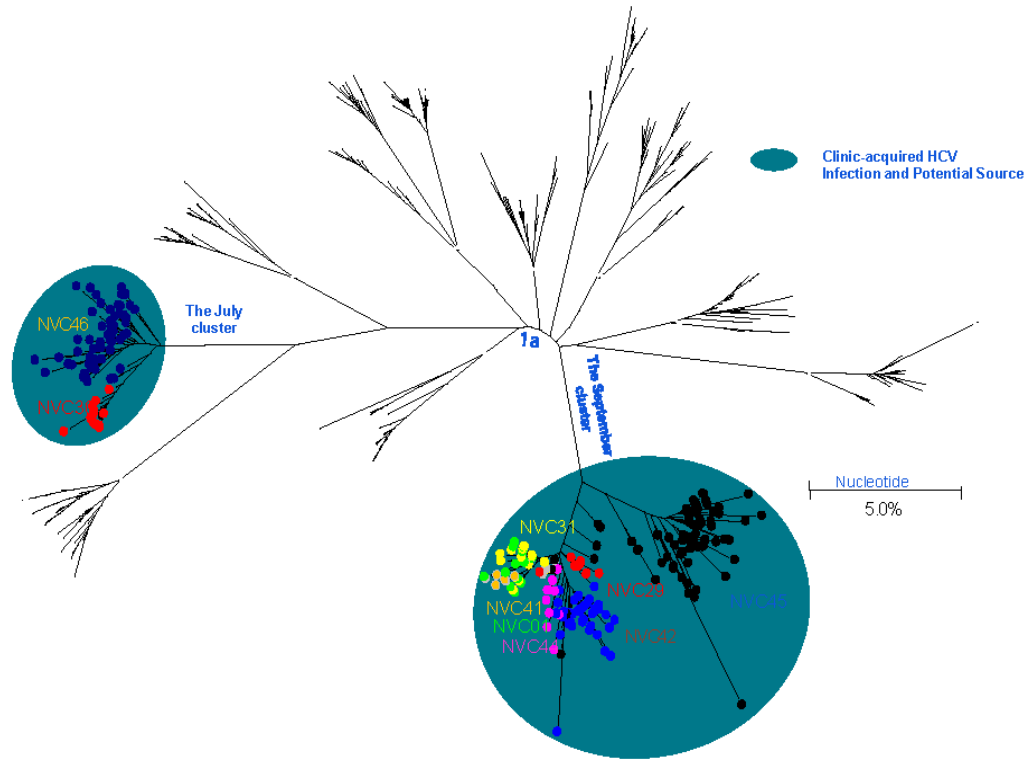
- ▶ Global Health Outbreak and Surveillance Technology (GHOST) is a new web-based system that harnesses the power of novel bioinformatics technology and automatically performs a comprehensive analysis at the click of a button. Once a user inputs an HCV sample's unique fingerprint, GHOST does a quality control check, identifies transmission links between other virus samples, and automatically creates a simple graph that shows plainly which cases are linked by transmission.

