Landmark Study Reveals Growth of Hepatitis C Epidemic Peaked around 1950

What is the study about?

Globally, 185 million people are living with hepatitis C virus (HCV). There are 300,000 people living with HCV in Canada and 3.5 million people living with HCV in the United States. The vast majority of adults infected with HCV in North America, as well as some other developed countries, are part of the generational cohort composed of individuals born between 1945 and 1964 (called "the baby boomers"). Previous studies implicated both use of

FACT BOX

The peak of the HCV genotype 1a, the most common form of HCV in North America, occurred in 1950 when the oldest members of the most severely affected demographic cohort were five years of age.

infected blood products (prior to the screening of the blood supply) and injection drug use as major contributors to the epidemic in this demographic group.

What are the key points of this study?

- The study, based on careful analysis of the evolution of North American hepatitis C virus sequences, revises previous estimates of the timing of peak spread of the HCV epidemic by 15 years.
- The increase in medical procedures following World War II and the use of glass and metal syringes both coincide with a spike in HCV transmission among baby boomers. The observed plateau in HCV spread between 1960 and 1990 is consistent with the hypothesis that changes in injection technology were a driving factor.
- The results dispute the notion that the HCV epidemic among baby boomers is primarily due to injection drug use and other high-risk behaviours (e.g. unsafe tattooing and high risk sex). Injection drug use peaked at the end of the 1960s in the United States.

What does this mean?

- Individuals born in North America between 1945 and 1964 should be tested for HCV because it could lead to elevated risk of liver cirrhosis, liver cancer and liver failure.
- Treatment can help to prevent the spread of the virus by eliminating HCV from individuals who complete their treatment, rendering them unable to spread it to others through blood-to-blood contact.

Citation: Joy JB, PhD, McCloskey RM, Nguyen T, Liang RH, Khudyakov Y, Olmstead A, Krajden M, Ward JW, Harrigan PR, Montaner JSG, Poon AFY (2016); The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study. Published in the Lancet Infectious Diseases.

