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Global Distribution of HCV Genotypes

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Background:

- In 2005, approximately 2.8% of the world's population, or >185 million people, were anti-HCV positive (1).
- Starting in 2014, new therapies are expected to launch with higher current 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 1995 containing the following search terms -

  PubMed: *(hcv OR (hepatitis c)) AND (genotype* OR hepacivirus/genetics*[mesh])*

  Embase: *'hepatitis c' OR 'hcv' AND ('genotype' OR genotyp*)*
- 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 n<100
  - *** Large study in a select population with n>100
  - **** Small study in the general population with n<100
  - ***** Large study in the general population with n>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).
- Globally, genotype 1 (G1) was the most common (42% of HCV cases), followed by G3 (26%) and G4 (17%).
- 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 predominately G1 (60-75%) with G1b accounting for 25%, 35%, and 50% 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 the region.
- Genotype 1 is more common in high income and upper middle income countries while genotypes 3 and 4 are more prevalent in low income and lower middle income countries. However, the latter observation was strongly influenced by Egypt, India, and Pakistan.

TABLE 1: Countries and Regions Studied

GBD Regions	Countries	Countries w/ Data	% Coverage
Asia Pacific, High Income	4	2	50%
Asia, Central	9	3	33%
Asia, East	3	2	67%
Asia, South	6	2	33%
Asia, Southeast	11	4	36%
Australiasia	2	1	50%
Caribbean	15	1	7%
Europe, Central	13	8	62%
Europe, East	7	4	57%
Europe, West	22	17	77%
Latin America, Andean	3	1	33%
Latin America, Central	9	3	33%
Latin America, South	3	2	67%
Latin America, Tropical	2	1	50%
North Africa/Middle East	19	12	63%
North America, High Income	2	2	100%
Oceania	9	0	0%
Sub-Saharan Africa, Central	6	2	33%
Sub-Saharan Africa, East	17	2	12%
Sub-Saharan Africa, South	6	1	17%
Sub-Saharan Africa, West	19	2	11%
NA	63	2	3%
Total	**250**	**74**	**30%**
World Bank Regions			
High income	71	37	52%
Upper Middle Income	52	20	38%
Lower Middle Income	47	10	21%
Low income	36	6	17%
NA	44	1	2%
Total	**250**	**74**	**30%**

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

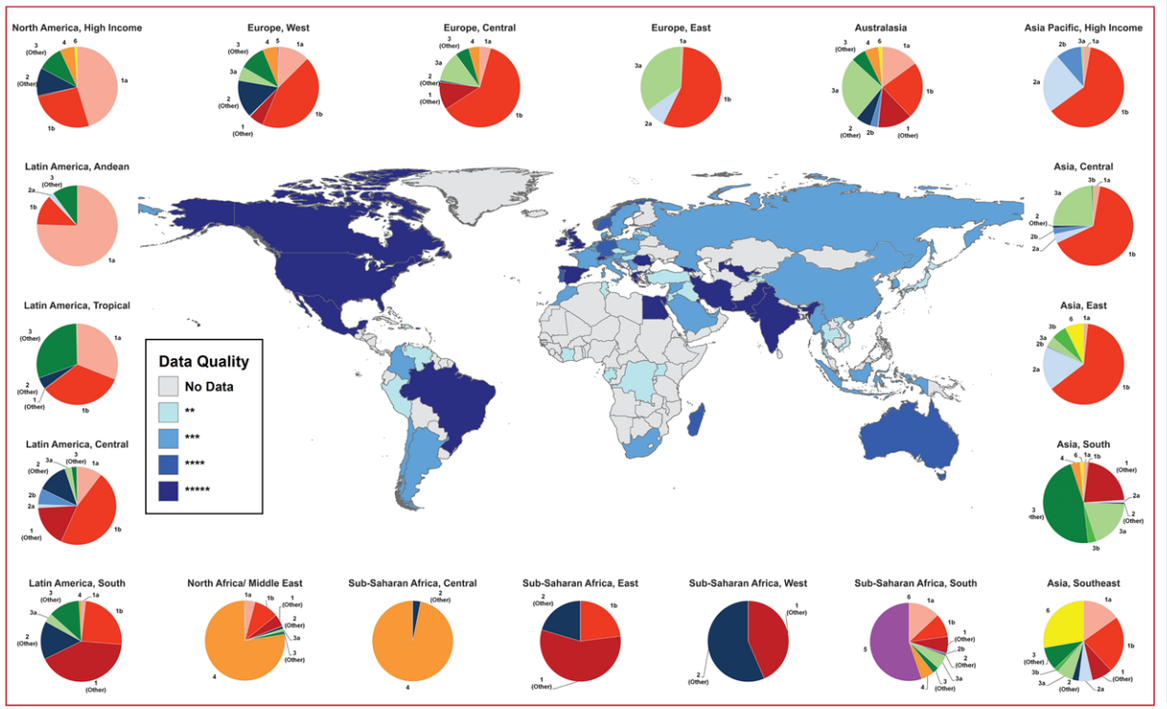
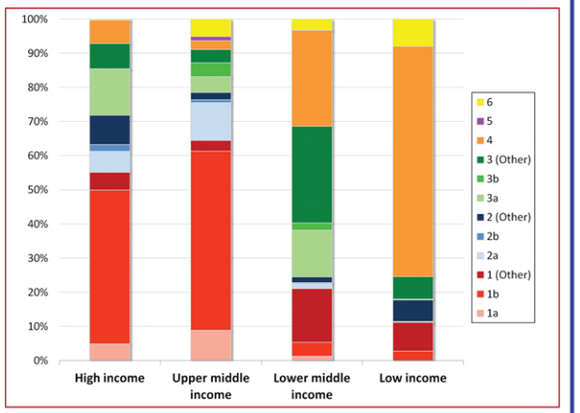


FIGURE 2: HCV genotype distribution by World Bank regions



Conclusions:

- Although this analysis found genotype distributions for 67% of the global HCV population, 70% 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:

1. Mohd HK, Groeger J, Flaxman AD, Wiersma ST. Global epidemiology of hepatitis C virus infection: New estimates of age-specific antibody to HCV seroprevalence. Hepatology 2013 Apr;57(4):1333-42.
2. Murray CJ, Ezzati M, Flaxman AD, Lim S, Lozano R, Michaud C, et al. GBD 2010: design, definitions, and metrics. Lancet 2012 Dec 15;380(9859):2063-6.

Disclosures:

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