Negative Hepatitis C Reporting and Linkage to Care Outreach

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New York City Department of Health and Mental Hygiene
### Hepatitis B and C Surveillance Registry

- >90% electronically reported from laboratories
- High volume of reports. In 2016:
  - >100,000 labs for hepatitis B
  - >200,000 labs for hepatitis C

<table>
<thead>
<tr>
<th>Hepatitis B labs</th>
<th>Hepatitis C labs</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Positive Core Antibody IgM, surface antigen, “e” antigen, DNA, genotype</td>
<td>• Positive antibody</td>
</tr>
<tr>
<td>• Negatives, non-reportables and ALTs reported if on same accession as a reportable lab</td>
<td>• Positive and negative RNA results, genotype</td>
</tr>
<tr>
<td>• Core Antibody total, surface antibody, “e” antibody</td>
<td>• ALTs reported if on same accession as a reportable lab</td>
</tr>
<tr>
<td></td>
<td>• Negative antibody tests</td>
</tr>
<tr>
<td></td>
<td>• Positive rapid antibody tests</td>
</tr>
</tbody>
</table>
Demographic Data Collected from Laboratory Reports

Demographic information received
- Name
- Date of birth
- Social security number
- Sex
- Age
- Address at time of report
- Current address
- Phone number

Do not receive
- Race/ethnicity
- Country of birth
- Risk factors
New York City Communicable Disease Reporting

- New York State maintains list of reportable diseases
- New York City must conduct surveillance for these diseases
- New York City Health Code Articles 11 and 13
  - Require providers and laboratories to report positive and, in select cases, negative findings or markers of reportable diseases
  - Amendments proposed and approved by the Board of Health
Amend Health Code to Require Lab Reporting of All Hepatitis C RNA Results

- For some conditions, receiving all laboratory results, not just those that are positive, greatly benefits disease surveillance (e.g., HIV viral load, hemoglobin A1C)
- Accurately classify the proportion of New Yorkers previously infected who are currently infected
- Identify providers and areas where screening, but not confirmatory testing, is performed to improve HCV care
- Estimate the proportion of patients cured annually, as we do for HIV
Negative Hepatitis C RNA Reporting Implementation

• Health Code change as of July 21, 2014
• Ensure laboratories report negative RNA tests
  • Check number of negative RNA tests by lab by month
  • Monitor percent of negative RNA tests by lab
• Import results in Maven
  • Negative RNA results associated with patients already in Maven with a positive HCV test
Hepatitis C Treatment and Cure Algorithm

• Treatment
  • Positive RNA test and a subsequent negative RNA test

• Cure
  • First negative, indeterminate, or low positive (<1000 IU/mL) RNA result after most recent high positive RNA result (proxy for 4 weeks into treatment)
  • Based on this date:
    • At least 1 subsequent negative RNA test
    • Most recent negative RNA test is at least 4 months later
    • No subsequent high positive RNA (≥1000 IU/mL)
Treatment and Cure Algorithm Validation

- Definitions validated using program data and chart reviews
  - High sensitivity, specificity, positive and negative predictive value

<table>
<thead>
<tr>
<th>Treatment</th>
<th>HCV Program Data</th>
<th>Chart review</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitivity</td>
<td>94.5</td>
<td>93.2</td>
</tr>
<tr>
<td>Specificity</td>
<td>85.7</td>
<td>83.8</td>
</tr>
<tr>
<td>Positive predictive value</td>
<td>80.3</td>
<td>92.6</td>
</tr>
<tr>
<td>Negative predictive value</td>
<td>96.2</td>
<td>84.9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cure</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitivity</td>
<td>86.7</td>
<td>93.8</td>
</tr>
<tr>
<td>Specificity</td>
<td>98.3</td>
<td>89.4</td>
</tr>
<tr>
<td>Positive predictive value</td>
<td>65.0</td>
<td>89.1</td>
</tr>
<tr>
<td>Negative predictive value</td>
<td>99.5</td>
<td>93.9</td>
</tr>
</tbody>
</table>
Hepatitis C Linkage to Care