GHOST Analysis

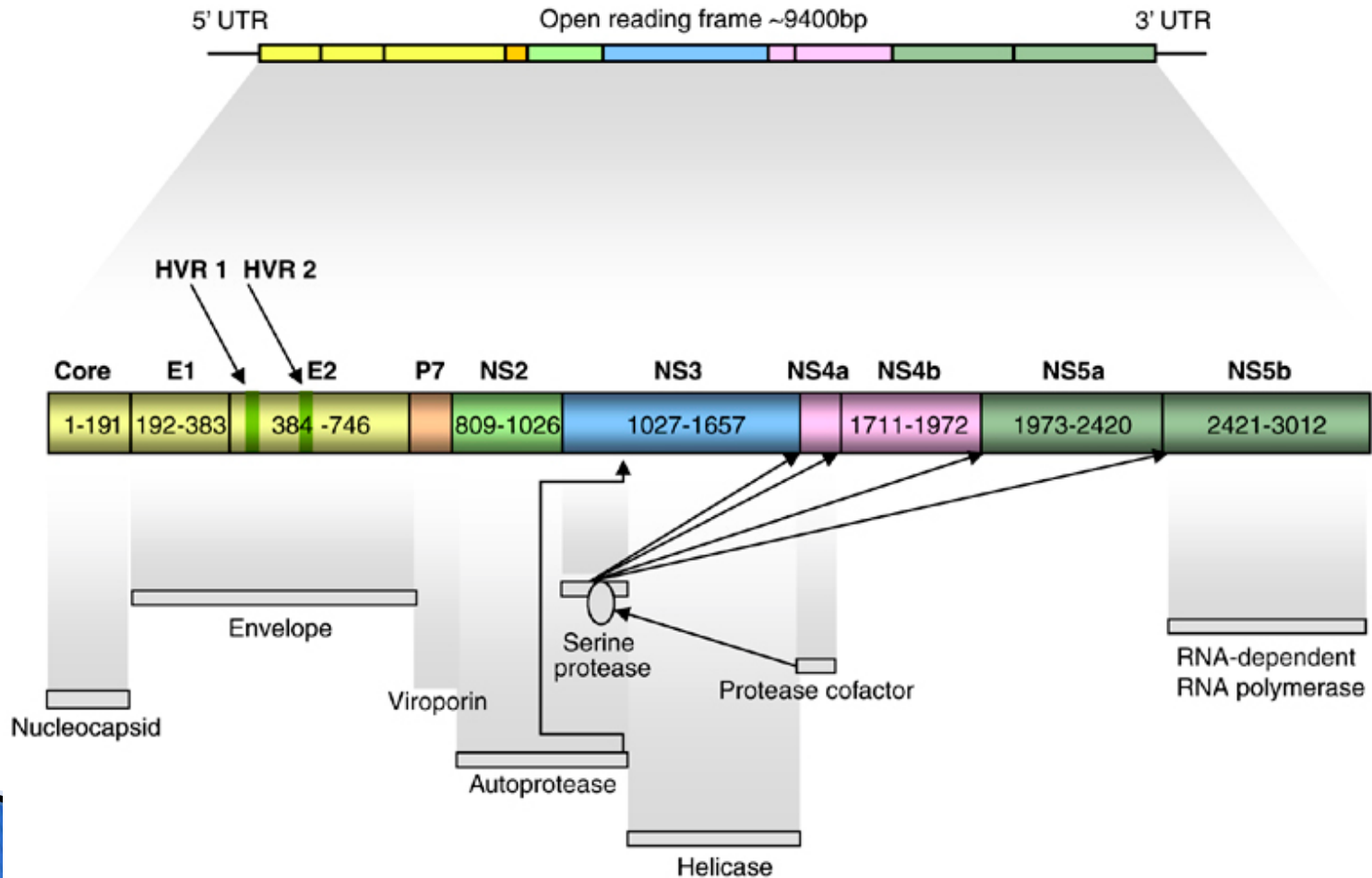


GHOST was an essential part of the “The Indiana Injection Drug Use-Associated HIV/HCV Outbreak Response Team”, which was selected as the winner of the 2015 CDC/ATSDR Honor Award for Excellence in Emergency Response – Domestic.

