Hepatitis C: The Global Spread of Genotype 1

This article which originally appeared in the HCV Advocate, discusses the the global spread of hepatitis C gneotype 1.

April 1, 2015 By Alan Franciscus

The origin of hepatitis C (HCV) is unknown. The current theory is that it may have originated in horses, but while the virus found in horses is similar to the hepatitis C virus the scientific evidence linking it to hepatitis C is far from clear. Where the virus originated is on more solid ground—it is believed to have originated in West Africa. Hepatitis C is spread by direct blood-to-blood contact. So how did it develop into such a huge problem with an estimated 130-150 million people infected worldwide? How did genotype 1 become the most common genotype worldwide? The answer to both questions is well-known—blood transfusions and unsafe injections.

In the study "The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis," by G Magiokinis et al., the authors used a complicated system of analysis with various models (molecular clock & the Bayesian skyline demographic). The model tracked how genotype 1a and 1b spread throughout the world. First it was found that genotype 1a had a steady rate of expansion from about 1906 through the 1960's. Moreover, it was found that from the 1960's through the 1980's it dramatically expanded. This corresponds to the increase in injection drug use from the 1960's through the present day. Genotype 1b on the other hand expanded at a steady rate from 1922 to the late 1940s. Then from the 1950's until the 1980s it showed the greatest expansion. Thus, the highest rate of expansion of genotype 1b was ~16 years before genotype 1a. An interesting observation was that early on in the hepatitis C epidemic it was thought that genotype 1b led to more cases of liver cancer. A possible explanation of this is that people with genotype 1b were infected longer and were more likely to have had more disease progression. As the authors pointed out, the connection between genotype 1b, liver cancer and the earlier spread of genotype 1b needs to be validated in future studies.

To validate their findings of the earlier expansion of genotype 1b, however, the authors pointed to other evidence:

- All US military recruit samples from 1948-1955 were genotype 1b.
- Older HCV-infected individuals are "systematically" or consistently genotype 1b.

Back to why genotype 1 is the most common genotype. The most likely reason is that genotype 1 was introduced into developed western countries and spread by the introduction of blood transfusions, plasma pooling and unsafe injections (reuse or improper needle sterilization) of medicines to treat many diseases. In the late 1920s through the present day the epidemic of injection drug use and sharing needles and drug preparation tools is another reason for the spread of HCV genotype 1.

One has to wonder how different it would be if genotype 2 had been 'the genotype' that had been the one that had greatly expanded instead of genotype 1. Treatment of genotype 2 produced very high cure rate early on in the history of treatment. Still with current treatments we have the potential to eradicate hepatitis C in a lifetime. If only we could increase treatment access for everyone with hepatitis C.

Facts about genotype 1:

- Genotype 1 is the most common genotype worldwide at 83.4 million (46.2%) people.
- Genotype 1 is the most common genotype in the United States at 70% of the population with HCV.
- Genotype 1a and 1b are the most common subtypes; subtypes 1c, d, e, f, g, h, i, k and l have been identified but are uncommon.
- The current standard of care for the treatment of hepatitis C can cure 90 to 100% of people who take the medications (HARVONI and VIEKIRA PAK). Treatment durations are usually 12 weeks but vary from 8 to 24 weeks.

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