- In 2016, ~11,000 people newly reported with hepatitis C
  - 3,781 confirmed infection (RNA positive), 2,684 antibody positive only
- Prioritize cases for outreach based on current infection status
  - Exclude people whose last RNA test is negative (i.e., people who initiated treatment)
- Linkage to care projects
  - Surveillance-based linkage to care
  - HIV/HCV co-infected individuals
  - Bronx RHIO (individuals with high fibrosis score)
# Linkage to Care Case Management Tool in Maven

<table>
<thead>
<tr>
<th>Field</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Do not contact in future</td>
<td>No</td>
</tr>
<tr>
<td>Patient consented to text</td>
<td>No</td>
</tr>
<tr>
<td>Moved out of NYC</td>
<td></td>
</tr>
<tr>
<td>Patient currently homeless</td>
<td></td>
</tr>
<tr>
<td>Date and time</td>
<td></td>
</tr>
<tr>
<td>Currently alive?</td>
<td>Yes</td>
</tr>
<tr>
<td>Primary language</td>
<td></td>
</tr>
</tbody>
</table>

**Method of contact:** Text

**Phone number used as contact method:**

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Undeliverable</td>
<td></td>
</tr>
<tr>
<td>Incorrect phone number/ email address</td>
<td></td>
</tr>
<tr>
<td>Opted out</td>
<td></td>
</tr>
<tr>
<td>Declined Services</td>
<td></td>
</tr>
<tr>
<td>Provided services</td>
<td></td>
</tr>
</tbody>
</table>

**Person contacted:**

**Date of contact:** 08/24/2017

**Start Time (Military time example: 1300 or 0900):** 1630

**End time (Military time):** 1632

**Total time (in h:mm):** 0.02

**Outreach Program:** Routine Linkage to Care

**Method of contact:** Call

**Phone number used as contact method:**

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>No Answer</td>
<td></td>
</tr>
<tr>
<td>Left voice message</td>
<td></td>
</tr>
<tr>
<td>Incorrect phone number/ email address</td>
<td></td>
</tr>
<tr>
<td>Out of service</td>
<td></td>
</tr>
<tr>
<td>Declined Services</td>
<td></td>
</tr>
<tr>
<td>Provided services</td>
<td></td>
</tr>
</tbody>
</table>

**Person contacted:**

**Date of contact:** 09/05/2017

**Start Time (Military time example: 1300 or 0900):** 1223

**End time (Military time):** 1225

**Total time (in h:mm):** 0.02

**Outreach Program:** Routine Linkage to Care
Require Reporting of Hepatitis B Negative DNA Test Results

• Allow the Health Department to estimate the proportion of New Yorkers infected with hepatitis B virus who are appropriately linked to care

• Identify gaps in access to care

• Develop targeted interventions to increase linkage to care and improve provider knowledge of HBV testing and treatment guidelines

• Increase monitoring of hepatitis B to decrease HBV-related morbidity and mortality
Hepatitis B Care Continuum Proposed Definitions

Positive hepatitis B surface antigen

Timely linkage to care: HBV DNA result within 6 months

No HBV DNA result could mean not done or negative
Need health code change to receive all negatives

HBV DNA ≥2000

No

Yes

No treatment candidate based on labs

ALT > 40

Treatment candidate

At least 2 subsequent HBV DNA within 9 months

No evidence of treatment

Treatment initiation

Viral load reduction defined as a declining HBV DNA viral load (>=1 log) in a test result in those in the treatment initiation group

Viral load suppression defined as HBV DNA <60 IU/mL in those in the viral load reduction group

-Based on EASL 2017 Guidelines:

- Treatment candidate defined as HBV DNA >=2000 and ALT >40
- Treatment initiation defined as treatment candidate followed by HBV DNA x 2 within 9 months

ALGORITHM DEFINITIONS

Linked to care defined as HBV DNA test within 6 months of newly reported HbsAg (current limitations = missing neg HBV DNA)
Acknowledgements

• New York City Department of Health and Mental Hygiene’s:
  • Viral Hepatitis Program
    • Miranda Moore, Kevin Guerra, Ann Winters
  • Bureau of Communicable Disease General Surveillance and Data Units
  • Division of Informatics and Information Technology
  • Rima Oken, Director of Policy, Division of Disease Control

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