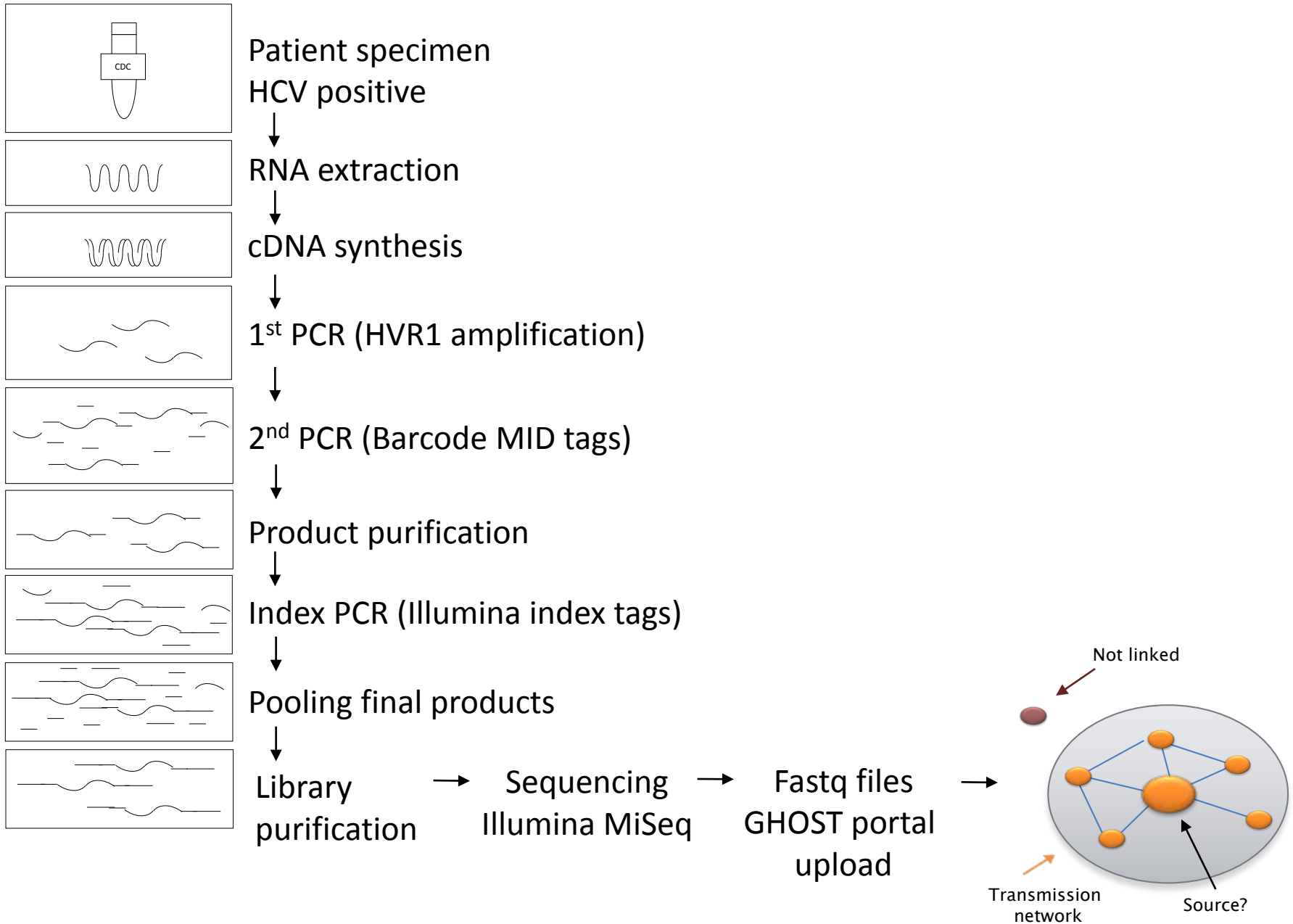
Traditional Phylogenetic Analysis



HCV Viral Genome

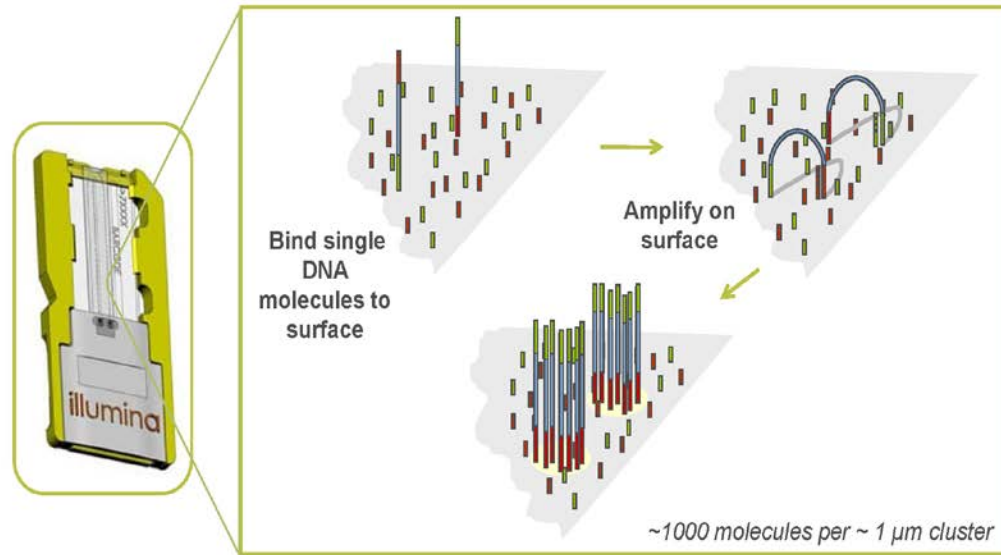


GHOST Lab Methodology Workflow



MISeq Flow Cell

Cluster Generation Overview



[Skip Details](#)





Data from MISEQ is a FastQ File

```
--->gzip -cd L2I_S1_L001_R1_001.fastq.gz | head
@M00805:5:000000000-A0VLL:1:1101:16473:1320 1:N:0:1
NTTGTTCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACAGGAAGCAGATTTTGCTAAT
TTGGAAGTCTAGGTCAGCTGAAGATCCTGTGAGCGAAGTTCCGGCAGTGTCACAGCAC
+
#55<<?BBDBDDDDDDFFFFFFHHHHHFHHAFHHHHHHHHHBHHHHHFFHHHHHHHHHDGDGHC
AFHFHHHHHHHFGHDDHFBFHDFHFFHHHFFA=@BEEED)@<B?BE3==?EEEE
@M00805:5:000000000-A0VLL:1:1101:15023:1321 1:N:0:1
NAGAAATCACAGACATAAAAGCAGTCTGTGTCCTTAGGTCCTGAGCAGCCTCCAGCACATTCT
AGCATCTGCCGTCACATTGTTCTGCACACACCGTCCTTGTCACTGCAGAAGACAGA
+
#55???BBDEDDDDDDGGGGGGIIIIIIIIIIIIIIIIIIIIHIIHIIHFGHHHIIIIIIIIIIHIIII
HHHHHHHHHHHHHHHHHHHHHHHHHHHHGGFGEGGGGGGGGGGGGGGGGGGGEGGGGCEGG>
@M00805:5:000000000-A0VLL:1:1101:14046:1321 1:N:0:1
NTTTCGTGGAAGTGGGTTACCTGACAGTGTGCACGCCCCCAGCAGGTTACAATATTCTCGTGG
ACATGAGTGCCTCTCTTTCAGAGCTGTCTGCTTTTTTCTGTCAAAGAAAGGAGCATT
```


