Hepatitis A Virus Infections: FAQs

What are the different types of Hepatitis A virus genotypes?

There are 6 HAV genotypes, with only genotypes I, II and III infecting humans. HAV genotypes I, II and III are further divided into subtypes A and B. HAV genotypes and subtypes have a distinctive geographic distribution (1).

- HAV genotype I is the most common genotype occurring around the world
  - HAV genotype IA is prevalent in South and North America, Europe, Asia and Africa
  - HAV genotype IB is predominant in the Middle East and South Africa
- HAV genotype II is not as common
- HAV genotype III is common around the world
  - HAV genotype IIIA circulates in Asia, Europe, Madagascar and the USA.

What are the clinical implications of different HAV genotypes?

No differences in clinical presentation of infections with different genotypes are clearly established. However, HAV genotype IB is found more frequently among acute liver failure cases compared to the non-liver failure cases, suggesting its potential greater virulence. Host factors such as age of patients and underlying liver diseases as well as viral factors such as HAV RNA levels and genomic mutations were reported in some studies to be associated with disease severity (2).

How does hepatitis A genotyping help to establish transmission in an outbreak setting?

Hepatitis A genotyping is done to determine genetic identity of the HAV sequences in an outbreak. Sequence differences in the VP1-P2A junction of the HAV genome has been widely used to identify HAV sub-genotypes, and evaluate genetic relatedness among sequences derived from hepatitis A infected individuals (3). Genotyping assists significantly in the identification of a common source of infection during hepatitis A outbreaks, especially when paired with epidemiologic evidence (4).
Reference


