Global Distribution of HCV Genotypes

Homie Razavi, Erin Gower, Sarah Hindman, and Chris Estes

Center for Disease Analysis, Louisville, Colorado, USA

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Background:
- In 2005, approximately 2.8% of the world’s population, or >165 million people, were anti-HCV positive (1).
- Starting in 2014, new therapies are expected to launch with higher cure rates and shorter duration of treatment than the current standard of care.
- In the near term, HCV genotype will continue to be an important factor influencing treatment decisions and clinical outcomes.

Objectives:
- Quantify the genotype distribution of HCV infected populations by region.
- Examine the genotype variations across regions.

Methodology:
- PubMed and Embase were searched for all articles published since 1999 containing the following search terms:
  - PubMed: (hcv OR hepatitis c*) AND (genotype* OR hepatitisvirus/genovirus* [Mesh])
  - Embase: (hepatitis c OR hcv) AND (genotype* OR genotype*)
- Approximately 17,000 studies were identified.
- The studies were reviewed and scored according to the following scale:
  - Estimate without a formal study
  - Small study in a select population with <100
  - Large study in a select population with 100-100
  - Small study in the general population with <100
  - Large study in the general population with >100
- All studies with a score of one star were ignored and the highest ranking study was selected for each country.
- Data from countries with available studies were grouped according to the Global Burden of Disease (GBD) classifications (2) and the World Bank regions.
- A regional estimate was calculated using a weighted average approach using the countries’ total infected HCV cases as the weighting factor.
- Regions where <10% of countries reported a genotype distribution were ignored.

Results:
- Genotype data were available for 74 countries, accounting for 67% of the total HCV infections (Table 1).
- Genotype 1b was the most common sub-type accounting for 27% of all infections. However, significant regional, country, and local variations existed.
- Infections in North America, Latin America, and Europe were predominantly G1 (60-75%) with G1b accounting for 25-35%, and 50-90% of all cases respectively.
- North Africa and the Middle East had a large G4 population (75%), which was attributable to the high prevalence of G4 in Egypt. When Egypt was excluded, the genotype distribution of this region was more similar to Europe with 54% of the HCV population being G1.
- The Asia Pacific region was predominately G1 (40%) followed by G3 (35%), largely driven by the HCV infected populations in India and Pakistan. G1b accounted for 30% of all infections in this region.
- Genotype 1 is more common in high income and upper middle income countries while genotypes 3 and 4 are more prevalent in low and lower middle income countries. However, the latter observation was strongly influenced by Egypt, India, and Pakistan.

TABLE 1: Countries and Regions Studied

<table>
<thead>
<tr>
<th>Region</th>
<th>Countries</th>
<th>Genotype 1</th>
<th>Genotype 2</th>
<th>Genotype 3</th>
<th>Genotype 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>5</td>
<td>3</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Latin America</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Europe</td>
<td>7</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Africa</td>
<td>16</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Asia</td>
<td>5</td>
<td>3</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>31</td>
<td>15</td>
<td>7</td>
<td>3</td>
<td>0</td>
</tr>
</tbody>
</table>

FIGURE 1: Data quality scores (by country) and HCV genotype distribution by Global Burden of Disease Regions

FIGURE 2: HCV genotype distribution by World Bank regions

Conclusions:
- Although this analysis found genotype distributions for 67% of the global HCV population, 75% of the countries did not have published data.
- Country level strategies are needed to manage HCV disease burden and until pan-genotypic therapies are available, genotyping will be required to determine the therapy type, duration, and expected response rate.
- Genotype studies in low-income and lower-middle-income countries are needed where ~<20% of the countries report a HCV genotype distribution.
- Genotype studies are needed in Africa to better plan the treatment of HCV infected population.
- Clinical trials in genotypes 3, 4, and 6 are required to provide access to the new therapies in lower middle and low income countries.

References:

Disclosures:
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