Converting FastQ to FastA File

```
>Sequence_1 assembly1
```

```
CCCTAAACCCTAAACCCTAAACCCTAAACCTCTGAATCCTTAATCCCTAAATCCCTAAAT  
CTTTAAATCCTACATCCATGAATCCCTAAATACCTAATTCCTAAACCCGAAACCGGTTT  
CTCTGGTTGAAAATCATTGTGTATATAATGATAATTTTATCGTTTTTATGTAATTGCTTA  
TTGTTGTGTGTAGATTTTTTAAAAATATCATTTGAGGTCAATACAAATCCTATTTCTTGT  
GGTTTTCTTTCCTTCACTTAGCTATGGATGGTTTATCTTCATTTGTTATATTGGATACAA  
GCTTTGCTACGATCTACATTTGGGAATGTGAGTCTCTTATTGTAACCTTAGGGTTGGTTT  
ATCTCAAGAATCTTATTAATTGTTTGGACTGTTTATGTTTGGACATTTATTGTCATTCTT
```

```
>Sequence_2
```

```
CCCTAAACCCTAAACCCTAAACCCTAAACCTCTGAATCCTTAATCCCTAAATCCCTAAAT  
CTTTAAATCCTACATCCATGAATCCCTAAATACCTAATTCCTAAACCCGAAACCGGTTT  
CTCTGGTTGAAAATCATTGTGTATATAATGATAATTTTATCGTTTTTATGTAATTGCTTA  
TTGTTGTGTGTAGATTTTTTAAAAATATCATTTGAGGTCAATACAAATCCTATTTCTTGT  
GGTTTTCTTTCCTTCACTTAGCTATGGATGGTTTATCTTCATTTGTTATATTGGATACAA  
GCTTTGCTACGATCTACATTTGGGAATGTGAGTCTCTTATTGTAACCTTAGGGTTGGTTT  
ATCTCAAGAATCTTATTAATTGTTTGGACTGTTTATGTTTGGACATTTATTGTCATTCTT
```

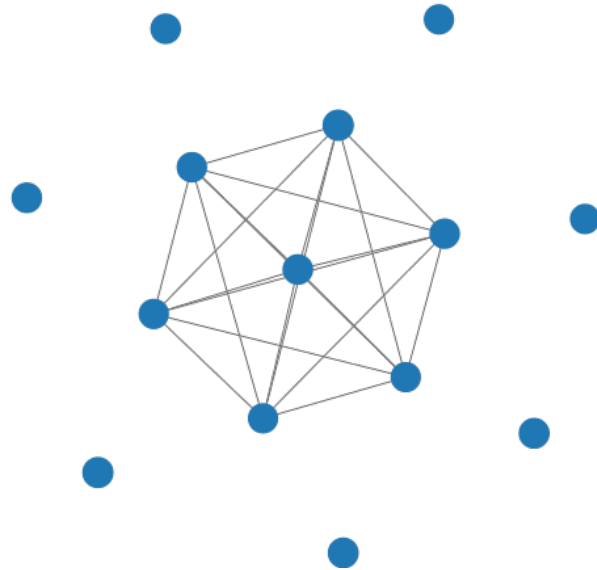


My Analysis
New | Edit | Delete | Share Find: Search database...

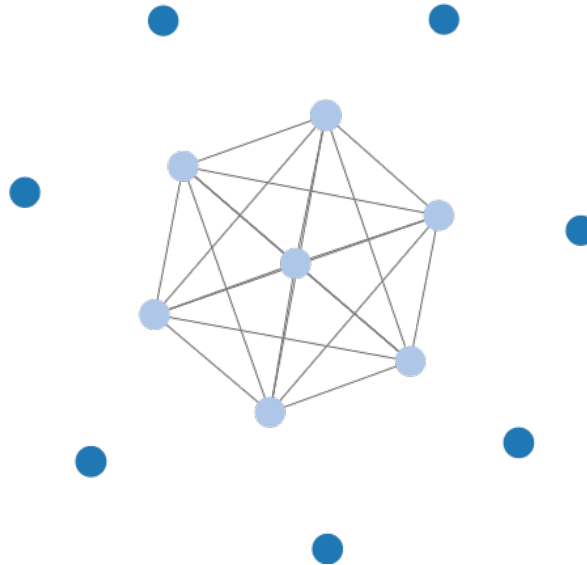
Rows per Page 10 Page 1 of 1 Displaying 1 to 9 of 9 items

Task ID	Name	Description	Task Type	Country	State	Status	Date	Data Sets	Owner
402	Kevin		Analysis	United States	MI	Complete	04/03/2017	CLEAN(4) ANALYSIS(Rodeman, Kevin
398	Michigan Specimens GHOST 3/31/2017	First set of 15	Analysis	United States	MI	Complete	03/31/2017	CLEAN(14) ANALYSIS	Rodeman, Kevin
391	Michigan GHOST Specimens 03/31/2017	First 15 specimens	Quality Control	United States	MI	Warning	03/31/2017	RAW(32) CLEAN(14)	Rodeman, Kevin
388	Michigan GHOST Panel II 03272017	Third Run different MISec	Analysis	United States	MI	Complete	03/27/2017	CLEAN(11) ANALYSIS	Rodeman, Kevin
387	Michigan GHOST Panel II 03272017		Quality Control	United States	MI	Warning	03/27/2017	RAW(48) CLEAN(11)	Rodeman, Kevin
383	GHOST Panel II-MI		Analysis	United States	MI	Complete	03/13/2017	CLEAN(8) ANALYSIS(Rodeman, Kevin
381	Michigan GHOST Panel II	verification panel	Quality Control	United States	MI	Warning	03/13/2017	RAW(48) CLEAN(8)	Rodeman, Kevin
327	Michigan-CDC GHOST Panel-02102017	on site procedure verifi	Analysis	United States	MI	Complete	02/10/2017	CLEAN(7) ANALYSIS(Rodeman, Kevin
324	Michigan GHOST Panel	Michigan CDC Verification	Quality Control	United States	MI	Warning	02/09/2017	RAW(16) CLEAN(7)	Rodeman, Kevin

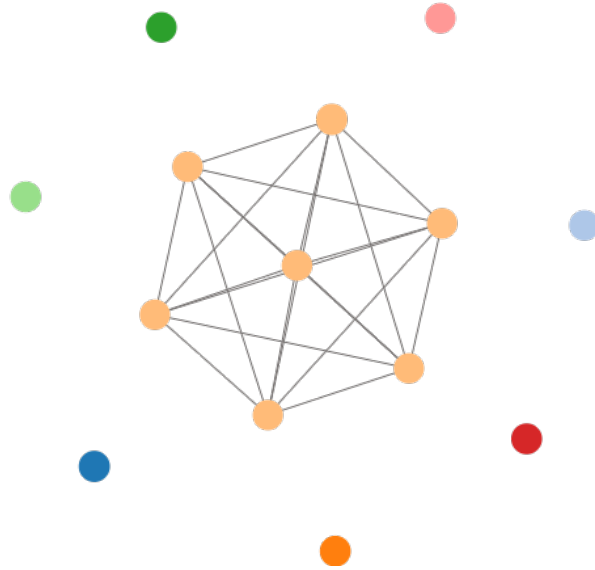
HCV Specimens Analyzed by GHOST-Genotype



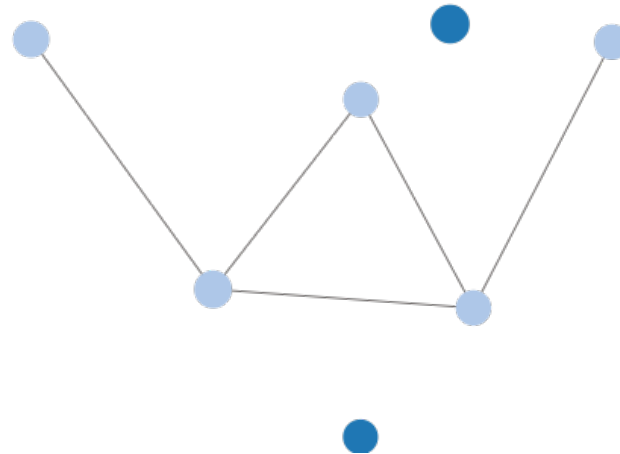
HCV Specimens Analyzed by GHOST-Cluster



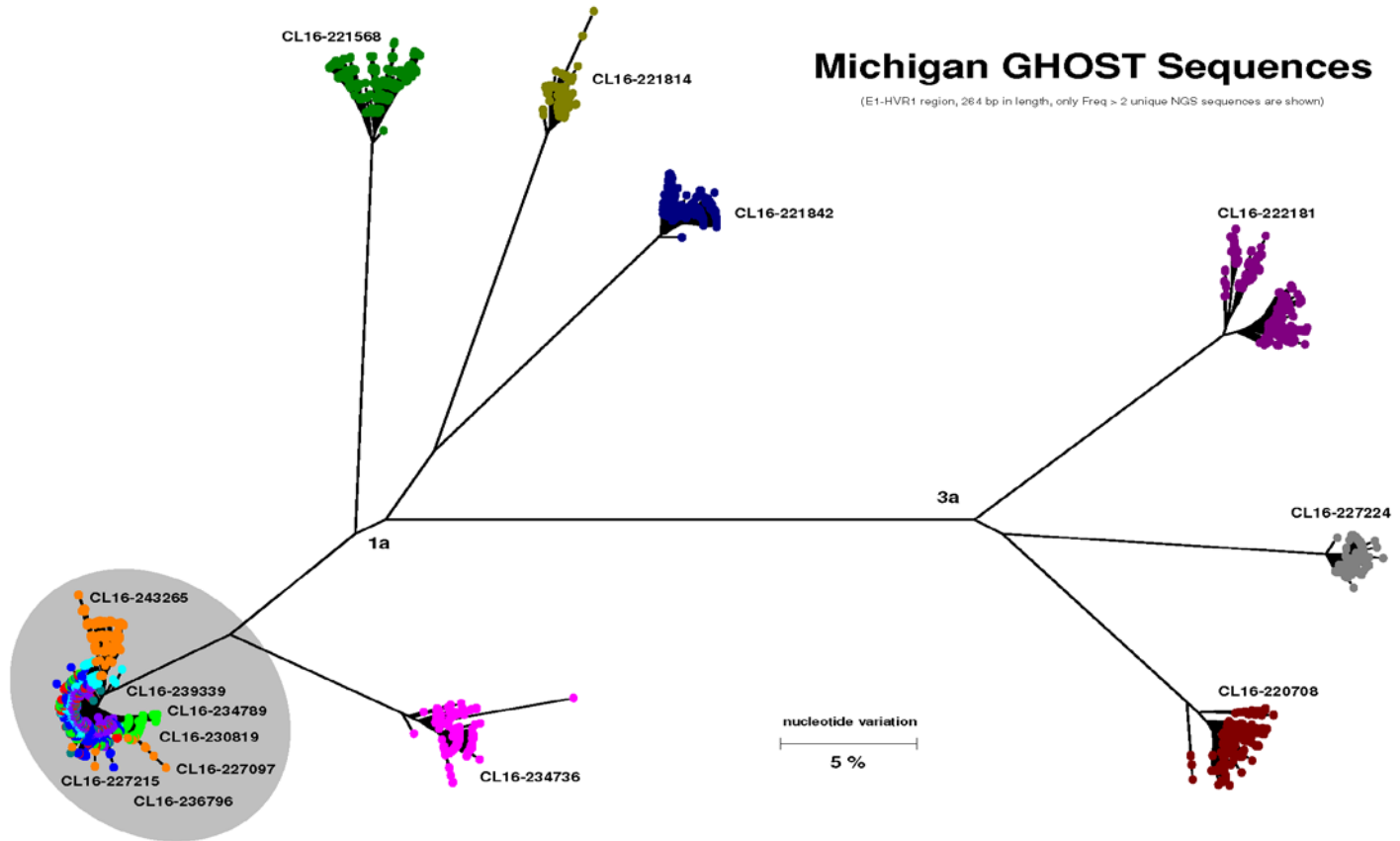
HCV Specimens Analyzed by GHOST-Strain



Unable to Determine Direction of Infection



Phylogenetic Tree MI GHOST Sequences



It's Modular

- We are currently testing new HCV modules that
 - Detect Persons Who Inject Drugs
 - Estimate duration of infection
 - Monitor for drug resistance
- Modules to investigate Hepatitis A and B are in the works
- Discussions with Malaria and HIV Divisions to integrate these other pathogens are in progress